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OM nucleic - nucleic search, using sw model
Run on: September 26, 2004, 09:37:58 ; Search time 18291 Seconds
(without alignments)
17478.444 Million cell updates/sec

Title: US-10-033-026-3
Perfect score: 7376
Sequence: 1 gggggcggtgcggcggt.....tgcttgagtacgtacgcg 7376

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Score	Match	Query %	Length	DB	ID	Description
1	7376	100.0	7376	6	AR198607	AR198607 Sequence	AR198607 Sequence
2	7342	99.5	7364	6	AR198608	AR198608 Sequence	AR198608 Sequence
3	7342	99.5	7364	6	AX333697	AX333697 Sequence	AX333697 Sequence
4	7342	99.5	7364	9	HUMCACHNT	M94172 Human N-typ	M94172 Human N-typ
5	7316.4	99.2	7362	6	AR022379	AR022379 Sequence	AR022379 Sequence
6	7316.4	99.2	7362	6	AR063882	AR063882 Sequence	AR063882 Sequence
7	7316.4	99.2	7362	6	AR067882	AR067882 Sequence	AR067882 Sequence
8	7316.4	99.2	7362	6	AR105183	AR105183 Sequence	AR105183 Sequence
9	7316.4	99.2	7362	6	AR431823	AR431823 Sequence	AR431823 Sequence
10	7223.2	97.9	7266	6	AR118079	AR118079 Sequence	AR118079 Sequence
11	6958	94.3	7177	6	AR198609	AR198609 Sequence	AR198609 Sequence
12	6958	94.3	7177	9	HUMCACHNTA	M94173 Human N-typ	M94173 Human N-typ
13	6932.4	94.0	7175	6	AR022380	AR022380 Sequence	AR022380 Sequence
14	6932.4	94.0	7175	6	AR063883	AR063883 Sequence	AR063883 Sequence
15	6932.4	94.0	7175	6	AR067883	AR067883 Sequence	AR067883 Sequence
16	6932.4	94.0	7175	6	AR105184	AR105184 Sequence	AR105184 Sequence
17	6932.4	94.0	7175	6	AR431824	AR431824 Sequence	AR431824 Sequence
18	5937	80.5	6232	6	A22938	A22938 H.sapiens m	A22938 H.sapiens m
19	5887.8	79.8	6232	6	AR150755	AR150755 Sequence	AR150755 Sequence
20	5717.4	77.5	7121	4	AF173882	AF173882 Bos tauru	AF173882 Bos tauru
21	5641	76.5	7713	4	RABBCBIII	D14157 Rabbit mRNA	D14157 Rabbit mRNA
22	5359.6	72.7	9695	10	AF055477	AF055477 Rattus no	AF055477 Rattus no
23	5327.4	72.2	9884	10	AF042317	AF042317 Mus muscu	AF042317 Mus muscu
24	5289.8	71.7	7011	6	AR198610	AR198610 Sequence	AR198610 Sequence
25	5289.8	71.7	7011	10	RATRBBI	M92905 Rat calcium	M92905 Rat calcium
26	5049.2	68.5	7185	6	BD095100	BD095100 N-Type ca	BD095100 N-Type ca
27	5049.2	68.5	7185	10	MMU04999	U04999 Mus musculu	U04999 Mus musculu
28	4865.4	66.0	5467	6	I12880	I12880 Sequence 12	I12880 Sequence 12
29	3817.2	51.8	7925	5	AF173018	AF173018 Gallus ga	AF173018 Gallus ga
30	3797.2	51.5	7920	5	AF173019	AF173019 Gallus ga	AF173019 Gallus ga
31	3758.8	51.0	7892	5	AF173014	AF173014 Gallus ga	AF173014 Gallus ga
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34	3713.8	50.3	7995	5	AF173013	AF173013 Gallus ga	AF173013 Gallus ga
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36	3693.6	50.1	7962	5	AF173017	AF173017 Gallus ga	AF173017 Gallus ga
37	3195.2	43.3	5438	6	AR150749	AR150749 Sequence	AR150749 Sequence
38	3194.2	43.3	5438	6	A22926	A22926 H.sapiens m	A22926 H.sapiens m
39	2833	38.4	6981	5	DYGCCALB	L12532 Discopryge o	L12532 Discopryge o
40	2732.8	37.0	7786	5	AF461708	AF461708 Oncorhync	AF461708 Oncorhync
41	2731.2	37.0	7835	5	AY319304	AY319304 Oncorhync	AY319304 Oncorhync
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44	2582.6	35.0	6639	10	RATBCCA1S	M64373 Rat calcium	M64373 Rat calcium
45	2577.8	34.9	7236	10	AB066608	AB066608 Mus muscu	AB066608 Mus muscu

ALIGNMENTS

RESULT 1
AR198607 LOCUS AR198607 7376 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 3 from patent US 6353091.
ACCESSION AR198607
VERSION AR198607.1 GI:20248456
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 7376)
AUTHORS Lipscombe,D. and Schorge,S.
TITLE Human N-type calcium channel isoform
JOURNAL Patent: US 6353091-A 3 05-MAR-2002;
FEATURES Location/Qualifiers

2041	Db	GGGACAGTTCAACTTCCAGGATGAGACTCCACAACCAACTTCGACACCTTCCTCGCCG	2100
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2281	Db	GGCCAAACGCCCAAGCAGCTGACCAAGGATGAAGAGGATGGAAGAAGCACCATCAGAA	2340
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2461	Qy	CAGCCAGCTACGGCTGCAGAACCTCGCGGCCAGCTCGAGGCGCTGTATACAGCAGATGGA	2520
2461	Db	CAGCCAGCTACGGCTGCAGAACCTCGCGGCCAGCTCGAGGCGCTGTATACAGCAGATGGA	2520
2521	Qy	CCCCGAGGAGCGGTGGCGCTTCGCCACTTACGCGCCACCTCGCGGCCGACATGAAGACGA	2580
2521	Db	CCCCGAGGAGCGGTGGCGCTTCGCCACTTACGCGCCACCTCGCGGCCGACATGAAGACGA	2580
2581	Qy	CCTCGAACCGGCGCTGTGTGTGTGAGCTTGGGCGCGAACCGGCGCGCGGGGCCCTGTGGAGG	2640
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2761	Qy	GAAAGCGGAGACGGGGAGCCCGGTGCCCGGAGAGAGCGGCGCGCGCGCACCGACGCCA	2820
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2881	Qy	CGAGGGCGCGCGCGGACACACCGCGCGGTCTCCCGAGAGAGCGGCGCGAGCGGGAGCC	2940
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DB GATGATGAAGTCTATGATGCAACCTATGAGTACGAGCTGATGCTGAAATGCTGAAACAT 4680
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QY 6061 AGGAGCACTGGCTGTGGAGCTTCCAGATGAGAGCTTCCATCTCCATCTCCATCGCTGCGGCCGA 6120
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DB GCGCCAGCTGGCTGTGGAGCTTCCAGATGAGAGCTTCCATCTCCATCTCCATCGCTGCGGCCGA 6180
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QY 6301 GTCGACACCAACCAACCGCTGCGCCAGGAGCAGGAGCAGGAGCAGAGCTGCTGGA 6360
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QY 6361 GAAGGGGCCAGCTGTCTGCGGATATGATGGCGCACCAAGCAGTGTGTGGGGCCGG 6420
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QY 1861 TGGGATCAGTGTGCGGCGCCTCCGCTGCTGAGGATCTTCAAAGTACAGAGTACTG 1920
Db 1861 TGGGATCAGTGTGCGGCGCCTCCGCTGCTGAGGATCTTCAAAGTACAGAGTACTG 1920
QY 1921 GAGCTCCCTCGGAACTGTGTGTCTCCCTGAACTCCATGAGTCCATCATCAGCCT 1980
Db 1921 GAGCTCCCTCGGAACTGTGTGTCTCCCTGAACTCCATGAGTCCATCATCAGCCT 1980

QY 1981 GCTCTCTTGTCTTCTCTGTTCAITTTGGTCTTCCGCTGCTGGGATGACAGCTGTTGG 2040
Db 1981 GCTCTCTTGTCTTCTCTGTTCAITTTGGTCTTCCGCTGCTGGGATGACAGCTGTTGG 2040
QY 2041 GGGACAGTTCAACTTCCAGGATGAGCTCCACAAACAACTTCCCTGCGGC 2100
Db 2041 GGGACAGTTCAACTTCCAGGATGAGCTCCACAAACAACTTCCCTGCGGC 2100
QY 2101 CATCTCTCACTCTCTTCCAGATCCTGACGGGAGAGACTGGAATGCAGTGTATCACGG 2160
Db 2101 CATCTCTCACTCTCTTCCAGATCCTGACGGGAGAGACTGGAATGCAGTGTATCACGG 2160
QY 2161 GATCGAATTCGCAAGCGGCGCTCAGCAAGGATGTTCTCGTCTTTTACTTCATTGTCT 2220
Db 2161 GATCGAATTCGCAAGCGGCGCTCAGCAAGGATGTTCTCGTCTTTTACTTCATTGTCT 2220
QY 2221 GACACTGTTTGGAACTTACACTCTGCTGAATGTTCTTCTGGCCATCGCTGTGACAACT 2280
Db 2221 GACACTGTTTGGAACTTACACTCTGCTGAATGTTCTTCTGGCCATCGCTGTGACAACT 2280
QY 2281 GGGCAACCGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAGAGAGAGAGAG 2340
Db 2281 GGGCAACCGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAGAGAGAGAGAG 2340
QY 2341 GCTTGTCTTCGAAAGGCGCAAGAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2400
Db 2341 GCTTGTCTTCGAAAGGCGCAAGAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2400
QY 2401 CTCATCTCGCGCGCAGCAGCAAACTCGGCCAAGGCGCTCGGTGTGGAGCAGCGGCG 2460
Db 2401 CTCATCTCGCGCGCAGCAGCAAACTCGGCCAAGGCGCTCGGTGTGGAGCAGCGGCG 2460
QY 2461 CAGCCAGCTACGGCTGGAGAACCTCGCGGCGCAGCTCGAGGCGCTGTACAGCAGATGA 2520
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QY 2521 CCCCGAGGAGCGCTCGGCTTCGCCACTACGCGCCACCTCGCGCGCGGCGGCGGCGG 2580
Db 2521 CCCCGAGGAGCGCTCGGCTTCGCCACTACGCGCCACCTCGCGCGCGGCGGCGGCGG 2580
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Db 2581 CTTGAGCCGCGCGCTGGTGGTGGAGCTGGGCGCGGAGCGCGCGCGGCGGCGGCGG 2640
QY 2641 CAAAGCCCGACCTGAGGCTGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2700
Db 2641 CAAAGCCCGACCTGAGGCTGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2700
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Db 2701 CCGGCACCGCGACAAAGGACAAAGACCCCGCGCGGCGGAGCAGGACCGAGCAGAGG 2760
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QY 2941 CCGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3000
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QY 3001 CGAGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3060
Db 3001 CGAGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3060

Db 5209 CGTCTCCTTCATCTTCCTGTGCTCTCTTTCTGATGTTGAACCTCTTTGTGCTGTGATCAT 5268
QY 5281 GGCAATTTTGTAGTACCTACGCGGAGCTCTTCCATCCTAGTCTCTCAACACTTGTGATGA 5340
Db 5269 GGCAATTTTGTAGTACCTACGCGGAGCTCTTCCATCCTAGTCTCTCAACACTTGTGATGA 5328
QY 5341 GTTATCCTCGGCTGTGGCTGAATACGACCCGGCTGCTGTGTGGCGCATCAGTTTACAATGA 5400
Db 5329 GTTATCCTCGGCTGTGGCTGAATACGACCCGGCTGCTGTGTGGCGCATCAGTTTACAATGA 5388
QY 5401 CATGTTTGTAGATGCTGAACACATGTCCTCGGCTCTGGGCTGTGGGAAAGAAATGCCCTGC 5460
Db 5389 CATGTTTGTAGATGCTGAACACATGTCCTCGGCTCTGGGCTGTGGGAAAGAAATGCCCTGC 5448
QY 5461 TCGAGTTGCTTTACAAGCGCTGTGTCGATGAACATGCCATCTCCAAACGAGGACATGAC 5520
Db 5449 TCGAGTTGCTTTACAAGCGCTGTGTTTCGATGAACATGCCATCTCCAAACGAGGACATGAC 5508
QY 5521 TGTTCATCTTCAAGCTCAAGCTGATGCTCTCATCCGACCGGCACTGGAGATCAAGCTGGC 5580
Db 5509 TGTTCATCTTCAAGCTCAAGCTGATGCTCTCATCCGACCGGCACTGGAGATCAAGCTGGC 5568
QY 5581 CCAGCTGGGACAAAGACATCAGTGTGACCGGAGTTGAGAAAGAGATTTCCGTTGT 5640
Db 5569 CCAGCTGGGACAAAGACATCAGTGTGACCGGAGTTGAGAAAGAGATTTCCGTTGT 5628
QY 5641 GTGGGCAATCTGCCCCAGAAGACTTTGGACTTGTGTTACCAACCCCATTAAGCTGTATGA 5700
Db 5629 GTGGGCAATCTGCCCCAGAAGACTTTGGACTTGTGTTACCAACCCCATTAAGCTGTATGA 5688
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Db 5689 GATGACAGTGGGAGAGTTTATGCACTCTGATGATATTTGACTTCTACAAGACAAACAA 5748
QY 5761 AACCACAGACACAGATCAGACAGCTCTCCGAGGCTCTCCAGATGAGTCTCTGATGATATTTGACTTCTACAAGACAAACAA 5820
Db 5749 AACCACAGACACAGATCAGACAGCTCTCCGAGGCTCTCCAGATGAGTCTCTGATGATATTTGACTTCTACAAGACAAACAA 5808
QY 5821 CTTGTTTCAACCTCTGAAGGCCACCTCGAGCAGACACAGCCGGCTGTGCTCCGAGGAGC 5880
Db 5809 CTTGTTTCAACCTCTGAAGGCCACCTCGAGCAGACACAGCCGGCTGTGCTCCGAGGAGC 5868
QY 5881 CCGGTTTTCCTTCACAGAAAGTTTCACTCCCTCAGCAATGCGGGGCGCATACAAAA 5940
Db 5869 CCGGTTTTCCTTCACAGAAAGTTTCACTCCCTCAGCAATGCGGGGCGCATACAAAA 5928
QY 5941 CCAAGAGAGTGATCAAAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC 6000
Db 5929 CCAAGAGAGTGATCAAAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC 5988
QY 6001 CCATGAGGCGGACCCCTGGAGCGTGGCCACTTCCACAGAGATCCCTGTGGGGCGGTC 6060
Db 5989 CCATGAGGCGGACCCCTGGAGCGTGGCCACTTCCACAGAGATCCCTGTGGGGCGGTC 6048
QY 6061 AGGAGCACTGGCTGTGGAGCAGAGGCTCAGATCAGAGCATTAACCGGAGGGGCGCTGTAGTGGGA 6120
Db 6049 AGGAGCACTGGCTGTGGAGCAGAGGCTCAGATCAGAGCATTAACCGGAGGGGCGCTGTAGTGGGA 6108
QY 6121 GCGCCAGCGCTGGCTGTGGAGCAGAGGCTCAGCGGCTCTCCATGCCCGGCTTGGCGCCGA 6180
Db 6109 GCGCCAGCGCTGGCTGTGGAGCAGAGGCTCAGCGGCTCTCCATGCCCGGCTTGGCGCCGA 6168
QY 6181 GACTCAGCGCTGACAGATGCGAGCCCATGAAGCGTCTCATCTCCACGCTGGGCCACGC 6240
Db 6169 GACTCAGCGCTGACAGATGCGAGCCCATGAAGCGTCTCATCTCCACGCTGGGCCACGC 6228
QY 6241 GCGCCGTGGGACTCATCTTTGACACACCCCGGAGCGGCCACCCCTAGCCAGGCGTC 6300
Db 6229 GCGCCGTGGGACTCATCTTTGACACACCCCGGAGCGGCCACCCCTAGCCAGGCGTC 6288
QY 6301 GTCGACCAACCAACCAACCTGCCACCGCGGAGGACAGGAAGCAGAGGTCCTCTGGA 6360
Db 6289 GTCGACCAACCAACCAACCTGCCACCGCGGAGGACAGGAAGCAGAGGTCCTCTGGA 6348

QY 6361 GAAGGGGCCCCAGCCTGTCTGCCGATATGATGGCGCAACCAAGCAGTGTCTGTGGGCGCGG 6420
Db 6349 GAAGGGGCCCCAGCCTGTCTGCCGATATGATGGCGCAACCAAGCAGTGTCTGTGGGCGCGG 6408
QY 6421 GCTGCCCGGGAGAGAGGGGCTCAGAGTGCCTGGGGGAGAGAGAGCGCTGGCAGGAGCG 6480
Db 6409 GCTGCCCGGGAGAGAGGGGCTCAGAGTGCCTGGGGGAGAGAGAGCGCTGGCAGGAGCG 6468
QY 6481 GGGCGGTTCCAGAGCGGAGGCGCTCATCTCTCTCTCGGAGAGAGAGCGCTTCTTA 6540
Db 6469 GGGCGGTTCCAGAGCGGAGGCGCTCATCTCTCTCTCGGAGAGAGAGCGCTTCTTA 6528
QY 6541 CTCCTGTGAGCGCTTTGGGGGCGTGTAGCCCCCGAAGCCCAAGCCCTCTCTACAGAGCGA 6600
Db 6529 CTCCTGTGAGCGCTTTGGGGGCGTGTAGCCCCCGAAGCCCAAGCCCTCTCTACAGAGCGA 6588
QY 6601 CCCAACGTGCGCAACAGCTGGCCAGGAGCGGAGCCCAACCCACAGGGCACTGTGTTCCGT 6660
Db 6589 CCCAACGTGCGCAACAGCTGGCCAGGAGCGGAGCCCAACCCACAGGGCACTGTGTTCCGT 6648
QY 6661 GAATGGAGCGCTTGTGTCAACATCTGTGTAGCAACCCCGGCGCGCTGTGGCGGAG 6720
Db 6649 GAATGGAGCGCTTGTGTCAACATCTGTGTAGCAACCCCGGCGCGCTGTGGCGGAG 6708
QY 6721 GCAGTCCCCAGACGCGCTGTGACTCCCGCCCGAGGAGTCACTTACAGAGCGGCAACTC 6780
Db 6709 GCAGTCCCCAGACGCGCTGTGACTCCCGCCCGAGGAGTCACTTACAGAGCGGCAACTC 6768
QY 6781 CTCACCATCACTTGGCGGGGCTCAGACCAAGCTCTCTGTGCTTCTCCACAGCGCGGT 6840
Db 6769 CTCACCATCACTTGGCGGGGCTCAGACCAAGCTCTCTGTGCTTCTCCACAGCGCGGT 6828
QY 6841 CAGCGTGGGCTTCCGAAACAAACGCGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 6900
Db 6829 CAGCGTGGGCTTCCGAAACAAACGCGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 6888
QY 6901 GGGCGCTGGCTTCGAATTTGGCTTCACTTACCTTACCTGGGGGAGCGTGTGAGAGTGGG 6960
Db 6889 GGGCGCTGGCTTCGAATTTGGCTTCACTTACCTTACCTGGGGGAGCGTGTGAGAGTGGG 6948
QY 6961 CTCTGTCCAGCGCTCTGAGGACAGCTCACTTTTCGAGGAGGCTGTGCGCCACCAACTC 7020
Db 6949 CTCTGTCCAGCGCTCTGAGGACAGCTCACTTTTCGAGGAGGCTGTGCGCCACCAACTC 7008
QY 7021 GGGCGCTCTCCAGAGCTTCTGAGTGTCTCTCCCTGAGCTTCCAGTCTTCCCTCTCCG 7080
Db 7009 GGGCGCTCTCTCAGGACTTCTTACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCG 7068
QY 7081 CCGCGTGGCCCAACGCTTACCACTGCAACCTTGGGACTCAGCTCGGGTGGCCAGCAGGCA 7140
Db 7069 CCGCGTGGCCCAACGCTTACCACTGCAACCTTGGGACTCAGCTCGGGTGGCCAGCAGGCA 7128
QY 7141 CAGTACCAACCCCTGACAGACCAACCACTGTGTGTAGCTGTGCAACCGTGAACCTCAGACGC 7200
Db 7129 CAGTACCAACCCCTGACAGACCAACCACTGTGTGTAGCTGTGCAACCGTGAACCTCAGACGC 7188
QY 7201 CTGATGACAGAGCGGTGTGTTCCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 7260
Db 7189 CTGATGACAGAGCGGTGTGTTCCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 7248
QY 7261 CCTCGGGGAGCGCTTGGCCACCTTGTGTAGGCTCTGTGGGCGCTCTCTCTCTCTCTCTCTCT 7320
Db 7249 CCTCGGGGAGCGCTTGGCCACCTTGTGTAGGCTCTGTGGGCGCTCTCTCTCTCTCTCTCTCT 7308
QY 7321 CCGCTCTTTTACTCTAGACAGAGATTAAGCCCTGTGTGCTGTAGTGTAGTGTAGTGTAGTGT 7376
Db 7309 CCGCTCTTTTACTCTAGACAGAGATTAAGCCCTGTGTGCTGTAGTGTAGTGTAGTGTAGTGT 7364

RESULT 3

AX333697

LOCUS

AX333697 7364 bp DNA linear PAT 09-JAN-2002

QY	1801	GGTCATCGTGGGAGCGCTCTTTGAAAGTGTCTGGGGCGGCATCAAGCCGGGAAGCTCCTT	1860		2881	CGAGGCGCGCGGGCAGCACACCCGGCGGGCTCCCGGAGAGGCGGCCAGCGGGAGCC	2940	
Db	1801	GGTCATCGTGGGAGCGCTCTTTGAAAGTGTCTGGGGCGGCATCAAGCCGGGAAGCTCCTT	1860		2941	CCGAGCGCACCGCGCGCACCGGCACACAGGATCCGAGCAAGAGTGCGCCGCGCAAGGG	3000	
QY	1861	TGGGATCAGTGTCTGGGGCCCTCCGCGTGTGAGGATCTTCAAGTCAAGAGTACTG	1920		2941	CCGAGCGCACCGCGCGCACCGGCACACAGGATCCGAGCAAGAGTGCGCCGCGCAAGGG	3000	
Db	1861	TGGGATCAGTGTCTGGGGCCCTCCGCGTGTGAGGATCTTCAAGTCAAGAGTACTG	1920		3001	CGAGCGCGCGCGCGCACCGCGCGGCCCGGAGCGGGGCCCGGAGAGCGGAGAGGG	3060	
QY	1921	GAGTCCTCTCGGAACTGGTGGTGTCCCTGTGTGAATCTCATGAAGTCCATCATAGCCT	1980		3001	CGAGCGCGCGCGCGCACCGCGCGGCCCGGAGCGGGGCCCGGAGAGCGGAGAGGG	3060	
Db	1921	GAGTCCTCTCGGAACTGGTGGTGTCCCTGTGTGAATCTCATGAAGTCCATCATAGCCT	1980		3061	GGAGGAGCGGCGCGCGCACCGCGCGGCCCGGAGCGGGGCCCGGAGAGCGGAGAGGG	3120	
QY	1981	GCTCTTTCTGCTCTCTGTTCAATGTGTCTTGGCGCTGTGGGATGCACTGTGTTGG	2040		3061	GGAGGAGCGGCGCGCGCACCGCGCGGCCCGGAGCGGGGCCCGGAGAGCGGAGAGGG	3120	
Db	1981	GCTCTTTCTGCTCTCTGTTCAATGTGTCTTGGCGCTGTGGGATGCACTGTGTTGG	2040		3121	GGAGAGGAGACACCGAGAGAGGAGCCACGGAGAGGAGGCTGAGATATGGAAGCCGA	3180	
QY	2041	GGGACAGTTCAACTCCAGAGTACAGTCCCAACCAACTTCGACACTTCCCTGCCGC	2100		3121	GGAGAGGAGACACCGAGAGAGGAGCCACGGAGAGGAGGCTGAGATATGGAAGCCGA	3180	
Db	2041	GGGACAGTTCAACTCCAGAGTACAGTCCCAACCAACTTCGACACTTCCCTGCCGC	2100		3181	CAAGGAAAGAGAGTCCCGGACCAACAGCCCGGAGCCACACTGTGACCCTGGAGACCAG	3240	
QY	2101	CATCTCACTGTCTTCCAGATCTGACGGGAGGAGCTGGAATGCAAGTATCATCAGG	2160		3181	CAAGGAAAGAGAGTCCCGGACCAACAGCCCGGAGCCACACTGTGACCCTGGAGACCAG	3240	
Db	2101	CATCTCACTGTCTTCCAGATCTGACGGGAGGAGCTGGAATGCAAGTATCATCAGG	2160		3241	TGGGACTGTGACTGTGGGTCCCATGCAACACTGCCAGCACCTGTCTCCAGAGGTGGA	3300	
QY	2161	GATCGAATGCAAGCGCGGTGAGCAAGGCAATGTTCTGCTTTTACTTCAATGTCT	2220		3241	TGGGACTGTGACTGTGGGTCCCATGCAACACTGCCAGCACCTGTCTCCAGAGGTGGA	3300	
Db	2161	GATCGAATGCAAGCGCGGTGAGCAAGGCAATGTTCTGCTTTTACTTCAATGTCT	2220		3301	GGAGACCCAGAGAGTGCAGACAATCAGCGGAAGCTCATCGCATGGGAGTCAAGGCCCC	3360	
QY	2221	GACACTGTTCCGAACTACACTCTGCTGAATGTCTTCTGGCCATCGCTGTGGCAACCT	2280		3301	GGAGACCCAGAGAGTGCAGACAATCAGCGGAAGCTCATCGCATGGGAGTCAAGGCCCC	3360	
Db	2221	GACACTGTTCCGAACTACACTCTGCTGAATGTCTTCTGGCCATCGCTGTGGCAACCT	2280		3361	AGACCCGAAACACTATTGTACATATCCAGTGTGCTGACGGGCCCTCTTGGGGAAGCCAC	3420	
QY	2281	GGCCAAAGCCCAAGAGTGAAGAGATGGAAGAGATGGAAGAGCAGCAATCAGAA	2340		3361	AGACCCGAAACACTATTGTACATATCCAGTGTGCTGACGGGCCCTCTTGGGGAAGCCAC	3420	
Db	2281	GGCCAAAGCCCAAGAGTGAAGAGATGGAAGAGATGGAAGAGCAGCAATCAGAA	2340		3421	GTTCTGTTCCAGTGTGTAAAGTGAACCTGGAAGCCAAAGCAGAGGGAAGAGAGTGA	3480	
QY	2341	GCTTGCTCTGCAAAAGGCCAAGAGTGCCTGAAGTCAAGCCCACTGTCTGCGCGCAACAT	2400		3421	GTTCTGTTCCAGTGTGTAAAGTGAACCTGGAAGCCAAAGCAGAGGGAAGAGAGTGA	3480	
Db	2341	GCTTGCTCTGCAAAAGGCCAAGAGTGCCTGAAGTCAAGCCCACTGTCTGCGCGCAACAT	2400		3481	AGCGGATGAGTGCATGAGGAGCGGCCCGGCTATCGTCCCATACAGCTCCATGTTCTG	3540	
QY	2401	CTCCATCGCGCCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGGAGCAGCGGC	2460		3481	AGCGGATGAGTGCATGAGGAGCGGCCCGGCTATCGTCCCATACAGCTCCATGTTCTG	3540	
Db	2401	CTCCATCGCGCCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGGAGCAGCGGC	2460		3541	TTTAAAGCCCAACAACTGCTCGCGCTTCTGCCACTACATCGTACCATAGGTTACTT	3600	
QY	2461	CAGCAGCTACGGCTGCAAGACCTCGGGCCAGCTGCGAGGCGTGTACAGCAGATGGA	2520		3541	TTTAAAGCCCAACAACTGCTCGCGCTTCTGCCACTACATCGTACCATAGGTTACTT	3600	
Db	2461	CAGCAGCTACGGCTGCAAGACCTCGGGCCAGCTGCGAGGCGTGTACAGCAGATGGA	2520		3601	CGAGGTGGTCAATCTCTGTTGATCGCTTGAAGAGCATCGCCCTGGCTGTGAGGAGCCC	3660	
QY	2521	CCCCAGGAGCGGCTGCGCTTCCGCACTACGCGCCACCTCGCGCCCGGACATGAAGCGCA	2580		3601	CGAGGTGGTCAATCTCTGTTGATCGCTTGAAGAGCATCGCCCTGGCTGTGAGGAGCCC	3660	
Db	2521	CCCCAGGAGCGGCTGCGCTTCCGCACTACGCGCCACCTCGCGCCCGGACATGAAGCGCA	2580		3661	AGTGCACACAGACTCGCCCGAGGAAACAAAGCTCTGAAATACCTGGATTACATTTTCACTGG	3720	
QY	2581	CCTGACCGCGCTGTGTGTGGAGCTGGGCGCGAGCGCGCGCGCGCGCGCGTGGGAGG	2640		3661	AGTGCACACAGACTCGCCCGAGGAAACAAAGCTCTGAAATACCTGGATTACATTTTCACTGG	3720	
Db	2581	CCTGACCGCGCTGTGTGTGGAGCTGGGCGCGAGCGCGCGCGCGCGCGTGGGAGG	2640		3721	TGCTTTTACCTTTGAGATGGTGAATAAGATGATCGACTTGGGACTGCTCTCACCCCTGG	3780	
QY	2641	CAAGCCCGAGCTGAGGCTGCGGAGGCCCCCGAGGGGTGACACCTCGCGCAGGCAACA	2700		3721	TGCTTTTACCTTTGAGATGGTGAATAAGATGATCGACTTGGGACTGCTCTCACCCCTGG	3780	
Db	2641	CAAGCCCGAGCTGAGGCTGCGGAGGCCCCCGAGGGGTGACACCTCGCGCAGGCAACA	2700		3781	AGCCTATTTTCCGGGACTTGTGAAACATTTCTGAACTTCAATGTGGTCAAGTGGCCCTGGT	3840	
QY	2701	CCGGCACCGCAGACAGGACAAAGACCCCGCGCGCGGGAGCCAGGACCGAGCAGAGGCC	2760		3781	AGCCTATTTTCCGGGACTTGTGAAACATTTCTGAACTTCAATGTGGTCAAGTGGCCCTGGT	3840	
Db	2701	CCGGCACCGCAGACAGGACAAAGACCCCGCGCGCGGGAGCCAGGACCGAGCAGAGGCC	2760		3841	GGCGTTTGTCTTCTC-----AGGATCCAAAGGGAAGACATCATATACCATCAA	3900	
QY	2761	GAAAGCGGAGAGCGGGAGCCCGGTGCCGAGGAGCGCGCGCGCGCGCGCGCAGGCA	2820		3841	GGCGTTTGTCTTCTC-----AGGATCCAAAGGGAAGACATCATATACCATCAA	3900	
Db	2761	GAAAGCGGAGAGCGGGAGCCCGGTGCCGAGGAGCGCGCGCGCGCGCGCAGGCA	2820		3901	GTCTCTGAGAGTCTTGTGTCTCGGGCCCTCAAGACCATCAAAAGCCGCTGCCCAAGCT	3960	
QY	2821	CAGCAAGGAGCGCGGGCCCCCGAGGCGCGAGGCGCGCGCGCGCGCGCGCGCGCG	2880		3889	GTCTCTGAGAGTCTTGTGTCTCGGGCCCTCAAGACCATCAAAAGCCGCTGCCCAAGCT	3948	
Db	2821	CAGCAAGGAGCGCGGGCCCCCGAGGCGCGAGGCGCGCGCGCGCGCGCGCGCGCG	2880		3961	CAAGGCTGTGTTGACTGTGTGGTGAACCTCCCTGAGGAATGTCTTCAACATTTGATTTGT	4020	
QY	2881	CGAGGCGCGCGCGCGGACCAACCAAGCGCGCTCCCGGAGGAGCGCGCGCGCGGAGCC	2940					

Db 3949 CAAGGCTGTGTGAAGTGTGTGTGAACCTCCCTGAAGAAATGTCTCTCAACATCTTGATGT 4008
Qy 4021 CTACATGCTCTTCATGTTCATATTTGCGGTCAATTCGCGGTGAGCTCTTCACAAAGGAGATT 4080
Db 4009 CTACATGCTCTTCATGTTCATATTTGCGGTCAATTCGCGGTGAGCTCTTCACAAAGGAGATT 4068
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Db 4069 TTTCTACTGCACAGATGAATCCAAAGAGCTGGAGAGGACCTGCAGGGGTCAATTTTGGGA 4128
Qy 4141 TTATGAAAGGAGAGTGGAGCTCAGCCAGCCAGCTGGAGAGAAATACACATTTTCACTA 4200
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Qy 4261 CATGGTGTCTGAACACTCCGTGGATGCCACTATGAGGAGAGGGTCCAAAGCCCTGGGTA 4320
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Db 4309 CCGCATGGAGCTGCCATCTTACGTGTGCTACTTTGTGGTCTTTTCCCTTCTTCTCGT 4368
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Qy 4441 TGAATGAGCTGGAGAGAAACGAGAGGGCTTGATTTGATTTGCCATCAGCGCCAAACC 4500
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Qy 4501 CCTGACAGCTGACATGCCCAACCGGAGCTGTTCCAGTATGAAGACGTGGACATTTGT 4560
Db 4489 CCTGACAGCTGACATGCCCAACCGGAGCTGTTCCAGTATGAAGACGTGGACATTTGT 4548
Qy 4561 GGTCTCCCGCCCTTTGAATACTTCATCATGCGGCATGATAGCCCTCAACACTGTGGTGT 4620
Db 4549 GGTCTCCCGCCCTTTGAATACTTCATCATGCGGCATGATAGCCCTCAACACTGTGGTGT 4608
Qy 4621 GATGATGAAGTCTTATGATGACCCCTATGATGATGAGCTGATGCTGAATTCGCTGAACAT 4680
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Qy 4681 CGTGTTCACATCCATGTTCTCCATGGAATGGGTGCTGAAGATCATCGCCTTTGGGGTGT 4740
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Qy 4741 GAACTATTTGAGATGCTGGAAATGCTTTGACTTTGTCACTGTGTGGGAAGTATTAC 4800
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Qy 4981 GCTGTCTTTCATCTACGCCATCATCGGATGCTGAGGTGTTTGGGAATATTCCTCGGATGA 5040
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Qy 5101 GTTCAGGAGCGCCACCGGGAGGCTTGGCACGAGATCATGCTGTCTCTGCTGAGCAACCA 5160
Db 5089 GTTCAGGAGCGCCACCGGGAGGCTTGGCACGAGATCATGCTGTCTCTGCTGAGCAACCA 5148
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Db 5209 CGTCTCTTTCATCTTCTGTCTCTCTTCTGTGTTGAACTCTTTGTGGCTGTGATCAT 5268
Qy 5281 GGCACAAATTTTGAATACCTCAACGGGACTCTTCCATCTCTAGGTCTTCCACCTTGGATGA 5340
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Db	7189	CTGCATG	CAGCAGCGTGTGTTCAGTGTGATGATTTTATCATCCACACGGGCGAGTGG		7248
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RESULT 4

HUMCACHNT 7364 bp mRNA linear PRI 31-OCT-1994

LOCUS Human N-type calcium channel alpha-1 subunit mRNA, complete cds.

DEFINITION M94172

ACCESSION M94172.1 GI:179757

VERSION N-type calcium channel alpha-1 subunit.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 7364)

AUTHORS Williams,M.E., Brust,P.F., Feldman,D.H., Patthi,S., Simerson,S., Maroufi,A., McCue,A.F., Velicellebi,G., Ellis,S.B. and Harpold,M.M.

TITLE Structure and functional expression of an omega-conotoxin-sensitive human N-type calcium channel

JOURNAL Science 257 (5068), 389-395 (1992)

MEDLINE 92355886

PUBMED 1321501

COMMENT Original source text: Homo sapiens CNS cDNA to mRNA.

FEATURES

Location/Qualifiers

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ORIGIN

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VERSION AR022379.1 GI:3976441
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7362)
AUTHORS Harpold,M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
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ORIGIN

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Db 4847 CCTCTTTCAGCTGCGCGGCTGATCAAGTGTCTCGCCAGGAGTACACCATCCGATCCT 4906
Qy 4921 GCTGTGAGCTTGTCTCAGTCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCT 4980
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Qy	5821	CCTGTTCCACCTCTGAAGGCCACCTGGAGCAGACACGCGGCTGTGCTCCGAGGAGC	5880
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RESULT 6
AR063882
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ACCESSION AR063882
VERSION AR063882.1 GI:5993190
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 7362)
AUTHORS Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.P.
and Brenner,R.
TITLE Human calcium channel .alpha..sub.1.1. .alpha..sub.2. and .beta.
subunits and assays using them
JOURNAL Patent: US 5846757-A 7 08-DEC-1998;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 99.2%; Score 7316.4; DB 6; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

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Qy 61 GCTGCTCCGCTCTGAGCGCTGCGGCGCGCGCGCTCCCTGCGGACGAGCTGGGCGCGCTA 180
Db 60 GCTGCTCCGCTCTGAGCGCT-GCGGCGCGCGCGCTCCCTGCGGCGCGCTGGGCGG 118

Qy 121 GGGATGACGCGGGGCGCGGAGCCATGTCGCTTCGGGACGAGCTGGGCGCGCTA 178
Db 119 GGGATGACGCGGGGCGCGGAGCCATGTCGCTTCGGGACGAGCTGGGCGCGCTA 178

Qy 181 TGGAGCGCGCGCGGAGAGCGGCGCGCGCGCTCCCTGCGGCGCGCGCGCGCGCGCG 240
Db 179 TGGAGCGCGCGCGGAGAGCGGCGCGCGCGCTCCCTGCGGCGCGCGCGCGCGCGCG 238

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Qy 301 CGCGGACCATGCGCGCTGTACAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 360
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Db 359 CGGCTCGCTCTTCGCTTTTACGAGGACAAAGTCTGTCGCAAAATACGAGCGCATCAC 418

Qy 421 CGAGTGGCTCCATTCGAGTATATGATCCTGGCCACCATCATGCCAACTGCTGCTGCT 480
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QY	4621	GATGATGAAGTTCATGATGACCCCTATGAGTACGAGCTGATGCTGAAATCCCTGAACAT	4680
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QY	4681	CGTGTTCATCCATGTTCTCCATGGAATGCGTGTGAAGATCATGCGCTTTGGGGTCT	4740
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QY	4741	GAACTATTTCAGAGATGCTGGAATGCTTTTGACTTTTGCTACTGTGTTGGGAAGTATTAC	4800
Db	4727	GAACTATTTCAGAGATGCTGGAATGCTTTTGACTTTTGCTACTGTGTTGGGAAGTATTAC	4786
QY	4801	TGATATTTTAGTACAGAGATTCGGGAAACGAAATTTTCATCAACCTCAGCTTCTCCCG	4860
Db	4787	TGATATTTTAGTACAGAGATTCGGGAAACGAAATTTTCATCAACCTCAGCTTCTCCCG	4846
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QY	4981	GCTGTCTTCTCATCTACGCCCATCATCGGCATCAGAGTGTTCGGGAATATTCCCTGGATGA	5040
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VERSION AR067882.1 GI:5999104
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
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AUTHORS Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McQue,A.F.
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Qy 61 GTGTCTCGCTTGTAGCGCTTGGCGCCCGCGCCCTCCCTGCGGGGCGGTGGGCGG 120
Db 60 GTGTCTCGCTTGTAGCGCTTGGCGCCCGCGCCCTCCCTGCGGGGCGGTGGGCGG 118
Qy 121 GGATGCACGCGGGGCGCGGAGCGGCGCGGGGCGGCGGGGCGGGGCGGGGCGGCGCTA 180
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Db 4727 GAACATTTTCAGAGATGCTTGGAAATGCTTTGACTTTGTCTGCTGTTGGGAAGTATTAC 4786

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QY	4861	CCTCTTTTGAGCTGCGCGCTGATCAAGCTGCTCGCGCAGGGCTACACATCCGGATCCT	4920
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QY	4921	GCTGTGGAACCTTTGTCCAGTCCTTCAAGCCCTCGCCCTACGTGTGTCTGTCTCATTTGCCAT	4980
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AUTHORS Harpold,M.M., Ellis,S.B., Williams,M.E. and McCue,A.F.

TITLE Human calcium channel compositions and methods

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ORIGIN

Query Match 99.2%; Score 7316.4; DB 6; Length 7362;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

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Db 60 GCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCCCTCCCTGCGGGGCGCTGGGCGG 118

Qy 121 GGGATGACGCGGGGCGCGGAGCCATGCTCCGCTTGGGGACAGCTGGGCGGCGCTA 180

Db 119 GGGATGACGCGGGGCGCGGAGCCATGCTCCGCTTGGGGACAGCTGGGCGGCGCTA 178

Qy 181 TGGAGGCGCGCGGCGGAGCGGCGCGGGGCGGCGGCGCGGCGGGGCGGCGGCGG 240

Db 179 TGGAGGCGCGCGGCGGAGCGGCGCGGGGCGGCGGCGGCGGCGGCGGCGGCGG 238

Qy 241 GGGTCCGGGGGCTGACGCGCGGCGGCGGCTCTCTACAAGCAATCGATCGCGCAGCG 300

Db 239 GGGTCCGGGGGCTGACGCGCGGCGGCGGCTCTCTACAAGCAATCGATCGCGCAGCG 298

Qy 301 CGCGCGGACCATGGCGCTGTACAACCCGATCCCGGTCAAGCAGAACTGCTTACCCTCAA 360

299 CGCGCGGACCATGGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTACCCTCAA 358

Qy 361 CGCTCGCTCTTCGTCTTTCAGCGAGGACAAACGTCGTCCGCAAAATACGCGAAGCGCATCAC 420

Db 359 CGCTCGCTCTTCGTCTTTCAGCGAGGACAAACGTCGTCCGCAAAATACGCGAAGCGCATCAC 418

Qy 421 CGAGTGGCTCCATTCGAGTATATGATCTGGGCCACCATCATCGCCAACTGCATCGTCT 480

Db 419 CGAGTGGCTCCATTCGAGTATATGATCTGGGCCACCATCATCGCCAACTGCATCGTCT 478

Qy 481 GGGCCCTGGAGCAGCACTCCCTCATGGGACAAAACGCCCATGTCCGAGCGGCTGACGCA 540

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Qy 1381 TTTTGGACGTCTCAAGAGCGGCGCCCAAGAGAGCAGAAATGACTGATCCACGAGA 1440

Db 1379 TTTTGGACGTCTCAAGAGCGGCGCCCAAGAGAGCAGAAATGACTGATCCACGAGA 1438

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AUTHORS     Harpold,M.M., Ellis,S.B., Williams,M.E., McCue,A.F., Gillespie,A.,
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Db AGACCCGAACACTATTGTACATATCCAGTGTGACGGGCGGCTCTTGGGGAAGCCAC 3418
Qy GGTCTTCCCACTGTGACCTGGACCTGGAAGCGGAGGAGGAGGAGGAGGAGGAGG 3480
Db GGTCTTCCCACTGTGACCTGGACCTGGAAGCGGAGGAGGAGGAGGAGGAGGAGG 3478
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Qy	4681	CGTGTTCACATCCATGTTCTCCAT	TGGAATGCGTGCTGAAGATCATCGCTTTGGGGTGCT	4740
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Db	4787	TGATATTTTATGTAACAGAGATTG	CGGAAAAGAACAAATTTTATCAAACTCTACGTTTCTCTCG	4846
Qy	4861	CCTCTTTGAGCTCGCGGCTGATCA	AGCTGCTCCGCGAGGGCTACACCATCCGCATCCT	4920
Db	4847	CCTCTTTGAGCTCGCGGCTGATCA	AGCTGCTCCGCGAGGGCTACACCATCCGCATCCT	4906
Qy	4921	GCTGTGACACTTTGCTCCAGTCTT	CAAGGCCCTCCCTACGTGTGCTGTCTCATTTGCCAT	4980
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Qy	5041	TGACACAGAGCATCAACCGCCACA	CAACTTCCGAGCGTTTTTTCGACGCCCTGATGCTGCT	5100
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Qy	5101	GTTTCAGAGCGCCACGGGGAGGCT	CGCAGAGATCATGCTGTCTGCGCTGAGCAACCA	5160
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Qy	5221	CGTCTCCTTCATCTTCTGTGCTCT	TTCTTGATGTTGAACTCTTTGTGGCTGTGATCAT	5280
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Qy	5401	CATGTTTGTAGATGCTGAAAACA	CATGTCCCCTCTCTGGGCTGGGGAAGAAATGCCCTGC	5460
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Qy	5701	GATGACAGTGGGAAAGGTTTATGAGCCTCTGATGATATATTTGACTTCTACAAGCGAACA	5761
Db	5687	GATGACAGTGGGAAAGGTTTATGAGCCTCTGATGATATATTTGACTTCTACAAGCAGAA	5746
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Qy	5881	CCGGGTTTTCTTTCGACAGAAGAGTTCCACTCCTCAGCAATGGCGGGCCATACAAAA	5940
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Qy	6181	GACTCAGCCCGTCAACAGATGCCAGCCCATGAAGAGCGTCCATCTCCACGCTGGGCCACGC	6240
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Qy	6721	GCAGCTCCCCAGACGCCCTGACTCCCGCCCGCCAGCATCACCTACAAAGACGCCAACTC	6780
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Qy	6781	CTCACCATCCACTTGGCCGGGGCTCAGACAGCCTCCCTGCGCTTCTCCCAAGCCGGCT	6840

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Qy      7021  GGGCCGCTCTCCAGGACTTCTTACGCTGCTCTCCCTGACCTCCAGCTCACTCTCTCG 7080
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SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE Unclassified.
AUTHORS   Franco,R., Chen,A.Ru.Sun. and Shuey,D.John.
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ORIGIN

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Db      61  GGGCGGGGATGACGCGGGGCCCGGAGCCATGGTTCGGTTCGGGAGCAGCTGGGCGG 120
Qy      175  CCGCTATGAGGCCCCCGCGCGGAGAGCGGCGCGGGCGCGGCGCGGCGGCGG 234
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Qy      295  GCAGCGCGCGGAGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTCTTTCAC 354
Db      241  GCAGCGCGCGGAGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTCTTTCAC 300
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Qy      475  CGTCTGGCCCTGGAGCAGCACTTCCCTGATGGGGAACAAACGCCCATATGTCCGAGCGGCT 534
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Qy      535  GGACGACACGAGCGCTTATTTTCATCGGATCTTTTCTTTCGAGGCGAGGATCAAAATCAT 594
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Qy      1195  GGTGTGGCGGTGTCTCTCGGGGAGTTTGGCAAGAGCGAGAGGGTGGAGAAACCGCGC 1254
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Qy      1255  CGCCTTCTGAGCTGCGCGCGGAGCAGCATCGAGGAGAGCTCAACCGGTTACTTGA 1314
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1201	Db	CGCCTTCTGAAAGCTGCGCGGACGACGACAGATGCAGCGAGAGCTCAA	CGGGTACTGTGA	1261
1315	Qy	GTGGATCTTCAAGCGGAGGAAGTCA	TGCTGGCGGAGGACAGGAATGCAGAGAGAA	1374
1261	Db	GTGGATCTTCAAGCGGAGGAAGTCA	TGCTGGCGGAGGACAGGAATGCAGAGAGAA	1320
1375	Qy	GTCCCTTTTGGACGTGCTGAAGAGAGCGGCCA	CCAGAAGAGAGAAATGACCTGATCCA	1434
1321	Db	GTCCCTTTTGGACGTGCTGAAGAGAGCGGCCA	CCAGAAGAGAGAAATGACCTGATCCA	1380
1435	Qy	CGCAGAGGAGGAGAGACCGGTTTG	CAGATCTCTGTGCTGTGGATCCCCCTTCGCCCG	1494
1381	Db	CGCAGAGGAGGAGAGACCGGTTTG	CAGATCTCTGTGCTGTGGATCCCCCTTCGCCCG	1440
1495	Qy	CGCCAGCCTCAAGACGCGGGAAGACAGAGAGCTCGT	CATATCTCCGAGGAGAGAAAGAT	1554
1441	Db	CGCCAGCCTCAAGACGCGGGAAGACAGAGAGCTCGT	CATATCTCCGAGGAGAGAAAGAT	1500
1555	Qy	GTTCGGGTTTTTATCCGGCGCATGTGTGAAGGCTCAGAGCTTCT	TACTGTGGTGTGTGTG	1614
1501	Db	GTTCGGGTTTTTATCCGGCGCATGTGTGAAGGCTCAGAGCTTCT	TACTGTGGTGTGTGTG	1560
1615	Qy	GTGTGGCGCCTGNAACACATGTGTGTGGGCATGGTGATTA	CAACGAGCGCGCGGGCT	1674
1561	Db	GTGTGGCGCCTGNAACACATGTGTGTGGGCATGGTGATTA	CAACGAGCGCGCGGGCT	1620
1675	Qy	TACCACAGCCTGTATTTTTCGAGAGTTTGT	TTTCTGGGTCTCTCTCACAGAGATGTC	1734
1621	Db	TACCACAGCCTGTATTTTTCGAGAGTTTGT	TTTCTGGGTCTCTCTCACAGAGATGTC	1680
1735	Qy	CTTGGAAGATGTATGGCTTGCGGCCAGAAAGCTACT	TCCGGTCTCTCTTCAACTGCTTCGA	1794
1681	Db	CTTGGAAGATGTATGGCTTGCGGCCAGAAAGCTACT	TCCGGTCTCTCTTCAACTGCTTCGA	1740
1795	Qy	CTTTGGGGTCATCGTGGGGAGCGCTTTGAAGTGTCTGGCGCGCCATCAAGCGCGGAG	1854	
1741	Db	CTTTGGGGTCATCGTGGGGAGCGCTTTGAAGTGTCTGGCGCGCCATCAAGCGCGGAG	1800	
1855	Qy	CTCCTTTTGGATCAGTGTGTGCGGGCCCTCGCGCTGCTCAGGATCTTCAAAGTCA	CAGAA	1914
1801	Db	CTCCTTTTGGATCAGTGTGTGCGGGCCCTCGCGCTGCTCAGGATCTTCAAAGTCA	CAGAA	1860
1915	Qy	GTACTGGAGCTCCTTGCGGAAACCTGTGGTGTCCCTGCTGAACTCCAATGAAGTCCATCAT	1974	
1861	Db	GTACTGGAGCTCCTTGCGGAAACCTGTGGTGTCCCTGCTGAACTCCAATGAAGTCCATCAT	1920	
1975	Qy	CAGCCTGCTCTTCTTGTCTCTTCTGTTCATGTGGTCTTTCGCCCTGCTGGGATGAGCT	2034	
1921	Db	CAGCCTGCTCTTCTTGTCTCTTCTGTTCATGTGGTCTTTCGCCCTGCTGGGATGAGCT	1980	
2035	Qy	GTTTGGGGGACAGTTCAACTTTCAGGATGAGACTCCCAACAACTTCGACACCTTCCC	2094	
1981	Db	GTTTGGGGGACAGTTCAACTTTCAGGATGAGACTCCCAACAACTTCGACACCTTCCC	2040	
2095	Qy	TGCGCCATCCTCACTGTTTCCAGATCTCTGACGGGAGAGACTTGGAAATGCAGTGATGA	2154	
2041	Db	TGCGCCATCCTCACTGTTTCCAGATCTCTGACGGGAGAGACTTGGAAATGCAGTGATGA	2100	
2155	Qy	TCAGGGATCGAATTCGCAAGCGCGCTCAGCAAAAGCATGTTCTCGTCTTTTACTTTTCAT	2214	
2101	Db	TCAGGGATCGAATTCGCAAGCGCGCTCAGCAAAAGCATGTTCTCGTCTTTTACTTTTCAT	2160	
2215	Qy	TGTCTCAGACTGTTTCGGAACATACCTCTGCTGAATGTCTTTCTGGCCATCGCTGTGA	2274	
2161	Db	TGTCTCAGACTGTTTCGGAACATACCTCTGCTGAATGTCTTTCTGGCCATCGCTGTGA	2220	
2275	Qy	CAACCTGGCCAAACGCCCAAGAGCTGACCAAGGATGAAGAGAGATGGAAAGACGACCAA	2334	
2221	Db	CAACCTGGCCAAACGCCCAAGAGCTGACCAAGGATGAAGAGAGATGGAAAGACGACCAA	2280	
2335	Qy	TCAGAGCTTGCTCTGCAAAAGGCCAAAGATGGTGAAGTCAAGCCCCATGTCTGCCG	2394	
2281	Db	TCAGAGCTTGCTCTGCAAAAGGCCAAAGATGGTGAAGTCAAGCCCCATGTCTGCCG	2340	

Qy	2395	GAACATCTCATCGCCGCCACGAGCAGCAAGAACTCGGCCCAAGCGCGCTCGGTGTGGGAGCA	2454
Db	2341	GAACATCTCATCGCCGCCACGAGCAGCAAGAACTCGGCCCAAGCGCGCTCGGTGTGGGAGCA	2400
Qy	2455	GGGGCCAGCGCAGCTACGGCTGCAGAACCTTGCGGCCAGCTGCAGAGCGCTGTACAGCGA	2514
Db	2401	GGGGCCAGCGCAGCTACGGCTGCAGAACCTTGCGGCCAGCTGCAGAGCGCTGTACAGCGA	2460
Qy	2515	GATGGACCCCGAGAGCGGTGCGCTTTGCGCACTTACGCGCACTTGCGGGCCCGACATGAA	2574
Db	2461	GATGGACCCCGAGAGCGGTGCGCTTTGCGCACTTACGCGCACTTGCGGGCCCGACATGAA	2520
Qy	2575	GAGCACTTCGACCGGGCCGCTGTGTGTGGAGCTTGGCGCGAGCGCGCGGGGGCCCGT	2634
Db	2521	GAGCACTTCGACCGGGCCGCTGTGTGTGGAGCTTGGCGCGAGCGCGCGGGGGCCCGT	2580
Qy	2635	GGGAGGCAAGACCCGACTCTGAGGCTGCGGAGGGCCCCGAGGGGCTGACCTTCGCGCAG	2694
Db	2581	GGGAGGCAAGACCCGACTCTGAGGCTGCGGAGGGCCCCGAGGGGCTGACCTTCGCGCAG	2640
Qy	2695	GCACCAACCGCAACGCGACAAGGACAAGACCCCGCGGGCGGGGGAACAGACACGAGCAGA	2754
Db	2641	GCACCAACCGCAACGCGACAAGGACAAGACCCCGCGGGCGGGGGAACAGACACGAGCAGA	2700
Qy	2755	GGCCCCGAAGCGGAGCGGGAGCCCGTGTCCCGGAGGAGCGGCGCGCGCCGACCG	2814
Db	2701	GGCCCCGAAGCGGAGCGGGAGCCCGTGTCCCGGAGGAGCGGCGCGCGCCGACCG	2760
Qy	2815	CAGCCACAGCAAGGAGCGCGGGGCCCCCGGAGGCGCGAGCGCGCGCGAGCGCC	2874
Db	2761	CAGCCACAGCAAGGAGCGCGGGGCCCCCGGAGGCGCGAGCGCGCGCGAGCGCC	2820
Qy	2875	AGGCGCGAGGGCGGCGCGGCACACACCGCGCGCTCCCGAGAGAGCGCGCGAGCG	2934
Db	2821	AGGCGCGAGGGCGGCGCGGCACACACCGCGCGCTCCCGAGAGAGCGCGCGAGCG	2880
Qy	2935	GGAGCCCCGACGCCACCGCGCGCACCGGCAACCAAGATCCGAGCAAGAGTGCCTCGCGC	2994
Db	2881	GGAGCCCCGACGCCACCGCGCGCACCGGCAACCAAGATCCGAGCAAGAGTGCCTCGCGC	2940
Qy	2995	CAAGGGCGAGCGGCGCGCGCACCGCGGGGCCCCCGAGCGGGGCCCCGGGAGGCGGA	3054
Db	2941	CAAGGGCGAGCGGCGCGCGCACCGCGGGGCCCCCGAGCGGGGCCCCGGGAGGCGGA	3000
Qy	3055	GAGCGGGAGGAGCGCGCGCGGGCACCGGGGCCCGGCACAAGCGCGAGCTGTCTACAGA	3114
Db	3001	GAGCGGGAGGAGCGCGCGCGGGCACCGGGGCCCGGCACAAGCGCGAGCTGTCTACAGA	3060
Qy	3115	GGCTGTGGAGAAAGAGACCAACGAGAAAGGAGGCCACGGAAGAGGCTGAGATAGTGGGA	3174
Db	3061	GGCTGTGGAGAAAGAGACCAACGAGAAAGGAGGCCACGGAAGAGGCTGAGATAGTGGGA	3120
Qy	3175	AGCGCAACGGAAGAGAGCTTCGGAGACCAACGAGCCCCCGGAGCGCACCTGTGACCTTGA	3234
Db	3121	AGCGCAACGGAAGAGAGCTTCGGAGACCAACGAGCCCCCGGAGCGCACCTGTGACCTTGA	3180
Qy	3235	GACCACTGGGACTGTGACTGTGGGTCCCATGCAACACTGCCAGCACCTGTCTCCAGAA	3294
Db	3181	GACCACTGGGACTGTGACTGTGGGTCCCATGCAACACTGCCAGCACCTGTCTCCAGAA	3240
Qy	3295	GGTGGAGGAACAGCCAGAGAGATGCAACATCAGCGGAACGTCACTCGCATGGGCACTCA	3354
Db	3241	GGTGGAGGAACAGCCAGAGAGATGCAACATCAGCGGAACGTCACTCGCATGGGCACTCA	3300
Qy	3355	GGCCCCAGACCCGAACACTATTGTACATATCCCAAGTATGCTGACGGGGCCCTCTTGGGGA	3414
Db	3301	GGCCCCAGACCCGAACACTATTGTACATATCCCAAGTATGCTGACGGGGCCCTCTTGGGGA	3360
Qy	3415	AGCCACGGTCTTCCAGTGGTAACTGTGGAACCTTGGAAAGCCAAAGCAGAGGGGAAGAAGGA	3474
Db	3361	AGCCACGGTCTTCCAGTGGTAACTGTGGAACCTTGGAAAGCCAAAGCAGAGGGGAAGAAGGA	3420

QY	3475	GGTGGAGCGGATGACGTGATGAGGAGCGGCCCCCGGCTATTCGTCCTCATACAGCTCCAT	3534
Db	3421	GGTGGAGCGGATGACGTGATGAGGAGCGGCCCCCGGCTATTCGTCCTCATACAGCTCCAT	3480
QY	3535	GTTCTGTTAAAGCCCAACCACTGCTCGCGCTTCGCCACATCATCTGTCACATCTGTCACCATG	3594
Db	3481	GTTCTGTTAAAGCCCAACCACTGCTCGCGCTTCGCCACATCATCTGTCACATCTGTCACCATG	3540
QY	3595	GTACTTCGAGGTGGTCAATTCCTCGTGGTCAATCGCTTGTGAGCAGCATCGCCCTGGCTGCTGA	3654
Db	3541	GTACTTCGAGGTGGTCAATTCCTCGTGGTCAATCGCTTGTGAGCAGCATCGCCCTGGCTGCTGA	3600
QY	3655	GAACCCAGTGCACAGACTCGCCCAAGNACAAAGCTCTGAAATACCTGGATTAATTTT	3714
Db	3601	GAACCCAGTGCACAGACTCGCCCAAGNACAAAGCTCTGAAATACCTGGATTAATTTT	3660
QY	3715	CACCTGGTCTTTACCTTTGAGATGGTGAATAAGATGATGACATTTGGAGCTGCTGCTTCA	3774
Db	3661	CACCTGGTCTTTACCTTTGAGATGGTGAATAAGATGATGACATTTGGAGCTGCTGCTTCA	3720
QY	3775	CCCTGGAGCTAATTTCCGGGACTTGTGGAAATTTCTGGAATTCATTTGTGTCTAGTGGCGC	3834
Db	3721	CCCTGGAGCTAATTTCCGGGACTTGTGGAAATTTCTGGAATTCATTTGTGTCTAGTGGCGC	3780
QY	3835	CCTGTTGGCGTTTGCTTTCTCGAGCTTCGTGGGAGGATCCAAAGGGAACACATCAATAC	3894
Db	3781	CCTGTTGGCGTTTGCTTTCTCGAGCTTCGTGGGAGGATCCAAAGGGAACACATCAATAC	3828
QY	3895	CATCAAGTCTCTGAGAGTCTTCTGTTGCTCGCGGCCCTCAAGACCATCAAAAGGCTGCC	3954
Db	3829	CATCAAGTCTCTGAGAGTCTTCTGTTGCTCGCGGCCCTCAAGACCATCAAAAGGCTGCC	3888
QY	3955	CAAGTCTCAAGGCTGTGTTTGACTGTGTGGTGAATCCCTCGAAGAAATGCTCTCAACATCTT	4014
Db	3899	CAAGTCTCAAGGCTGTGTTTGACTGTGTGGTGAATCCCTCGAAGAAATGCTCTCAACATCTT	3948
QY	4015	GATTTGCTACATGCTTTCTATGTTTCATATTTGCGGTCAATTTGCGGTGAGCTTTCAAAGG	4074
Db	3949	GATTTGCTACATGCTTTCTATGTTTCATATTTGCGGTGAGCTTTCAAAGG	4008
QY	4075	GAAAGTTTTCTACTGACAGATGAATCCAAAGGAGCTGGAGAGGATTCAGCGGTGAGCTT	4134
Db	4009	GAAAGTTTTCTACTGACAGATGAATCCAAAGGAGCTGGAGAGGATTCAGCGGTGAGCTT	4068
QY	4135	TTTGGATTATGAGAGGAGGAGTGGAACTCAGCCAGGACAGGTGGAAGAAATACGATTT	4194
Db	4069	TTTGGATTATGAGAGGAGGAGTGGAACTCAGCCAGGACAGGTGGAAGAAATACGATTT	4128
QY	4195	TCATCTACAGAAATGCTCTGGGCTCTGTCAGCGCTTTTCACAGTGTCCACGGGAGAAG	4254
Db	4129	TCATCTACAGAAATGCTCTGGGCTCTGTCAGCGCTTTTCACAGTGTCCACGGGAGAAG	4188
QY	4255	CTGCCCCATGGTGTGMAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCCC	4314
Db	4189	CTGCCCCATGGTGTGMAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCCC	4248
QY	4315	TGGGTACCGATGGAGCTGTCATCTTCTACGTGGTCTACTTTGTGGTCTTTCCCTCTCTT	4374
Db	4249	TGGGTACCGATGGAGCTGTCATCTTCTACGTGGTCTACTTTGTGGTCTTTCCCTCTCTT	4308
QY	4375	CTTCGTCAACATCTTTGTGGCTTTGATCATCATCTTCCAGGAGCAGGGGGAACAAGT	4434
Db	4309	CTTCGTCAACATCTTTGTGGCTTTGATCATCATCTTCCAGGAGCAGGGGGAACAAGT	4368
QY	4435	GATGTCTGAATGAGCCTTGAGAGAAACAGAGGGCTTGCATTTGACTTCGCCATCAGCGC	4494
Db	4369	GATGTCTGAATGAGCCTTGAGAGAAACAGAGGGCTTGCATTTGACTTCGCCATCAGCGC	4428
QY	4495	CAAAACCCCTGACACGGTACATGCCCCAAAACCGGAGTCTGTTCCAGTATTAAGACGTGGAC	4554
Db	4429	CAAAACCCCTGACACGGTACATGCCCCAAAACCGGAGTCTGTTCCAGTATTAAGACGTGGAC	4488
QY	4555	ATTTGTGGTCTCCCCGCCCTTTGAATATTTTCATATGCGCATGATAGCGCTTCAACACTGT	4614

[illegible]

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5695	QY	TGATGAGATGACAGTGGGGAGGTTTATATGCAAGCTCTGATGATATTTTGACTTCTACAAGCA	5754
5623	DB	TGATGAGATGACAGTGGGGAAGGTTTATGTCAGCTCTGATGATATTTTGACTTCTACAAGCA	5682
5755	QY	GAACAAACCAACAGAGACCAAGATGCAGCAGGCTCTCTGGAGGCTCTCCACAGATGGGTCC	5814
5683	DB	GAACAAACCAACAGAGACCAAGATGCAGCAGGCTCTCTGGAGGCTCTCCACAGATGGGTCC	5742
5815	QY	TGTGTCTCTGTTTCCACCCTCTGAAGGCCACCTCTGGAGCAGACACAGCCGCTGTGTCCTCG	5874
5743	DB	TGTGTCTCTGTTTCCACCCTCTGAAGGCCACCTCTGGAGCAGACACAGCCGCTGTGTCCTCG	5802
5875	QY	AGGAGCCCGGGTTTTCTTCCAGACAAGAGTTCCACCTCTCAGCAATGGCGGGGCCAT	5934
5803	DB	AGGAGCCCGGGTTTTCTTCCAGACAAGAGTTCCACCTCTCAGCAATGGCGGGGCCAT	5862
5935	QY	ACAAACCAAGAGAGTGGCATCAAAAGATCTGTCTCTCTGGGGCACTCAAAAGGACCCAGGA	5994
5863	DB	ACAAACCAAGAGAGTGGCATCAAAAGATCTGTCTCTCTGGGGCACTCAAAAGGACCCAGGA	5922
5995	QY	TGCACCCCATGAGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGG	6054
5923	DB	TGCACCCCATGAGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGG	5982
6055	QY	CGGCTCAGGAGCACTGGCTGTGGACGTTTCAGATGCAGAGCATAAACCGGAGGGCCCTGA	6114
5983	DB	CGGCTCAGGAGCACTGGCTGTGGACGTTTCAGATGCAGAGCATAAACCGGAGGGCCCTGA	6042
6115	QY	TGGGGAGCCCCAGCCTCGGCTGGAGACCCAGGGTTCGAGCGGCTTCATGCCCCCGCTTGC	6174
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6175	QY	GGCCGAGACTCAGCCCGTTCAGATGCCAGCCCATGAAGGGCTCCATCTCCAGCGTGGC	6234
6103	DB	GGCCGAGACTCAGCCCGTTCAGATGCCAGCCCATGAAGGGCTCCATCTCCAGCGTGGC	6162
6235	QY	CCAGCGCCCGCTGGGACTCATCTTTTCAGCACCAACCCCGGACCGGCCACCCCTAGCCA	6294
6163	DB	CCAGCGCCCGCTGGGACTCATCTTTTCAGCACCAACCCCGGACCGGCCACCCCTAGCCA	6222
6295	QY	GGGCTCTGCAACCAACCAACCGCTGCACCCGCGCAGGACAGGAAGCAGAGGTC	6354
6223	DB	GGGCTCTGCAACCAACCAACCGCTGCACCCGCGCAGGACAGGAAGCAGAGGTC	6282
6355	QY	CCTGGAGAGGGGCCAGCCTGTCTGCCGATATGATGGGCGCACCAAGCAGTCTGTGGG	6414
6283	DB	CCTGGAGAGGGGCCAGCCTGTCTGCCGATATGATGGGCGCACCAAGCAGTCTGTGGG	6342
6415	QY	GCCGGGCTGCCCCCGGAGAGGGGCTTACAGGCTGCCGCGGGAACGAGAGCGCCGCA	6474
6343	DB	GCCGGGCTGCCCCCGGAGAGGGGCTTACAGGCTGCCGCGGGAACGAGAGCGCCGCA	6402
6475	QY	GGAGCGGGGCGGTTCCAGGAGCGGAGGCACTCTCTCTCTCTCGGAGAGCAGCG	6534
6403	DB	GGAGCGGGGCGGTTCCAGGAGCGGAGGCACTCTCTCTCTCTCGGAGAGCAGCG	6462
6535	QY	CTTCTACTCTGCGAACCGCTTTTGGGGGCGGTGAGCCCCCGAGCCCAAGCCCTCTCTCAG	6594
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6523	DB	CAGCCACCCACGTCGCCACAGCTGGCCAGGAGCCGGGACCCACCCACAGGGCAGTGG	6582
6655	QY	TTCCGTGAATGGGAGCCCTTGTGTCAACATCTGTGTCTAGCACCCCGCGCGCGGTGG	6714
6583	DB	TTCCGTGAATGGGAGCCCTTGTGTCAACATCTGTGTCTAGCACCCCGCGCGCGGTGG	6642
6715	QY	GCGGAGCAGCTCCCCCAGACGCCCTTGACTCCCCCGCCCCCAGCATCACTACAAGACGGC	6774
6643	DB	GCGGAGCAGCTCCCCCAGACGCCCTTGACTCCCCCGCCCCCAGCATCACTACAAGACGGC	6702

Qy	6775	CAAACTCCTACCCATTCACATTCGCGCGGGCTCAGACACAGCCTCCTCGCTTCCTTCCCCAGG	6834
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Qy	6835	CCGGCTCAGCCGTGGGCTTTCGAAACACACACGCCCTGCTGCAGAGAGACACCCCTCAGCCA	6894
Db	6763	CCGGCTCAGCCGTGGGCTTTCGAAACACACACGCCCTGCTGCAGAGAGACACCCCTCAGCCA	6822
Qy	6895	GCCTCTGGCCCTCGGCTCTCGAATTGGCTCTGACCCCTTACTCTGGGGCAGCGTCTGGACAG	6954
Db	6823	GCCTCTGGCCCTCGGCTCTCGAATTGGCTCTGACCCCTTACTCTGGGGCAGCGTCTGGACAG	6882
Qy	6955	TGAGGCTCTGTGCCACGCGCTCGCTCAGGACACGCTCACCTTTTCGAGGAGCGTGTGGCCAC	7014
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Qy	7015	CAACTGGGCGCGCTCCTCAGAGGACTTCTTACGTGTCTCTCCCTGACCTCCACAGTCTCACCC	7074
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Qy	7075	TCTCCGCGCGGTGCCAAACGGTTACCACTGCACCCCTGGGACTCAGTTCGGGTGGCCGAGC	7134
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Qy	7135	ACGGCACAGTACCAACCCCTGACCAAGACCACTGCTGTAGCTGCACCGTGACCGCTC	7194
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Qy	7195	AGAGGCTGTAGTACGAGCGCGTGTTCACGTGGATAGTATTCATCCACACCGGGC	7254
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Qy	7255	AGTGGGCCCTCGGGGAGGCGTTTGCCACCTTGTGTAGGCTCCTGTGGCCCTCCCTCCC	7314
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Qy	7315	CCCTCTCCCTCTTTTACTCTAGA	7338
Db	7243	CCCTCTCCCTCTTTTACTCTAGA	7266
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VERSION	AR198609.1	GI:20248458	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1. (bases 1 to 7177)		
AUTHORS	Lipscombe, D. and Schorge, S.		
TITLE	Human N-type calcium channel isoform		
JOURNAL	Patent: US 6353091-A 7 05-MAR-2002;		
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	/mol_type="unassigned DNA"		
ORIGIN			
Query Match	94.3%;	Score 6958;	DB 6; Length 7177;
Best Local Similarity	97.3%;	Pred. No. 0;	
Matches 7177; Conservative	0;	Mismatches	0; Indels 199; Gaps 2;
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Db	1	GCGCAGCGCGCTCGCGCGTGGGCGCGGCGAGGTCCGCTCGCGTCCCGCGGTCCGTG	60
Qy	61	GCTGTCTCCGCTCTGAGCGCTCGCGCGCCCGCGCCCTCTCCCTCGCGGGCGCGTGGGCGG	120
Db	61	GCTGTCTCCGCTCTGAGCGCTCGCGCGCCCGCGCCCTCTCCCTCGCGGGCGCGTGGGCGG	120

Db 2281 GGCACCGCCCAAGAGTGAACCAAGGATGAAGAGGAGATGAAGAGACGACCCAAATCAGAA 2340
QY 2341 GCTTGTCTCTCAAAAGGCCAAAGAGTGGCTGAAGTCAGGCCCATGTCTCTCCCGCAACAT 2400
Db 2341 GCTTGTCTCTCAAAAGGCCAAAGAGTGGCTGAAGTCAGGCCCATGTCTCTCCCGCAACAT 2400
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Db 2401 CTCATCCGCGCCAGGCGAGCAGAACTCGGCCAAAGGCGCGTCTCGGTGTGGGAGCAGCGGGC 2460
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Db 2581 CTTGGACCGCCGCTGGTGTGAGCTGGCCCGGACGCGCGCGGGGCCCCGTGGGAGG 2640
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Db 3721 TGTCTTTTACCTTTGAGATGATGAATGATCGACTTGGGACTGCTGCTTCAACCTGG 3780
QY 3781 AGCTATTTTCCGGGACTTGTGGAACTTCTGGACTTTCATTGTGGTCAAGTGGCCCTGGT 3840
Db 3781 AGCTATTTTCCGGGACTTGTGGAACTTCTGGACTTTCATTGTGGTCAAGTGGCCCTGGT 3840
QY 3841 GGGCTTTGCTTTCGAGCTTCGAGGATCCAAAGGGAAGACATCAATACCATCAA 3900
Db 3841 GGGCTTTGCTTTCGCTC-----AGGATCCAAAGGGAAGACATCAATACCATCAA 3988
QY 3901 GTCTCTGAGAGTCTTCTGCTGCTGCGGCCCTCAAGACCATCAAGCGCTGCCAGCT 3960
Db 3889 GTCTCTGAGAGTCTTCTGCTGCTGCGGCCCTCAAGACCATCAAGCGCTGCCAGCT 3948
QY 3961 CAAGGCTGTGTTTGAAGTGTGTTGAAGTGTCTTGAAGATGTCTTCAACATCTTGATTGT 4020
Db 3949 CAAGGCTGTGTTTGAAGTGTGTTGAAGTGTCTTGAAGATGTCTTCAACATCTTGATTGT 4008
QY 4021 CTACATGCTTTCATGTTTCATATTTGCGGTCAATGCGGTGAGCTCTTCAAGGGAAGTT 4080
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QY 4081 TTTCTACTCCACAGATGAATCCAGGAGCTGGAGAGGAGTGCAGGGTCAAGTATTGGA 4140
Db 4069 TTTCTACTGACAGATGAATCCAGGAGCTGGAGAGGAGTGCAGGGGTCAAGTATTGGA 4128
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QY 4201 CGACAATGTGCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCACGGGAGAGGGTGGCC 4260
Db 4189 CGACAATGTGCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCACGGGAGAGGGTGGCC 4248
QY 4261 CATGTGCTGAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAGGCCCTCGGTA 4320
Db 4249 CATGTGCTGAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAGGCCCTCGGTA 4308
QY 4321 CCGCATGGAGCTGTCCATCTTCTACGTGGTCTACTTTGTGGTCTTTCCCTTCTTCTCGT 4380
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QY 4441 TGAATCAGCTGGAGAAACGAGAGGGCTTGCATTTGATTTGCTTCCCATCAGCGCCAAAC 4500
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QY	4561	GGTCTCCCGCCCTTTGAATACATTTTCATATGGCCATGATAGCCCTCAACACATGTGGTGT	4620
Db	4549	GGTCTCCCGCCCTTTGAATACATTTTCATATGGCCATGATAGCCCTCAACACATGTGGTGT	4608
QY	4621	GATGATGAAGTTCTATGATGCACCCCTATGATAGTACGAGCTGATGCTGAATGCTCGAACAT	4680
Db	4609	GATGATGAAGTTCTATGATGCACCCCTATGATAGTACGAGCTGATGCTGAATGCTCGAACAT	4668
QY	4681	CGTGTTCACATCCATGTTCTCCATGGAAATGCTGTGAAATCATATGCTTTGGGGTGT	4740
Db	4669	CGTGTTCACATCCATGTTCTCCATGGAAATGCTGTGAAATCATATGCTTTGGGGTGT	4728
QY	4741	GAACATATTTACAGATGCTCGGAATGCTTTTGTACCTTTGTACCTGTTGGGAAGTATTAC	4800
Db	4729	GAACATATTTACAGATGCTCGGAATGCTTTTGTACCTTTGTACCTGTTGGGAAGTATTAC	4788
QY	4801	TGATATTTTAAACAGAGATTCGGAAACGAAATTTTCATCAACCTCAGCTTCTCTCG	4860
Db	4789	TGATATTTTAAACAGAGATTCGGAAACGAAATTTTCATCAACCTCAGCTTCTCTCG	4848
QY	4861	CCTCTTTTCAGAGCTCGCGGCTGATCAAGCTGCTCCGCCAGGGCTACCATCCGCATCCT	4920
Db	4849	CCTCTTTTCAGAGCTCGCGGCTGATCAAGCTGCTCCGCCAGGGCTACCATCCGCATCCT	4908
QY	4921	GCTGTGACCTTTGTCAGTCCCTTCAAGGCCCTGCCCTCAGTGTGTCTCAATTTGCCAT	4980
Db	4909	GCTGTGACCTTTGTCAGTCCCTTCAAGGCCCTGCCCTCAGTGTGTCTCAATTTGCCAT	4968
QY	4981	GCTGTTCCTTACATACGCCATCATCGGCATGACAGTGTGTTGGGAATATTGCCCTCGATGA	5040
Db	4969	GCTGTTCCTTACATACGCCATCATCGGCATGACAGTGTGTTGGGAATATTGCCCTCGATGA	5028
QY	5041	TGACACGAGATCAACCGGCACACAACTTCGCGAGCTTTTGGAGCCCTGATGCTCT	5100
Db	5029	TGACACGAGATCAACCGGCACACAACTTCGCGAGCTTTTGGAGCCCTGATGCTCT	5088
QY	5101	GTTTCAGGAGCGCACGGGGAGGCTGGCACGAGATCATGCTCTCCCTGAGCAACCA	5160
Db	5089	GTTTCAGGAGCGCACGGGGAGGCTGGCACGAGATCATGCTCTCCCTGAGCAACCA	5148
QY	5161	GGCTGTGATGAGCGGCAATGCCACCGAGTGTGGAAGTGACTTTGCTACTTCTACTT	5220
Db	5149	GGCTGTGATGAGCGGCAATGCCACCGAGTGTGGAAGTGACTTTGCTACTTCTACTT	5208
QY	5221	CGTCTCCTTTCATCTTCTGCTCCTTCTGATGTTGAACCTCTTTGTTGGCTGTGATCAT	5280
Db	5209	CGTCTCCTTTCATCTTCTGCTCCTTCTGATGTTGAACCTCTTTGTTGGCTGTGATCAT	5268
QY	5281	GGACAATTTGATGATCCTCAGCGGGAATCTTTCCATCCTAGGTCTCTCACCCTTTGGATGA	5340
Db	5269	GGACAATTTGATGATCCTCAGCGGGAATCTTTCCATCCTAGGTCTCTCACCCTTTGGATGA	5328
QY	5341	GTTTCATCCGGTCTGGGCTGAATACGACCCGGCTGCTGGGCGCATCAGTTTCAATGA	5400
Db	5329	GTTTCATCCGGTCTGGGCTGAATACGACCCGGCTGCTGGGCGCATCAGTTTCAATGA	5388
QY	5401	CATGTTTGAGATGCTGAAACACATGTCCTCCCTCTGGGGCTGGGAAGAAATGCCCTGC	5460
Db	5389	CATGTTTGAGATGCTGAAACACATGTCCTCCCTCTGGGGCTGGGAAGAAATGCCCTGC	5448
QY	5461	TCGAGTTGCTTACAGCGCCTGGTTGCAATGAACATGCCCATCTCCAAACGAGGACATGAC	5520
Db	5449	TCGAGTTGCTTACAGCGCCTGGTTGCAATGAACATGCCCATCTCCAAACGAGGACATGAC	5508
QY	5521	TGTTCACTTCAGTCCAGCTGATGGCCCTCATCCGACCGGCACTGAGATCAAGCTGGC	5580
Db	5509	TGTTCACTTCAGTCCAGCTGATGGCCCTCATCCGACCGGCACTGAGATCAAGCTGGC	5568

QY	5581	CCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCCGTTGT	5640
Db	5569	CCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCCGTTGT	5628
QY	5641	GTGGGCCAATCTGCCCCAGAGACTTTGGACTTCTGGTACCACCCCATATAGCCTGATGA	5700
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QY	5701	GATGACATGTGGGAAGGTTTATGCAGCTCTGATGATATTTGACTTCTACAGAGACAACAA	5760
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QY	5761	AACACACAGAGACAGATGACAGAGGCTCTTGAGAGGCTCTCCACAGATGGTCTCTGTGTC	5820
Db	5749	AACACACAGAGACAGATGACAGAGGCTCTTGAGAGGCTCTCCACAGATGGTCTCTGTGTC	5808
QY	5821	CCTGTTCCACCTCTGAAGGCCACCTTGAGGACACACCGCGGCTGTGCTCGAGGAGC	5880
Db	5809	CCTGTTCCACCTCTGAAGGCCACCTTGAGGACACACCGCGGCTGTGCTCGAGGAGC	5868
QY	5881	CCGGGTTTTCTTCGACAGAAAGATTCACCTCCTCAGCAATGGCGGGGCTCATACAAA	5940
Db	5869	CCGGGTTTTCTTCGACAGAAAGATTCACCTCCTCAGCAATGGCGGGGCTCATACAAA	5928
QY	5941	CCAAGAGATGGGCATCAAGAGTCTGCTCTCTGGGGCACTCAAGAGACCCAGATGACCC	6000
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QY	6001	CCATGAGGCGAGGCCACCCCTTGAGGCTGCGCCACTCCACAGAGATCCCTGTGGGGGGTCC	6060
Db	5989	CCATGAGGCGAGGCCACCCCTTGAGGCTGCGCCACTCCACAGAGATCCCTGTGGGGGGTCC	6048
QY	6061	AGGAGCACTGGCTGTGAGCGTTTCAGATGACAGAGATTAACCCGAGGGGCTCTGATGGGA	6120
Db	6049	AGGAGCACTGGCTGTGAGCGTTTCAGATGACAGAGATTAACCCGAGGGGCTCTGATGGGA	6108
QY	6121	GCCTCAGCTGGGCTGGAGAGCCAGGGTTCAGCGGCTCCATGCCCCGCTTGGGGCCGA	6180
Db	6109	GCCTCAGCTGGGCTGGAGAGCCAGGGTTCAGCGGCTCCATGCCCCGCTTGGGGCCGA	6168
QY	6181	GACTCAGCGCTGCACAGATGCGGCCCATGAAGCGCTCCATCTCCACGCTGGCCAGCG	6240
Db	6169	GACTCAGCGCTGCACAGATGCGGCCCATGAAGCGCTCCATCTCCACGCTGGCCAGCG	6228
QY	6241	GCCTCCTGCGACTCATCTTTGAGCAGCACCCCGGACCGCCCTTACCCCTTACCGAGCGTC	6300
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QY	6301	GTGCAACCAACCAACCAACCGCTGCGACCGCGCAGGGACAGGAAGACAGACGTCCCTGGA	6360
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QY	6361	GAAGGGCCCCAGCCTGTCTGCCGATATGATGCGGCAACAAGCAGTGTGTGGGGCCGG	6420
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QY	6421	GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGGGGAACGAGAGCGCCGCGAGAGCG	6480
Db	6409	GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGCGGGGAACGAGAGCGCCGCGAGAGCG	6468
QY	6481	GGGCGGCTCCAGAGAGCGGAGGCGCTCATCTCTCTCTCGGAGAAAGCAGCGCTTCTA	6540
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QY	6541	CTCTCTGCGACCGCTTTTGGGGCCGCTGAGCCCCCGAAGCCCAAGCCCTTCCCTCAGCAGCA	6600
Db	6529	CTCTCTGCGACCGCTTTTGGGGCCGCTGAGCCCCCGAAGCCCAAGCCCTTCCCTCAGCAGCA	6588
QY	6601	CCCAACGCTGCGCAACAGCTGCGCAGGAGCGCGGACCCCAACCAACAGGCGAGTGTGTCGT	6660
Db	6589	CCCAACGCTGCGCAACAGCTGCGCAGGAGCGCGGACCCCAACCAACAGGCGAGTGTGTCGT	6631
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Db	6632	-----	6631
Qy	6721	GCAGCTCCCCAGACGCCCTGACTCCCGCCCGCCAGCATCACCTACAAAGACGCCAACTC	6780
Db	6632	-----	6631
Qy	6781	CTCACCATTCCACTTCGCGCGGGCTCAGACAGCGCTCCCTGCCTTCTCCCGACGGCGGCT	6840
Db	6632	-----	6641
Qy	6941	CAGCGTGGCTTTCGAAACACACACAGCGCTGCTGCAGAGAGACCCCTCAGCAGCCCT	6900
Db	6642	CAGCGTGGCTTTCGAAACACACAGCGCTGCTGCAGAGAGACCCCTCAGCAGCCCT	6701
Qy	6901	GGCCCTGGCTCTCGAATTGGCTCTGACCTTACTCGGCGAGCGCTCTGCACAGTAGGCG	6960
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Qy	6961	CTGTGTCCACGCCCTGCTCAGGACACGCTCACTTTCGAGAGCGCTGTGCCACCAACTC	7020
Db	6762	CTGTGTCCACGCCCTGCTCAGGACACGCTCACTTTCGAGAGCGCTGTGCCACCAACTC	6821
Qy	7021	GGCGCGTCTCTCAGGACTTCTACGTGTCTCTCCCTGACCTCCAGTCTCACCTCTCCG	7080
Db	6822	GGCGCGTCTCTCAGGACTTCTACGTGTCTCTCCCTGACCTCCAGTCTCACCTCTCCG	6981
Qy	7081	CCGCGTCCCAACGGTTTACCACTGCACCTCGGACTCAGCTCGGCTGGCGGCGAGCAGCGCA	7140
Db	6882	CCGCGTCCCAACGGTTTACCACTGCACCTCGGACTCAGCTCGGCTGGCGGCGAGCAGCGCA	6941
Qy	7141	CAGTACCAACCCCTCAGCAACCACTCGTGTAGCTGCACCGTCAACCGCTCAGACGC	7200
Db	6942	CAGTACCAACCCCTCAGCAACCACTCGTGTAGCTGCACCGTCAACCGCTCAGACGC	7001
Qy	7201	CTGATCAGCAGCGGTGTCTCAGTGGATGAGTTTATCATCCACACGGGCGAGTCCG	7260
Db	7002	CTGATCAGCAGCGGTGTCTCAGTGGATGAGTTTATCATCCACACGGGCGAGTCCG	7061
Qy	7261	CCCTCGGGGAGGCTTGGCCACCTTGGTAGGCTCTGTGGCCCTCCCTCCCGCTCT	7320
Db	7062	CCCTCGGGGAGGCTTGGCCACCTTGGTAGGCTCTGTGGCCCTCCCTCCCGCTCT	7121
Qy	7321	CCCTCTTTTACTCTAGACGACGAATAAGCCCTGTTGCTGTAGTGTACGTACCGC	7376
Db	7122	CCCTCTTTTACTCTAGACGACGAATAAGCCCTGTTGCTGTAGTGTACGTACCGC	7177
RESULT 12			
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LOCUS	Human N-type calcium channel alpha-1 subunit mRNA, complete cds.		
DEFINITION	M94173		
ACCESSION	M94173.1 GI:179759		
VERSION	N-type calcium channel alpha-1 subunit.		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 7177)		
AUTHORS	Williams,M.E., Brust,P.F., Feldman,D.H., Patthi,S., Simerson,S., Maroufi,A., McCue,A.F., Velicelebi,G., Ellis,S.B. and Harpold,M.M.		
TITLE	Structure and functional expression of an omega-conotoxin-sensitive human N-type calcium channel		
JOURNAL	Science 257 (5068), 389-395 (1992)		
MEDLINE	92335886		
PUBMED	1321501		
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		Matches 7177; Conservative 0; Mismatches 0; Indels 199; Gaps 2;	
Qy	1	GC	CGCGCGGCTCGCGCGGTGGCGCGGCGAGGTCCGCTGCGGTCCCGCGCGCTCCGTG 60
Db	1	GC	CGCGCGGCTCGCGCGGTGGCGCGGCGAGGTCCGCTGCGGTCCCGCGCGCTCCGTG 60
Qy	61	GCT	GCTCCGCTCTGAGCGCTGCGCGCGCGCGCGCTCCCTGCGCGCGCGCGCGCGCG 120
Db	61	GCT	GCTCCGCTCTGAGCGCTGCGCGCGCGCGCGCTCCCTGCGCGCGCGCGCGCGCG 120
Qy	121	GG	GATGACGCGCGCGCGCGCGGAGCCATGCTCCCTTTCGGGAGCAGAGTGGCGCGCGCTA 180
Db	121	GG	GATGACGCGCGCGCGCGCGGAGCCATGCTCCCTTTCGGGAGCAGAGTGGCGCGCGCTA 180
Qy	181	TG	GAGGCGCGCGCGCGGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 240

[illegible]

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Qy	1321	CTTTCAAGCGGAGGAAGTCATCTGCGCGGAGGAGCAGGAATCG	CAGAGTACGAGAGTCCCC	1380
Db	1321	CTTTCAAGCGGAGGAAGTCATCTGCGCGGAGGAGCAGGAATCG	CAGAGTACGAGAGTCCCC	1380
Qy	1381	TTTGGACGTGTGAAGAGAGCGGCCACCAAGAAGAGCAGAAATG	ACCTGATCCACGCAGA	1440
Db	1381	TTTGGACGTGTGAAGAGAGCGGCCACCAAGAAGAGCAGAAATG	ACCTGATCCACGCAGA	1440
Qy	1441	GGAGGGAGAGACCGGTTTTCAGATCTCTGTGCTGTTGGATCC	CCCTTCCCGCGGCAG	1500
Db	1441	GGAGGGAGAGACCGGTTTTCAGATCTCTGTGCTGTTGGATCC	CCCTTCCCGCGGCAG	1500
Qy	1501	CCTCAAGAGCGGGAAGCAGAGAGCTCGTTCATATCTCCGAGG	GAAGAGLAGATGTTCCG	1560
Db	1501	CCTCAAGAGCGGGAAGCAGAGAGCTCGTTCATATCTCCGAGG	GAAGAGLAGATGTTCCG	1560
Qy	1561	GTTTTTTTATCCGGCGCATGTGTGAAGGCTCAGAGCTTCTACT	CGGTGTGTGCTGTGCGTGGT	1620
Db	1561	GTTTTTTTATCCGGCGCATGTGTGAAGGCTCAGAGCTTCTACT	CGGTGTGTGCTGTGCGTGGT	1620
Qy	1621	GGCCCTGAAACACACTGTGTGTGGCCATGTGTGCATTACAA	CAGCGCGCGGGCTTACCAC	1680
Db	1621	GGCCCTGAAACACACTGTGTGTGGCCATGTGTGCATTACAA	CAGCGCGCGGGCTTACCAC	1680
Qy	1681	GACCTGTATTTTGCAGAGTTTGTTCCTTGGGTCTCTTCTCA	CAGAGATGCCCTGTAA	1740
Db	1681	GACCTGTATTTTGCAGAGTTTGTTCCTTGGGTCTCTTCTCA	CAGAGATGCCCTGTAA	1740
Qy	1741	GATGTATGGCTGGGGCCCAGAGACTACTTCCGGTCTCTCTCA	ACTGCTTCCACTTTGG	1800
Db	1741	GATGTATGGCTGGGGCCCAGAGACTACTTCCGGTCTCTCTCA	ACTGCTTCCACTTTGG	1800
Qy	1801	GGTCATCGTGGGAGCGCTTTTGAAGTGGTCTGGCGGCCATCA	AGCGGGAAGCTCCTT	1860
Db	1801	GGTCATCGTGGGAGCGCTTTTGAAGTGGTCTGGCGGCCATCA	AGCGGGAAGCTCCTT	1860
Qy	1861	TGGGATCAGTGTCTCGGGCGCTCCGCTGCTGAGGATCTTCAA	AGTACGAGTACTG	1920
Db	1861	TGGGATCAGTGTCTCGGGCGCTCCGCTGCTGAGGATCTTCAA	AGTACGAGTACTG	1920
Qy	1921	GAGCTCCCTCGGAACTCGTGGTGTCCCTGTGAACTCCATGA	AGTCCATCAGCCT	1980
Db	1921	GAGCTCCCTCGGAACTCGTGGTGTCCCTGTGAACTCCATGA	AGTCCATCAGCCT	1980
Qy	1981	GCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	CT	2040
Db	1981	GCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	CT	2040
Qy	2041	GGGACAGTTTCAACTTCCAGGATGAGACTCCCAACCAACTTC	CGACACCTTCCCTGCCG	2100
Db	2041	GGGACAGTTTCAACTTCCAGGATGAGACTCCCAACCAACTTC	CGACACCTTCCCTGCCG	2100
Qy	2101	CATCTCTCAGTGTCTTCAGATCTCTGACGGAGAGGAGTGA	AGTGCAGTGCAGCG	2160
Db	2101	CATCTCTCAGTGTCTTCAGATCTCTGACGGAGAGGAGTGA	AGTGCAGTGCAGCG	2160
Qy	2161	GATCGAATCCGAAGCGGCGTTCAGAAAGCAATGTTCTCGT	CT	2220
Db	2161	GATCGAATCCGAAGCGGCGTTCAGAAAGCAATGTTCTCGT	CT	2220
Qy	2221	GACACTGTTTCGGAAAATACACTCTGCTGAATGTCTTCTTG	GGCCATCGCTGTGGCAACCT	2280
Db	2221	GACACTGTTTCGGAAAATACACTCTGCTGAATGTCTTCTTG	GGCCATCGCTGTGGCAACCT	2280
Qy	2281	GGCCAAAGCCCAAGAGCTGACCAAGATGGAAGGAGATGGA	AGGAGCAGTCAATCAGAA	2340
Db	2281	GGCCAAAGCCCAAGAGCTGACCAAGATGGAAGGAGATGGA	AGGAGCAGTCAATCAGAA	2340
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Db	2341	GCTTGTCTGCAAAAGCCCAAGAGTGGCTGAAGTCAAGCTT	CGTCTGTGCGGCAACAT	2400

QY 2401 CTCATCCGCGCCAGGAGAGAGAACTCGGCGAAGAGCGCGCTCGGTGGGAGCAGCGGGC 2460
DB 2401 CTCATCCGCGCCAGGAGAGAGAACTCGGCGAAGAGCGCGCTCGGTGGGAGCAGCGGGC 2460
QY 2461 CAGCAGCTAGGCTGCAGAACCTGCGGCGCAGCTGCGAGCGCTGTACAGCGAGTGA 2520
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QY 2521 CCCGAGGAGCGGTGCGCTTCGCGCACTAGCGCGCACCTGCGGCCCCGACATGAAGACGA 2580
DB 2521 CCCGAGGAGCGGTGCGCTTCGCGCACTAGCGCGCACCTGCGGCCCCGACATGAAGACGA 2580
QY 2581 CTTGGACCGGCGCTGTGTGTGGAGCTGGGCGCGGACCGGCGCGCGGGCCCCGTGGGAGG 2640
DB 2581 CTTGGACCGGCGCTGTGTGTGGAGCTGGGCGCGGACCGGCGCGCGGGCCCCGTGGGAGG 2640
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DB 2641 CAAAGCCGACCTGAGGCTCGGAGGCCCCCGAGGGGCTCGACCTCCGCGCAGGACCA 2700
QY 2701 CCGGCACCGCGACAAGACCAAGACCCCGCGGCGGGGGAACAGACCGAGCAGAGGCCCC 2760
DB 2701 CCGGCACCGCGACAAGACCAAGACCCCGCGGCGGGGGAACAGACCGAGCAGAGGCCCC 2760
QY 2761 GAAGCGGAGAGCGGGAGCCCGGTGCCCGGAGGAGCGGCGCGCGCCGACCGCAGCCA 2820
DB 2761 GAAGCGGAGAGCGGGAGCCCGGTGCCCGGAGGAGCGGCGCGCGCCGACCGCAGCCA 2820
QY 2821 CAGCAAGAGGCGCGGGCCCCCGAGGCGCGGAGCGAGGCGGCGCGGCCCCAGGCC 2880
DB 2821 CAGCAAGAGGCGCGGGCCCCCGAGGCGCGGAGCGAGGCGGCGGCCCCAGGCC 2880
QY 2881 CGAGGCGCGCGGCGCACCAACCGCGCGCTCCCGAGGAGCGCGCCGAGCGGGAGCC 2940
DB 2881 CGAGGCGCGCGGCGCACCAACCGCGCGCTCCCGAGGAGCGCGCCGAGCGGGAGCC 2940
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DB 2941 CCGACGCCACCGCGCGCACCGCGCACCAAGGATCCGAGCAAGAGTGC CGCGCGCAGAGG 3000
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DB 3001 CGAGCGGCGCGGCGCACCGCGGCGCCCCCGAGCGGGCCCCCGGAGCGGAGAGCGG 3060
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DB 3061 GGAGAGCTCGGCGCGGCGCACCGGCGCCCCGACCAAGCGCGAGCTGCTCAACAGGCTGT 3120
QY 3121 GGAGAGGAGACCAAGAGAGGAGGCGCACCGGAGAGGCTGAGATAGTGAAGCCGA 3180
DB 3121 GGAGAGGAGACCAAGAGAGGAGGCGCACCGGAGAGGCTGAGATAGTGAAGCCGA 3180
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DB 3301 GGAACAGCCAGAGGATCAGACATCAGCGGAACGTCACCTCGCATGGGCGAGTCAGCCCCC 3360
QY 3361 AGACCCGAACACTATTGTGATATCCAGTGATGCTGACGGGCCCTCTTGGGAGGCCAC 3420
DB 3361 AGACCCGAACACTATTGTGATATCCAGTGATGCTGACGGGCCCTCTTGGGAGGCCAC 3420
QY 3421 GGTGTTCCAGTGGTAACTGGACCTGGAAAGCCAGAGAGGGGAAGAGGTTGA 3480
DB 3421 GGTGTTCCAGTGGTAACTGGACCTGGAAAGCCAGAGAGGGGAAGAGGTTGA 3480

QY 3481 AGCGGATGAGTGATGAGGAGCGGCCCCCGGCTATGCTGCCATACAGCTCCATGTTCTG 3540
DB 3481 AGCGGATGAGTGATGAGGAGCGGCCCCCGGCTATGCTGCCATACAGCTCCATGTTCTG 3540
QY 3541 TTTAAGCCCCACCAACCTGCTCCGCGCTTCTGCCACTACATGTCACCATGAGGTACTT 3600
DB 3541 TTTAAGCCCCACCAACCTGCTCCGCGCTTCTGCCACTACATGTCACCATGAGGTACTT 3600
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DB 3601 CGAGGTGGTCATTCTCGTGGTCAATCGCCTTTGAGCAGCATCGCCCTGCTGAGGACC 3660
QY 3661 AGTGGCGCAGACTCGCCCGAGGAACAACGCTCTGAATACCTGGATACATTTTCACTGG 3720
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QY 3721 TGTCTTTTACCTTTGAGATGGTATAAGATGATCGACTTTGGGACTGCTGCTTCAACCTGG 3780
DB 3721 TGTCTTTTACCTTTGAGATGGTATAAGATGATCGACTTTGGGACTGCTGCTTCAACCTGG 3780
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QY 3901 GTCTCTGAGAGTCCTTCGTGCTCGGCCCCCTCAAGACCATCAACCGGCTGCCAAGCT 3960
DB 3901 GTCTCTGAGAGTCCTTCGTGCTCGGCCCCCTCAAGACCATCAACCGGCTGCCAAGCT 3960
QY 3961 CAAAGCTGTGTTTGAAGTGTGTGTAACCTCCCTGAAGAATGCTCTCAACATCTTGATTGT 4020
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QY 4021 CTACATGCTCTTCATGTTTCAATTTGCGGCTCATTTGCGGTGAGCTCTTCAAAGGGAAGTT 4080
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QY 4081 TTTCTACTGCACAGATGAATCCAAAGAGCTGGAGAGGAGCTGCAGGGGTCAAGTATTTGGA 4140
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QY 4381 CAACATCTTTTGTGGCTTTGATCATCATCTTTCCAGGAGCAGGGGACAAGGTGATGTC 4440
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QY 4441 TGAATCGAGCTGGAGGAACGAGAGGCTTGCATTGCTCCAGTATAAGACGTGGACATTTGT 4500
DB 4429 TGAATCGAGCTGGAGGAACGAGAGGCTTGCATTGCTCCAGTATAAGACGTGGACATTTGT 4488
QY 4501 CTTGACACGCTACATGCCCCCAAAACCGGCAAGTGGTCCAGTATAAGACGTGGACATTTGT 4560
DB 4489 CTTGACACGCTACATGCCCCCAAAACCGGCAAGTGGTCCAGTATAAGACGTGGACATTTGT 4548
QY 4561 GGTCTCCCCGCCCTTTTGAATATCTTCATATGCGCATGATAGCCCTCAACTGTGTGCT 4620

Db		4549	GGTCTCCCGCCCTTTGAATACTTCATCATGGCCATGATAGCCCTCAACACATGTGGTCT	4608
Qy		4621	GATGATGAAGTCTTATGATGACCCCTATGATGAGGAGCTGATGCTGAATATGCTGAACAT	4680
Db		4609	GATGATGAAGTCTTATGATGACCCCTATGATGAGGAGCTGATGCTGAATATGCTGAACAT	4668
Qy		4681	CGTGTTCACATCCATGTTCTCCATGGAATGCGTGTGTAAGATCATCGCTTTGGGGTGTCT	4740
Db		4669	CGTGTTCACATCCATGTTCTCCATGGAATGCGTGTGTAAGATCATCGCTTTGGGGTGTCT	4728
Qy		4741	GAATATTTTACAGATGCTCTGGAATGTCTTTGATCTTTGTCACTGTGTTGGGAAGTATTAC	4800
Db		4729	GAATATTTTACAGATGCTCTGGAATGTCTTTGATCTTTGTCACTGTGTTGGGAAGTATTAC	4788
Qy		4801	TGATATTTTGTAGTAACAGAGATTGCGGAACGACAAATTTTATCAACCTCAGCTTCTCGG	4860
Db		4789	TGATATTTTGTAGTAACAGAGATTGCGGAACGACAAATTTTATCAACCTCAGCTTCTCGG	4848
Qy		4861	CTCTTTTCAGAGCTGCGCGGTGATCAAGCTGTCTCCGCAAGGCTACACCATCCGATCCT	4920
Db		4849	CTCTTTTCAGAGCTGCGCGGTGATCAAGCTGTCTCCGCAAGGCTACACCATCCGATCCT	4908
Qy		4921	CGTGTGGACCTTTGTCCAGTCTTTAAAGCCCTGACCTTACGTGTGTCTCATTTGCCAT	4980
Db		4909	CGTGTGGACCTTTGTCCAGTCTTTAAAGCCCTGACCTTACGTGTGTCTCATTTGCCAT	4968
Qy		4981	GCTGTTCTTTCATCTACGCCATCATCGGCATGAGAGTGTGGAATATTTGCCCTGGATGA	5040
Db		4969	GCTGTTCTTTCATCTACGCCATCATCGGCATGAGAGTGTGGAATATTTGCCCTGGATGA	5028
Qy		5041	TGACACAGCATCAACCGGCCAACAACTTCCGGAGCTTTTTCGAAGCCCTGATCCTGCT	5100
Db		5029	TGACACAGCATCAACCGGCCAACAACTTCCGGAGCTTTTTCGAAGCCCTGATCCTGCT	5088
Qy		5101	GTTTCAGGAGCCACGGGGAGCCCTGSCACAGATCATGCTGTCTCCTGAGCAACCA	5160
Db		5089	GTTTCAGGAGCCACGGGGAGCCCTGSCACAGATCATGCTGTCTCCTGAGCAACCA	5148
Qy		5161	GGCCTGTGATGAGCAGGCGCAATGCCACCGAGTGTGGAAGTGAATTTTGCTACTTCTACTT	5220
Db		5149	GGCCTGTGATGAGCAGGCGCAATGCCACCGAGTGTGGAAGTGAATTTTGCTACTTCTACTT	5208
Qy		5221	CGTCTCTTCTATCTTCTGTGTCTCTTTCTGATGTTGAACCTCTTTTGGTGTGATCAT	5280
Db		5209	CGTCTCTTCTATCTTCTGTGTCTCTTTCTGATGTTGAACCTCTTTTGGTGTGATCAT	5268
Qy		5281	GGACAAATTTGATGATACCTCAGCGGAGCTCTTCCATCCTTAGTCTTCCACCTTTGGATGA	5340
Db		5269	GGACAAATTTGATGATACCTCAGCGGAGCTCTTCCATCCTTAGTCTTCCACCTTTGGATGA	5328
Qy		5341	GTTTATCCGGGTCTGGGTGTAATACGACCCGGCTGCGTGTGGGGCATCAGTTACAATGA	5400
Db		5329	GTTTATCCGGGTCTGGGTGTAATACGACCCGGCTGCGTGTGGGGCATCAGTTACAATGA	5388
Qy		5401	CATGTTTGATGATGCTGAAACATGATGCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460
Db		5389	CATGTTTGATGATGCTGAAACATGATGCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5448
Qy		5461	TCGAGTTGCTTACAGCGCCCTGTTTCGATCAATGCCATCTCCACGAGGACATGAC	5520
Db		5449	TCGAGTTGCTTACAGCGCCCTGTTTCGATCAATGCCATCTCCACGAGGACATGAC	5508
Qy		5521	TGTTCACTTTCAGCTGATGGCCCTCATCCGACGSCACTGGAGATCAAGCTGGC	5580
Db		5509	TGTTCACTTTCAGCTGATGGCCCTCATCCGACGSCACTGGAGATCAAGCTGGC	5568
Qy		5581	CCCAGCTGGGAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGAGATTTCCGTTGT	5640
Db		5569	CCCAGCTGGGAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGAGATTTCCGTTGT	5628
Qy		5641	GTGGGCCAATCTGCCCCAGAGAATTTTGGATCTTCTGTATCCACCCCATTAAGCTGATGA	5700

Db		5629	GTGGGCCAATCTGCCCCAGAAAGACTTTGGACTTGTGTGTATCCACCCCATTAAGCCTGATGA	5688
Qy		5701	GATGACAGTGGGAAGGTTTATGAGCTCTGATGATATTTTGAATCTTCTACAGAGCAACAA	5760
Db		5689	GATGACAGTGGGAAGGTTTATGAGCTCTGATGATATTTTGAATCTTCTACAGAGCAACAA	5748
Qy		5761	AACACACAGAGACACAGATGACAGAGGCTCTTGGAGGCTCTCCACAGATGCTCTGTGTCT	5820
Db		5749	AACACACAGAGACACAGATGACAGAGGCTCTTGGAGGCTCTCTCCAGATGCTCTGTGTCT	5808
Qy		5821	CCTGTTTCCACCTCTGAAGGCCACCTCTGGAGCAGACACAGCCGCTGTGCTCCAGAGAGC	5880
Db		5809	CCTGTTTCCACCTCTGAAGGCCACCTCTGGAGCAGACACAGCCGCTGTGCTCCAGAGAGC	5868
Qy		5881	CCGGGTTTTTCTTCGACAGAAAGATTCCACTCTCCCTCAGCAATGGCGGGGCCATACAAA	5940
Db		5869	CCGGGTTTTTCTTCGACAGAAAGATTCCACTCTCCCTCAGCAATGGCGGGGCCATACAAA	5928
Qy		5941	CCAAGAGATGGCATCAAGAGTCTGCTCTGGGCACTTCAAGAGACCCAGATGACCC	6000
Db		5929	CCAAGAGATGGCATCAAGAGTCTGCTCTGGGCACTTCAAGAGACCCAGATGACCC	5988
Qy		6001	CCATGAGGCCAGGCCACCCCTCTGGAGCGTGGCCACTCCACAGAGATCCCTCTGGGGCGGTC	6060
Db		5989	CCATGAGGCCAGGCCACCCCTCTGGAGCGTGGCCACTCCACAGAGATCCCTCTGGGGCGGTC	6048
Qy		6061	AGGAGCACTGGCTGTGAGACGTTTCAAGATGACAGATAAACCCGAGAGGCGCTTATGAGGA	6120
Db		6049	AGGAGCACTGGCTGTGAGACGTTTCAAGATGACAGATAAACCCGAGAGGCGCTTATGAGGA	6108
Qy		6121	GCCCCAGCTCTGGCTGGAGAGCCAGGCTCGAGCGGCTCCATCCCGCCCTCTGGGGCCGA	6180
Db		6109	GCCCCAGCTCTGGCTGGAGAGCCAGGCTCGAGCGGCTCCATCCCGCCCTCTGGGGCCGA	6168
Qy		6181	GACTAGCCGCTCACAGATGCCAGCCCATGAAAGCTTCCATCTCCACGCTGCTCCAGCG	6240
Db		6169	GACTAGCCGCTCACAGATGCCAGCCCATGAAAGCTTCCATCTCCACGCTGCTCCAGCG	6228
Qy		6241	GCCCCGTGGAGCTCATCTTTTGGAGACCAACCCCGGACCCGCGACCCCTTACAGAGGCTC	6300
Db		6229	GCCCCGTGGAGCTCATCTTTTGGAGACCAACCCCGGACCCGCGACCCCTTACAGAGGCTC	6288
Qy		6301	GTCCGACACCAACCAACCGCTGCCACCGCCGAGGAGCAGGAAGCAGAGTCTCCCTGGA	6360
Db		6289	GTCCGACACCAACCAACCGCTGCCACCGCCGAGGAGCAGGAAGCAGAGTCTCCCTGGA	6348
Qy		6361	GAAGGGCCGAGCTGTCTGCGGATATGATGCGCACCAAGCAGTGTCTTGGGGCCGGG	6420
Db		6349	GAAGGGCCGAGCTGTCTGCGGATATGATGCGCACCAAGCAGTGTCTTGGGGCCGGG	6408
Qy		6421	GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGGGGGAACGAGAGCGCCGAGAGAGCG	6480
Db		6409	GCTGCCCCCGGAGAGGGGCTTACAGGCTGCGGGGGAACGAGAGCGCCGAGAGAGCG	6468
Qy		6481	GGGCGGCTCCAGGAGCGGAGCGCTTCTCTCTCTCGGAGAACGAGCGCTTCTA	6540
Db		6469	GGGCGGCTCCAGGAGCGGAGCGCTTCTCTCTCTCTCGGAGAACGAGCGCTTCTA	6528
Qy		6541	CTCTCTCGACCGCTTTTGGGGGCGGTGAGCCCGGAGCCAAAGCCCTCCCTCAGAGCCA	6600
Db		6529	CTCTCTCGACCGCTTTTGGGGGCGGTGAGCCCGGAGCCAAAGCCCTCCCTCAGAGCCA	6588
Qy		6601	CCCAAGCTCGCAACAGCTTGGCGAGCGGGAGCCCAACCCAGGAGGAGTGGTTCGT	6660
Db		6589	CCCAAGCTCGCAACAGCTTGGCGAGCGGGAGCCCAACCCAGGAGGAGTGGTTCGT	6631
Qy		6661	GAATGGAGCCCTTGTGTCAACATCTGTGTCTAGCACCCCGCGCGCTGGGGGAG	6720
Db		6632	-----	6631
Qy		6721	GCAGCTCCCCCAGAGCCCTGACTCCCCCGCCCCCAGCATCACACAGACGGCCAACTC	6780
Db		6632	-----	6631

Qy	6781	CTCACCATCCACTTCCCGGGGCTCAGACAGCCTCCCTGCTTCTCCCGAGCGGCT	6840
Db	6632	-----CAGCGCGCT	6641
Qy	6841	CAGCGTGGCTTTCGAAACACACACGCTGCTGCAGAGAGACCCCTCAGCCAGCCCT	6900
Db	6642	CAGCGTGGCTTTCGAAACACACGCTGCTGCAGAGAGACCCCTCAGCCAGCCCT	6701
Qy	6901	GGCCCTGGCTCTCGAATTGGCTCTGACCTTACTTGGGGCAGCGTCTGGACAGTGAGGC	6960
Db	6702	GGCCCTGGCTCTCGAATTGGCTCTGACCTTACTTGGGGCAGCGTCTGGACAGTGAGGC	6761
Qy	6961	CTCTGTCCACGCGCTGCTGAGGACACGCTCACTTTTCGAGAGGCTGTGGCCACCAACTC	7020
Db	6762	CTCTGTCCACGCGCTGCTGAGGACACGCTCACTTTTCGAGAGGCTGTGGCCACCAACTC	6821
Qy	7021	GGGCGGCTCTCCAGGACTTCTACGTGTCTCTCCCTGACCTCCAGTCTCACCTCTCCG	7080
Db	6822	GGGCGGCTCTCTCCAGGACTTCTACGTGTCTCTCCCTGACCTCCAGTCTCACCTCTCCG	6881
Qy	7081	CCGCGTCCCAACGGTTTACCACCTGCACCTGGGACTCAGCTCGGGTGGCCGAGCAGCGCA	7140
Db	6882	CCGCGTCCCAACGGTTTACCACCTGCACCTGGGACTCAGCTCGGGTGGCCGAGCAGCGCA	6941
Qy	7141	CAGTACCAACCCCTCAGCAAGACCACTGGTGTAGCTGCACCGTGACCGCTCAGACGC	7200
Db	6942	CAGTACCAACCCCTCAGCAAGACCACTGGTGTAGCTGCACCGTGACCGCTCAGACGC	7001
Qy	7201	CTGCATCAGCAGCGGTGTTCAGTGGATGAGTTTATCATCCACAGGGGAGTCCG	7260
Db	7002	CTGCATCAGCAGCGGTGTTCAGTGGATGAGTTTATCATCCACAGGGGAGTCCG	7061
Qy	7261	CCCTCGGGGAGGCTTGGCCACCTTGGTGAGGCTCTGTGGCCCTCCCTCCCGCTCTCT	7320
Db	7062	CCCTCGGGGAGGCTTGGCCACCTTGGTGAGGCTCTGTGGCCCTCCCTCCCGCTCTCT	7121
Qy	7321	CCCTCTTTTACTTAGACGACGAATAAGCCCTGTGTGCTGTAGTGTACGTACCGC	7376
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Human calcium channel compositions and methods			
JOURNAL			
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Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;			
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Db	1	GCGCGCGGCTGCGGGGTGGGCGCGGAGGTCCG-TGCGGTCCCGGCGGCTCCGCTG	59
Qy	61	GCTGCTCGGCTGAGGCGCTTGGGCGCGCGCGCGCTCCCTGCGGGGCGGCTGGGCGG	120

Db	60	GCTGCTCGGCTGTGAGGCGCTT-GGGCGCGCGCGCGCGCTCCCTGCGGGGCGGCTGGGCGG	118
Qy	121	GGGATGCACGCGGGGCGCGGAGCCATGTGTCGCTTCGGGGACGAGCTGGGCGGCGCTA	180
Db	119	GGGATGCACGCGGGGCGCGGAGCCATGTGTCGCTTCGGGGACGAGCTGGGCGGCGCTA	178
Qy	181	TGAGGCGCGCGGGGCGGAGGCGGCGCGGGGCGGCGGGGCGGCGGGGCGGCGGCGG	240
Db	179	TGAGGCGCGCGGGGCGGAGGCGGCGCGGGGCGGCGGGGCGGCGGGGCGGCGGCGG	238
Qy	241	GGGTCCCGGGGGGCTGCAGCGCGCGGCGGCGGGGCTCTTACAAGCAATCGATCGCGAGCG	300
Db	239	GGGTCCCGGGGGGCTGCAGCGCGCGGCGGCGGGGCTCTTACAAGCAATCGATCGCGAGCG	298
Qy	301	CGGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGTTCACCGTCAA	360
Db	299	CGGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGTTCACCGTCAA	358
Qy	361	CGGCTGCTCTTGTTCAGCGAGGACACGTCGTCCGCAAAATACGCGAAGCGCATCAC	420
Db	359	CGGCTGCTCTTGTTCAGCGAGGACACGTCGTCCGCAAAATACGCGAAGCGCATCAC	418
Qy	421	CGAGTGGCTTCCATTCGAGTATATGATCTTGGCCACCATCATCGCCAACTGCAATCGTCT	480
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Qy	481	GGCCCTGGAGCAGCACCTCCCTGATGGGACAAAACGCGCATGTCCGAGCGGCTGACGA	540
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Qy	541	CAGGAGCGCTATTTTTCATCGGGATCTTTTTCGAGGCGAGGATCAAAATCATCGCTCT	600
Db	539	CAGGAGCGCTATTTTTCATCGGGATCTTTTTCGAGGCGAGGATCAAAATCATCGCTCT	598
Qy	601	GGCTTTGCTTCCACAAAGGCTCTTACCTCGCGAACGCGTGAACCTCATGACATTCGT	660
Db	599	GGCTTTGCTTCCACAAAGGCTCTTACCTCGCGAACGCGTGAACCTCATGACATTCGT	658
Qy	661	GGTCTGCTCCTCAGAGGATCCTTGCACGCGTGGAACTGACTTCGACCTCGAAACACTGAG	720
Db	659	GGTCTGCTCCTCAGAGGATCCTTGCACGCGTGGAACTGACTTCGACCTCGAAACACTGAG	718
Qy	721	GGCTGCTGCTGCTGAGGCGCTTGAAGCTGTGTCTGGGATTCGAGTTTTCAGGTTGAGTGGT	780
Db	719	GGCTGCTGCTGCTGAGGCGCTTGAAGCTGTGTCTGGGATTCGAGTTTTCAGGTTGAGTGGT	778
Qy	781	GCTCAAGTCCATCATGAAGGCGCTTCCACCTCGCAGATTTGGGCTGCTCTTCTTCTT	840
Db	779	GCTCAAGTCCATCATGAAGGCGCTTCCACCTCGCAGATTTGGGCTGCTCTTCTTCTT	838
Qy	841	TGCGCATCCTCATGTTTGGCATCATTTGGCTTGGAGTTCTACATGGGCAAGTTTCCACAAAGC	900
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Qy	901	CTGTTTTCCTCCAAACAGACAGATCGGAGCGCGGTGGGTGACTTCCCTGTGGCAAGGAGGC	960
Db	899	CTGTTTTCCTCCAAACAGACAGATCGGAGCGCGGTGGGTGACTTCCCTGTGGCAAGGAGGC	958
Qy	961	CCGAGCGGCTGCTGCGAGGCGCACCTGAGTCCCGGAGTACTTGGCCAGACCCCAACTT	1020
Db	959	CCGAGCGGCTGCTGCGAGGCGCACCTGAGTCCCGGAGTACTTGGCCAGACCCCAACTT	1018
Qy	1021	TGGCATCACCAACTTTTGACAATATCTGTTTGGCATCTTTCAGCGGTGTTCCAGTGCATCAC	1080
Db	1019	TGGCATCACCAACTTTTGACAATATCTGTTTGGCATCTTTCAGCGGTGTTCCAGTGCATCAC	1078
Qy	1081	CATGAGGGGTGAGTGCATCTCTATATAAATAAAGATGCGGCGCGCAACCTTGGAA	1140
Db	1079	CATGAGGGGTGAGTGCATCTCTATATAAATAAAGATGCGGCGCGCAACCTTGGAA	1138
Qy	1141	CTGGCTCTACTTCTCATCTCTCATCATCGCTCTTCTTCTTCTCATCTCAACCTGGTCT	1200
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Qy	1201	GGGCGTGTCTCTCGGGGAGTTTGCCAAAGACGAGAGAGGGTGCAGAAACCGCCGCGCTT	1261
Db	1199	GGGCGTGTCTCTCGGGGAGTTTGCCAAAGACGAGAGAGGGTGCAGAAACCGCCGCGCTT	1258
Qy	1261	CCTGAAGTGTCCGCGGCAGCAGCAGATCAGCGAGAGCTCAACGGGTACCTTGGAGTGGAT	1320
Db	1259	CCTGAAGTGTCCGCGGCAGCAGCAGATCAGCGAGAGCTCAACGGGTACCTTGGAGTGGAT	1318
Qy	1321	CTTCAAGCGCGAGGAAGTCATGCTTGGCCGAGGAGCAGGAATCCAGAGGAAGTCCCC	1380
Db	1319	CTTCAAGCGCGAGGAAGTCATGCTTGGCCGAGGAGCAGGAATCCAGAGGAAGTCCCC	1378
Qy	1381	TTTGGACGTGTGAAGAGAGCGGCCAACAAAGACGAGAAATGACCTGATCCACGCAGA	1440
Db	1379	TTTGGACGTGTGAAGAGAGCGGCCAACAAAGACGAGAAATGACCTGATCCACGCAGA	1438
Qy	1441	GGAGGGAGAGACCGGTTTGAGATCTCTGTGTCTGTGTGGATCCCCCTTCGCCCGCGCCAG	1500
Db	1439	GGAGGGAGAGACCGGTTTGAGATCTCTGTGTCTGTGTGGATCCCCCTTCGCCCGCGCCAG	1498
Qy	1501	CCTCAAGACGGGAAGACAGAGAGCTCGTCATCTCCGGAGGAAGCAGGAAGATGTTCCG	1560
Db	1499	CCTCAAGACGGGAAGACAGAGAGCTCGTCATCTCCGGAGGAAGCAGGAAGATGTTCCG	1558
Qy	1561	GTTTTTTATCCGGCGCATGTGTGAAGGTCAGAGCTTCTACTCTGGGTGGTGTGTCGTGGT	1620
Db	1559	GTTTTTTATCCGGCGCATGTGTGAAGGTCAGAGCTTCTACTCTGGGTGGTGTGTCGTGGT	1618
Qy	1621	GGCCCTCAACACACTGTGTGGCCATGTGTGCATTACAAACGCGCGCGGCTTACCAC	1680
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Qy	1921	GAGCTCCCTCGGAACTCGTGTGTGTCCCTGTCTGAATCCATGAAGTCCATCATCAGCT	1980
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Qy	2041	GGGACAGTTTCAACTCCAGATGAGACTCCCAACCAACTTTCGACACCTTCCCTGCGCG	2100
Db	2039	GGGACAGTTTCAACTCCAGATGAGACTCCCAACCAACTTTCGACACCTTCCCTGCGCG	2098
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Db	2879	CGAGGGCGCGCGCGGACCAACCGGCGCGCTCCCGGAGGAGGCGGCGCGAGCGCGGAGCC	2938
QY	2941	CCGACGCCACCGCGCACAACCGGACCAAGGATCCGAGCAAGGAGTGCCTCGCGCGCAAGGG	3000
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QY	3061	GGAGGAGCGCGCGCGCGCACAACCGGCGCGCGCACAAGGCGAGCTGCTCAGAGGCTGT	3120
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Qy
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ACCESSION AR063883
VERSION AR063883.1 GI:5993191
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7175)
AUTHORS Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
TITLE Human calcium channel .alpha. .sub.1. .alpha. .sub.2. and .beta.
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ORIGIN

Query Match 94.0%; Score 6932.4; DB 6; Length 7175;
Best Local Similarity 97.3%; Pred. No. 0;

Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;			
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Db	60	GCTGCTCCGCTCTGAGCGCTT-GCGCGCGCGCGGCTTCCCTGCGCGGCGCTGGGCGG	118
Qy	121	GGGATGACGCGGCGCGCGGAGCATTGTCGCTTCGGGACAGACTGGGCGGCGCCTA	180
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Qy	421	CGAGTGCCTCCATTCGAGTATATGATCTTGGCCACCATCATGTCGCAACTGCTGCT	480
Db	419	CGAGTGCCTCCATTCGAGTATATGATCTTGGCCACCATCATGTCGCAACTGCTGCT	478
Qy	481	GGCCTCGAGCAGCACCTCCCTGATGGGACAAACGCCATGTCGAGCGGCTGGACGA	540
Db	479	GGCCTCGAGCAGCACCTCCCTGATGGGACAAACGCCATGTCGAGCGGCTGGACGA	538
Qy	541	CACGAGCCCTATTTCATCGGGATCTTTTGTCTCGAGCGAGGATCAAAATCATCGCTCT	600
Db	539	CACGAGCCCTATTTCATCGGGATCTTTTGTCTCGAGCGAGGATCAAAATCATCGCTCT	598
Qy	601	GGGCTTGTCTTCCAAAGGGCTTTACCTGCGGAAACGGCTGGAAACGTATGACATTCGT	660
Db	599	GGGCTTGTCTTCCAAAGGGCTTTACCTGCGGAAACGGCTGGAAACGTATGACATTCGT	658
Qy	661	GGTGGCTTCCACAGGGATCCTTGGCCACGGCTGGAACTGACTTCGACCTGCGAACACTG	720
Db	659	GGTGGCTTCCACAGGGATCCTTGGCCACGGCTGGAACTGACTTCGACCTGCGAACACTG	718
Qy	721	GGCTGTGCGTGTGCTGAGGCGCCCTGAAAGCTGGTGTCTGGGATTCAAAGTTTGCAGGTGGT	780
Db	719	GGCTGTGCGTGTGCTGAGGCGCCCTGAAAGCTGGTGTCTGGGATTCAAAGTTTGCAGGTGGT	778
Qy	781	GCTCAAGTCCATATGAAGCCATGTTTCCATCCTCTGAGATTGGGCTGCTTCTTCTT	840
Db	779	GCTCAAGTCCATATGAAGCCATGTTTCCATCCTCTGAGATTGGGCTGCTTCTTCTT	838
Qy	841	TGCCATCCTCATGTTTGGCCATCATTCGCTGGAGTTCTACATGGCAAGTTCCACAGGC	900
Db	839	TGCCATCCTCATGTTTGGCCATCATTCGCTGGAGTTCTACATGGCAAGTTCCACAGGC	898
Qy	901	CTGTTTCCCAACAGCAGATGCGGAGCCCGTGGGTGACTTCCCTCTGTGGCAAGGAGGC	960
Db	899	CTGTTTCCCAACAGCAGATGCGGAGCCCGTGGGTGACTTCCCTCTGTGGCAAGGAGGC	958
Qy	961	CCCAGCCCGGTGTCGAGGCGCAGACTGAGTGCAGGAGTACTGGCCAGGACCCAACTT	1020
Db	959	CCCAGCCCGGTGTCGAGGCGCAGACTGAGTGCAGGAGTACTGGCCAGGACCCAACTT	1018
Qy	1021	TGGCATCACCAACTTTCACATATCCTGTTGGCATCTTGAACGTTTCCAGTGCATCAC	1080
Db	1019	TGGCATCACCAACTTTCACATATCCTGTTGGCATCTTGAACGTTTCCAGTGCATCAC	1078

Qy	1081	CATGGAGGGCTGGACTGAACATCTCTATATAAACAACGATGCGGCGGCAACCTGGAA	1140
Db	1079	CATGGAGGGCTGGACTGAACATCTCTATATAAACAACGATGCGGCGGCAACCTGGAA	1138
Qy	1141	CTGGCTCTACTTTCATCCCTCTCATCATCGGCTCTTCTTCTATGCTCAACCTGGTGT	1200
Db	1139	CTGGCTCTACTTTCATCCCTCTCATCATCGGCTCTTCTTCTATGCTCAACCTGGTGT	1198
Qy	1201	GGCGCTGCTCTCGGGGGAGTTTCCAAAGAGCGAGAGGGTGGAGAACCGCGCGCTT	1260
Db	1199	GGCGCTGCTCTCGGGGGAGTTTCCAAAGAGCGAGAGGGTGGAGAACCGCGCGCTT	1258
Qy	1261	CCTGAAGCTGCGCGCGGAGCGAGAGATCGAGCGAGAGCTCAACGGGTACTCTGAGTGGAT	1320
Db	1259	CCTGAAGCTGCGCGCGGAGCGAGAGATCGAGCGAGAGCTCAACGGGTACTCTGAGTGGAT	1318
Qy	1321	CTTCAAGCGGAGGAAGTCAATGCTGCGCGGAGGACAGGAATGCAGAGAGAGTCCCC	1380
Db	1319	CTTCAAGCGGAGGAAGTCAATGCTGCGCGGAGGACAGGAATGCAGAGAGAGTCCCC	1378
Qy	1381	TTTGGACGTGCTGAAGAGAGCGGCCAACAAAGAGACAGAAATGACCTGATCCACGAGA	1440
Db	1379	TTTGGACGTGCTGAAGAGAGCGGCCAACAAAGAGAGAGAAATGACCTGATCCACGAGA	1438
Qy	1441	GGAGGAGAGGACCGGTTTGCAGATCTCTGTGCTGTGGATCCCTTTCGCCCGCGCAG	1500
Db	1439	GGAGGAGAGGACCGGTTTGCAGATCTCTGTGCTGTGGATCCCTTTCGCCCGCGCAG	1498
Qy	1501	CCTCAAGCGGGAACACAGAGAGCTGTCATACTTCCGGAGGAAGAGAGATGTCG	1560
Db	1499	CCTCAAGCGGGAACACAGAGAGCTGTCATACTTCCGGAGGAAGAGAGATGTCG	1558
Qy	1561	GTTTTTTATCCGCGCATGTTGAAGCTCAGAGCTTCTACTGGGTGGTGTGCTGCGTGGT	1620
Db	1559	GTTTTTTATCCGCGCATGTTGAAGCTCAGAGCTTCTACTGGGTGGTGTGCTGCGTGGT	1618
Qy	1621	GGCCCTGAAACACACTGTGTGTGGCCATGTFGCAATTAACAACGCGCGCGGCTTACAC	1680
Db	1619	GGCCCTGAAACACACTGTGTGTGGCCATGTFGCAATTAACAACGCGCGCGGCTTACAC	1678
Qy	1681	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTCCTCACAGAGATGTCCTGAA	1740
Db	1679	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTCCTCACAGAGATGTCCTGAA	1738
Qy	1741	GATGTATGGCTCGGCGCCACAGAGTACTTCCGGTCTCTCTCAACTGCTTCGACTTTGG	1800
Db	1739	GATGTATGGCTCGGCGCCACAGAGTACTTCCGGTCTCTCTCAACTGCTTCGACTTTGG	1798
Qy	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGCGGCGCATCAAGCGGGAAGCTCTT	1860
Db	1799	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGCGGCGCATCAAGCGGGAAGCTCTT	1858
Qy	1861	TGGGATCAGTGTCTCGGGCCCTCGCGCTGTGAGGATCTTCAAAGTCAAGTACTG	1920
Db	1859	TGGGATCAGTGTCTCGGGCCCTCGCGCTGTGAGGATCTTCAAAGTCAAGTACTG	1918
Qy	1921	GAGCTCCCTCGGAACTCGTGGTGTCTCTGCTGAACTCCATGAAGTCCATCATCAGCCT	1980
Db	1919	GAGCTCCCTCGGAACTCGTGGTGTCTCTGCTGAACTCCATGAAGTCCATCATCAGCCT	1978
Qy	1981	GCTCTTCTTGTCTTCTCTTCAATGTTGTCTTTCGCCCTGCTGGGATCAGCTGTTGG	2040
Db	1979	GCTCTTCTTGTCTTCTCTTCAATGTTGTCTTTCGCCCTGCTGGGATCAGCTGTTGG	2038
Qy	2041	GGGACAGTTCAACTTCCAGATGAGACTCCCAACAACCTTCGACACTTCCCTGCCG	2100
Db	2039	GGGACAGTTCAACTTCCAGATGAGACTCCCAACAACCTTCGACACTTCCCTGCCG	2098
Qy	2101	CATCTCACCTGCTTCCAGATCCTGAGGAGAGGACTGGAATGCAAGTATGATCACGG	2160
Db	2099	CATCTCACCTGCTTCCAGATCCTGAGGAGAGGACTGGAATGCAAGTATGATCACGG	2158

QY	2161	GATCGAATCGCAAGCGGGTTCAGCAAGGCATGTTCTCGTCTCTTTACTTTACTTTGTCCT	2220
Db	2159	GATCGAATCGCAAGCGGGTTCAGCAAGGCATGTTCTCGTCTCTTTACTTTACTTTGTCCT	2218
QY	2221	GACACTGTTTCGGAAATACACTCTGCTGTAATGTCCTTTCTGGCATCGCTGTGGACAACCT	2280
Db	2219	GACACTGTTTCGGAAATACACTCTGCTGTAATGTCCTTTCTGGCATCGCTGTGGACAACCT	2278
QY	2281	GGCCAAACGCCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAGAGCAGGCAATCAGAA	2340
Db	2279	GGCCAAACGCCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAGAGCAGGCAATCAGAA	2338
QY	2341	GCTTGCTCTGCAAAAGGCCAAAGAAAGTGTGAAGTCAGCCCCCATGTCTGCGCGCAACAT	2400
Db	2339	GCTTGCTCTGCAAAAGGCCAAAGAAAGTGTGAAGTCAGCCCCCATGTCTGCGCGCAACAT	2398
QY	2401	CTCCATCGCGCCGAGCAGCAGCAATCGCGCCCAAGCGCGCTCGGTGTGGAGCAGCGGGC	2460
Db	2399	CTCCATCGCGCCGAGCAGCAGCAATCGCGCCCAAGCGCGCTCGGTGTGGAGCAGCGGGC	2458
QY	2461	CAGCCAGCTACGGCTCGAGAACCTCGCGGCCAGCTGCGAGGGCGCTGTACAGCGAGATGGA	2520
Db	2459	CAGCCAGCTACGGCTCGAGAACCTCGCGGCCAGCTGCGAGGGCGCTGTACAGCGAGATGGA	2518
QY	2521	CCCCGAGGAGCGGCTCGCTTCGCCACTACGCGCCACTGCGGCCCGCATGNAAGCGCA	2580
Db	2519	CCCCGAGGAGCGGCTCGCTTCGCCACTACGCGCCACTGCGGCCCGCATGNAAGCGCA	2578
QY	2581	CTTGGAACCGGCGCTGGTGGTGGAGCTGGGCGCGCAACGCGCGCGCGGGGCCCGTGGAGG	2640
Db	2579	CTTGGAACCGGCGCTGGTGGTGGAGCTGGGCGCGCAACGCGCGCGCGGGGCCCGTGGAGG	2638
QY	2641	CAAAGCCGACCTGAGGCTGCGAGGCGCCCGCGAGGGCGTGCACCTCCGCGCAGGACCA	2700
Db	2639	CAAAGCCGACCTGAGGCTGCGAGGCGCCCGCGAGGGCGTGCACCTCCGCGCAGGACCA	2698
QY	2701	CCGGCACCCGACAGGAACAAGCCCGCGCGCGGGGACAGGACCCAGCAGAGGCGCCC	2760
Db	2699	CCGGCACCCGACAGGAACAAGCCCGCGCGCGGGGACAGGACCCAGCAGAGGCGCCC	2758
QY	2761	GAAGCGGAGAGCGGGAGCGCGGTCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG	2820
Db	2759	GAAGCGGAGAGCGGGAGCGCGGTCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG	2818
QY	2821	CAGCAAGAGGCGCGGGCGCCCGGAGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG	2880
Db	2819	CAGCAAGAGGCGCGGGCGCCCGGAGGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG	2878
QY	2881	CGAGGCG	2940
Db	2879	CGAGGCG	2938
QY	2941	CCGAGCGCACCGCGCGCACCGGACACAGATCCGAGCAAGAGTGCAGCGCGCGCGCGCGCGG	3000
Db	2939	CCGAGCGCACCGCGCGCACCGGACACAGATCCGAGCAAGAGTGCAGCGCGCGCGCGCGCGG	2998
QY	3001	CGAGCGCGCGCGCGCGCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG	3060
Db	2999	CGAGCGCGCGCGCGCGCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG	3058
QY	3061	GGAGGAGCGCGCGCGCGCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGT	3120
Db	3059	GGAGGAGCGCGCGCGCGCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGT	3118
QY	3121	GGAGAGGAGACCAAGAGAGGAGGCCACCGAGAGAGGAGGCTGAGATAGTGGAGCGCGA	3180
Db	3119	GGAGAGGAGACCAAGAGAGGAGGCCACCGAGAGAGGAGGCTGAGATAGTGGAGCGCGA	3178
QY	3181	CAAGGAAAGAGGCTCCGGAACCAAGCCCGGAGGACCACTGTGTGACCTTGGAGACCGAG	3240
Db	3179	CAAGGAAAGAGGCTCCGGAACCAAGCCCGGAGGACCACTGTGTGACCTTGGAGACCGAG	3238
QY	3241	TGGGACTGTGACTGTGGGTCCCATGTCACACTGCCGAGCACCTGTCTCCAGAGAGGTGGA	3300

Db	3239	TGGGACTGTGACTGTGGGTCCCATGTCACACTGCCGAGCACCTGTCTCCAGAGAGGTGGA	3298
QY	3301	GGAAACAGCAGAGGATGAGACAATCAGCGGAAAGTCACTCGCATGGCGTGTGACGCCCCC	3360
Db	3299	GGAAACAGCAGAGGATGAGACAATCAGCGGAAAGTCACTCGCATGGCGTGTGACGCCCCC	3358
QY	3361	AGACCCGAACACTATGTCATATCCCAAGTATGCTGACGGGCCCTCTTGGGGAAGCCAC	3420
Db	3359	AGACCCGAACACTATGTCATATCCCAAGTATGCTGACGGGCCCTCTTGGGGAAGCCAC	3418
QY	3421	GGTCGTTCCCAAGTATGTCATATCCCAAGTATGTCGAGGGGCCCTCTTGGGGAAGCCAC	3480
Db	3419	GGTCGTTCCCAAGTATGTCATATCCCAAGTATGTCGAGGGGCCCTCTTGGGGAAGCCAC	3478
QY	3481	AGCCGATGACGTATGAGGAGCGGCCCGCGGCTATCGTCCCATACAGTCTCATGTTCTG	3540
Db	3479	AGCCGATGACGTATGAGGAGCGGCCCGCGGCTATCGTCCCATACAGTCTCATGTTCTG	3538
QY	3541	TTTAAGCCCCACCAACCTGCTCCGCGCTTCTGCACTATCATCGTGACCATGAGGTACTT	3600
Db	3539	TTTAAGCCCCACCAACCTGCTCCGCGCTTCTGCACTATCATCGTGACCATGAGGTACTT	3598
QY	3601	CGAGGTGGTCAATTCCTGCTGCTCATCGCTTTGAGCAGCATCGCCCTGCTGCTGAGGACCC	3660
Db	3599	CGAGGTGGTCAATTCCTGCTGCTCATCGCTTTGAGCAGCATCGCCCTGCTGCTGAGGACCC	3658
QY	3661	AGTCGCGACAGACTCGCCAGGAAACACGCTCTGAAATACCTGGATTACAATTTCTACTGG	3720
Db	3659	AGTCGCGACAGACTCGCCAGGAAACACGCTCTGAAATACCTGGATTACAATTTCTACTGG	3718
QY	3721	TGCTTTTACCTTTGAGATGTTGAAACATTTCTGGACTTCATTGTTGTTGTTGTTGTTGTTG	3780
Db	3719	TGCTTTTACCTTTGAGATGTTGAAACATTTCTGGACTTCATTGTTGTTGTTGTTGTTGTTG	3778
QY	3781	AGCCTATTTCCGGGACTTTGGAACATTTCTGGACTTCATTGTTGTTGTTGTTGTTGTTGTTG	3840
Db	3779	AGCCTATTTCCGGGACTTTGGAACATTTCTGGACTTCATTGTTGTTGTTGTTGTTGTTGTTG	3838
QY	3841	GGCGTTTGTCTTCTCGAGCTTCGTTGGAGGATCCAAAGGGAAGACATCAATACCATCAA	3900
Db	3839	GGCGTTTGTCTTCTCGAGCTTCGTTGGAGGATCCAAAGGGAAGACATCAATACCATCAA	3886
QY	3901	GTCTCTGAGAGTCTTCTGTTCTCTGCGGCCCTCAAGACCATCAACGGGCTGCCCAAGCT	3960
Db	3887	GTCTCTGAGAGTCTTCTGTTCTCTGCGGCCCTCAAGACCATCAACGGGCTGCCCAAGCT	3946
QY	3961	CAAGGCTGTTTGTGACTGTGTGTGAACTCCCTCGAAGAAATGTCCTCAACAATCTTGATTGT	4020
Db	3947	CAAGGCTGTTTGTGACTGTGTGTGAACTCCCTCGAAGAAATGTCCTCAACAATCTTGATTGT	4006
QY	4021	CTACATGCTCTTCTCATGTTTCAATTTTTCGGTCAATTTGCGGTGTCAGCTCTTCAAGGGAGTT	4080
Db	4007	CTACATGCTCTTCTCATGTTTCAATTTTTCGGTCAATTTGCGGTGTCAGCTCTTCAAGGGAGTT	4066
QY	4081	TTTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGAGGAGCTGAGGGGTCGATTTTGA	4140
Db	4067	TTTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGAGGAGCTGAGGGGTCGATTTTGA	4126
QY	4141	TTATGAGAGGAGGAGTGGAGCTCAGCCAGGCGAGTGGAGAAATACGATTTTCACTA	4200
Db	4127	TTATGAGAGGAGGAGTGGAGCTCAGCCAGGCGAGTGGAGAAATACGATTTTCACTA	4186
QY	4201	CGACAATGTGCTTGGGCTCTGCTGACGCTGTTCACAGTGTCCACGGGAGAGGCTGGCC	4260
Db	4187	CGACAATGTGCTTGGGCTCTGCTGACGCTGTTCACAGTGTCCACGGGAGAGGCTGGCC	4246
QY	4261	CATGTTGCTGAAACACTCCGTTGGATGCCACCTATGAGGAGCAGGGTCCCAAGCCTTGGA	4320
Db	4247	CATGTTGCTGAAACACTCCGTTGGATGCCACCTATGAGGAGCAGGGTCCCAAGCCTTGGA	4306
QY	4321	CCGATGAGGAGTGTCCATCTTCTACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	4380

Db 4307 CCGATGGAGCTGTCATCTTTACGTGGTCTACTTTGTGGTCTTTCCCTCTTCTTCTCGT 4366
Qy 4381 CAACATCTTTGTGGCTTTGTATCATCATCACTTCCAGGAGCAGGGGACAAAGTGTATGTC 4440
Db 4367 CAACATCTTTGTGGCTTTGTATCATCATCACTTCCAGGAGCAGGGGACAAAGTGTATGTC 4426
Qy 4441 TGAATGAGCTTGAGAAAGAACGAGAGGGCTTGTGATTTGACTTGGCCATCAGCGCCAAACC 4500
Db 4427 TGAATGAGCTTGAGAAAGAACGAGAGGGCTTGTGATTTGACTTGGCCATCAGCGCCAAACC 4486
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Db 4487 CCTGACACGTTACATGCTCCCAAAACCGGCAGTCTTCCAGTATTAAGACGTGGACATTTGT 4546
Qy 4561 GGTCTCCCGCCCTTTGAATACCTTCATATGGCCATGATAGCCCTCAACACTGTGTGCT 4620
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Db 4607 GATGATGAAGTCTATGATGACCCCTATGATGATGATGATGATGATGATGATGATGATGAT 4666
Qy 4681 CGTGTTCACATCCATGTTCTCCATGGAATGCTGCTGAAGATCATGSCCTTTTGGGGTGTCT 4740
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Qy 4741 GAACTATTTTCAGAGATGCTTGAATGTCTTTGACTTTGTCACTGTGTGTGGGAAGTATTAC 4800
Db 4727 GAACTATTTTCAGAGATGCTTGAATGTCTTTGACTTTGTCACTGTGTGTGGGAAGTATTAC 4786
Qy 4801 TGATATTTTATAGTAACAGAGATTTGCGGAAACGAAACAAATTTTCATCAACCTCAGCTTCCTCCG 4860
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Db 5567 CCAGCTGGGACAAAACGAGCATCAGTGTGACGCGGAGTTGAGGAAGAGATTTCCGTTGT 5626
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7175)
AUTHORS Harpold,M.M., Ellis,S.B., Williams,M.E., Feldman,D.H., McCue,A.F.
and Brenner,R.
TITLE Human calcium channel .alpha.-1C/.alpha.-1D, .alpha.-2, .beta.-1,
and .gamma.subunits and cells expressing the DNA
JOURNAL Patent: US 5851824-A 8 22-DEC-1998;

FEATURES
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Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Query Match
Best Local Similarity 94.0%; Score 6932.4; DB 6; Length 7175;
Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;
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Db	5627	GTGGGCCAAATCTGCCCCAGAAAGACTTTGGACTTGTCTGATACCAACCCCATTAAGCCTGATGA	5686
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Db	5687	GATGACAGTGGGGAAGTTTATGACGCTCTGATGATATTTGACTTCTTACAAAGCAGAACAA	5746
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Db	5747	AACACACAGAGACCATGACGAGGCTCTGGAGGCTCTCCAGATGGTCTCTGTGTC	5806
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Qy	6181	GACTCAGCCGCTCAGATGCCAGCCCATCAAGCGCTTCCATCTCCACGCTGGGCCAGCG	6240
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Qy	6241	GGCCCGTGGGACTCATCTTTGACACACCCCGGACCCGCCATCCCTAGCCAGCGCTC	6300
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Qy	6661	GAATGGGAGCCCTTGTCTGAACATCTGTGTAGTACACCCCGCGCGGTGGGGGAG	6720
Db	6630	-----	6629
Qy	6721	GCAGTCTCCCAAGACGCGCCCTGTACTCCCGCCGCCAGCATCATCTACAAGACGGCCAACTC	6780
Db	6630	-----	6629
Qy	6781	CTCACCCATCCATTTCGCGGGGCTCAGACCAGCTTCCCTGCTTCTCCCAAGCCGGCT	6840
Db	6630	-----	6639
Qy	6841	CAGCCGTGGGCTTTCCGAACACAAACCGCTGTGTCAGAGAGACCCCTCAGCCAGGCCCCCT	6900
Db	6640	CAGCCGTGGGCTTTCCGAACACAAACCGCTGTGTCAGAGAGACCCCTCAGCCAGGCCCCCT	6699
Qy	6901	GGCCCTTGGCTCTCGAATTTGGCTCTGACCTTACCTTGGGGCAGGCTTGACAGTGAAGC	6960
Db	6700	GGCCCTTGGCTCTCGAATTTGGCTCTGACCTTACCTTGGGGCAGGCTTGACAGTGAAGC	6759
Qy	6961	CTCTGTCCAGCCCTGCTGAGGACAGCGCTCACTTTCGAGGAGGCTTGCCACCACTC	7020
Db	6760	CTCTGTCCAGCCCTGCTGAGGACAGCGCTCACTTTCGAGGAGGCTTGCCACCACTC	6819
Qy	7021	GGGCGCTCTCCAGGACTTCTACGCTGTCTCCCTGACCTCCAGTCTCACCTCTCTCCG	7080
Db	6820	GGGCGCTCTCTCCAGGACTTCTACGCTGTCTCCCTGACCTCCAGTCTCACCTCTCTCCG	6879
Qy	7081	CCGCGTCCCAACCGTTTACCACTGCAACCTTGGGACTCAGCTCGGGTGGCGAGCAGGCA	7140
Db	6880	CCGCGTCCCAACCGTTTACCACTGCAACCTTGGGACTCAGCTCGGGTGGCGAGCAGGCA	6939
Qy	7141	CAGCTACCAACCCCTGACCAAGACCACTGGTGTCTAGCTGCAACGCTGACCGCTCAGACGC	7200
Db	6940	CAGCTACCAACCCCTGACCAAGACCACTGGTGTCTAGCTGCAACGCTGACCGCTCAGACGC	6999
Qy	7201	CTGCATGACGAGCGGTGTTCCAGTGGATGATGTTTTTATCATCCACACGGGGCAGTCCG	7260
Db	7000	CTGCATGACGAGCGGTGTTCCAGTGGATGATGTTTTTATCATCCACACGGGGCAGTCCG	7059
Qy	7261	CCCTCGGGGAGGCTTGGCCACCTTGGTGAAGCTCTCTGTGGCCCTTCCCTCCCTCTCT	7320
Db	7060	CCCTCGGGGAGGCTTGGCCACCTTGGTGAAGCTCTCTGTGGCCCTTCCCTCCCTCTCT	7119
Qy	7321	CCCTCTTTTACTCTAGACGACGAATAAAGCCCTTGTGTTGAGTGTAGTACGCGC	7376
Db	7120	CCCTCTTTTACTCTAGACGACGAATAAAGCCCTTGTGTTGAGTGTAGTACGCGC	7175

Search completed: September 26, 2004, 22:19:17
Job time : 18363 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: September 26, 2004, 03:06:37 ; Search time 1700 Seconds
(without alignments)
18432.182 Million cell updates/sec

Title: US-10-033-026-3
Perfect score: 7376
Sequence: 1 gggcgccgctgcggcggt.....tgcttgagtgctaccgc 7376

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N_Geneseq_29Jan04.*
- 1: Geneseqn1980s.*
 - 2: Geneseqn1990s.*
 - 3: Geneseqn2000s.*
 - 4: Geneseqn2001as.*
 - 5: Geneseqn2001bs.*
 - 6: Geneseqn2002s.*
 - 7: Geneseqn2003as.*
 - 8: Geneseqn2003bs.*
 - 9: Geneseqn2003cs.*
 - 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	7376	100.0	7376	2 AAX88001	Aax88001 N-type ca
2	7342	99.5	7364	6 AB165869	Ab165869 Lung canc
3	7342	99.5	7364	7 ABZ58366	Abz58366 Human N-t
4	7316.4	99.2	7362	2 AAV42685	AAV42685 DNA encod
5	7316.4	99.2	7362	3 AAA71703	Aaa71703 Human cal
6	7316.4	99.2	7362	6 AAD39955	Aad39955 Human cal
7	7314.8	99.2	7362	2 AAQ84657	Aaq84657 Human neu
8	7313.2	99.1	7362	2 AAQ37817	Aaq37817 Sequence
9	7223.2	97.9	7266	2 AAV29059	Aav29059 Human cal
10	6958	94.3	7177	7 ABZ58367	Abz58367 Human N-t
11	6932.4	94.0	7175	2 AAQ84658	Aaq84658 Human neu
12	6932.4	94.0	7175	2 AAV42686	Aav42686 DNA encod
13	6932.4	94.0	7175	3 AAA71704	Aaa71704 Human cal
14	6932.4	94.0	7175	6 AAD39956	Aad39956 Human cal
15	6913.2	93.7	7175	2 AAQ37818	Aaq37818 Sequence
16	5935.4	80.5	6232	2 AAQ29269	Aaq29269 Human cal
17	5049.2	68.5	7185	4 AAH21860	Aah21860 Mouse N-c
18	3173	43.0	5438	2 AAQ29263	Aaq29263 Human cal
19	2582.6	35.0	6639	6 ABK63679	Abk63679 Rat sequ
20	2512	34.1	7808	2 AAQ84659	Aaq84659 Human neu
21	2512	34.1	7808	3 AAA71718	Aaa71718 Human cal
22	2512	34.1	7808	6 AAD39970	Aad39970 Human cal
23	2512	34.1	7808	7 ABZ58368	Abz58368 Human cal

24	2502.8	33.9	6822	4 AAF32541	Aaf32541 Rabbit P/
25	2502.2	33.9	7791	2 AAQ84660	Aaq84660 Human neu
26	2502.2	33.9	7791	3 AAA71719	Aaa71719 Human cal
27	2502.2	33.9	7791	6 AAD39971	Aad39971 Human cal
28	2502.2	33.9	7791	7 ABZ58369	Abz58369 Human cal
29	2488.2	33.7	7827	6 ABZ35311	Abz35311 Human gen
30	2449.6	33.2	6789	2 AAV29372	Aav29372 Calcium i
31	2408.4	32.7	7179	8 ADA13409	Ada13409 Human tra
32	2402.4	32.6	7032	2 AAQ84662	Aaq84662 Human neu
33	2402.4	32.6	7032	3 AAA71720	Aaa71720 Human cal
34	2402.4	32.6	7032	6 AAD39972	Aad39972 Human cal
35	2356.2	31.9	7089	2 AAQ84663	Aaq84663 Human neu
36	2356.2	31.9	7089	3 AAA71721	Aaa71721 Human cal
37	2356.2	31.9	7089	6 AAD39973	Aad39973 Human cal
38	2354.6	31.9	6922	2 AAQ83735	Aaq83735 Calcium c
39	2341.6	31.7	7088	6 ABZ35344	Abz35344 Human gen
40	1624.8	22.0	4919	2 AAQ29260	Aaq29260 Human cal
41	1225.2	16.6	3563	2 AAZ23429	Aaz23429 Human SCA
42	1225.2	16.6	3596	2 AAV61588	Aav61588 Alpha-1A
43	1177.6	16.0	3632	2 AAV61586	Aav61586 Alpha-1A
44	1153.2	15.6	3632	2 AAV61587	Aav61587 Alpha-1A
45	1091.4	14.8	1100	2 AAQ29275	Aaq29275 Human cal

ALIGNMENTS

RESULT 1
AAX88001
ID AAX88001 standard; cDNA; 7376 BP.
XX
AC AAX88001;
XX
DT 06-DEC-1999 (first entry)
XX
DE N-type calcium channel h-alpha-1B+SFVG subunit IIIS3-S4 cDNA.
XX
KW N-type calcium channel; h-alpha-1B+SFVG; human; splice variant;
XX signal transduction; stroke; pain; brain injury; therapy; diagnosis; ss.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 146..7177
FT /*tag= a
FT misc_difference 3856..3867
FT /*tag= b
FT /*note= "12-base insert"
XX
PN WO9946383-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US005392.
XX
PR 13-MAR-1998; 98US-0077901P.
XX (UYBR-) UNIV BROWN RES FOUND.
XX
PI Lipscombe D, Schorge S;
XX
DR WPI; 1999-561677/47.
DR P-PSDB; AAY31809.
XX
PT New isolated human N-type calcium channel isoform, used to develop
PT products, for treating, e.g. stroke or traumatic brain injury.
XX
PS Claim 7; Page 73-84; 141pp; English.
XX
CC This the nucleotide sequence of cDNA coding for a human N-type calcium
CC channel isoform (splice variant), h-alpha-1B-SFVG (see AAY31808), that is
CC involved in central nervous system signalling. The sequence includes a 12
CC nucleotide insert (see also AAX88000) that is not present in previously

published human alpha-1B Ca channel isoform sequences. The insert encodes a 4-amino acid insert (see AAV31808) corresponding to residues 1238-41 of the protein. The h-alpha-1B+SVFG subunit makes up a significant portion of the N-type Ca channel alpha-1B subunit mRNA in human brain, and is differentially distributed in different parts of the brain. The invention also includes fragments and biologically functional variants of the h-alpha-1B+SVFG channel, as well as inhibitors of h-alpha-1B+SVFG expression or function. The h-alpha-1B+SVFG nucleic acids, polypeptides and inhibitors can be used in the treatment and/or diagnosis of conditions characterized by aberrant brain neuronal calcium current, such as stroke, pain (e.g. neuropathic pain) and traumatic brain injury.

XX Sequence 7376 BP; 1445 A; 2280 C; 2222 G; 1429 T; 0 U; 0 Other;

Query Match		100.0%;	Score 7376;	DB 2;	Length 7376;		
Best Local Similarity		100.0%;	Pred. No. 0;				
Matches 7376;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	1	CGCGCGCGCTGCGCGGTGGGGCCGGGAGGTCCGCTGGCGTCCCGCGCGCTCCGTTG	60				
Db	1	CGCGCGCGCTGCGCGGTGGGGCCGGGAGGTCCGCTGGCGTCCCGCGCGCTCCGTTG	60				
Qy	61	GCTGCTCCGCTCTGAGCGCTGCGCGGCCCGCGGCCCTCCCTGCGGGGCCCTGGGCG	120				
Db	61	GCTGCTCCGCTCTGAGCGCTGCGCGGCCCGCGGCCCTCCCTGCGGGGCCCTGGGCG	120				
Qy	121	GGGATGACGCGCGGGCCCGGGAGCCATGCTCGCTTCGGGGACGAGCTGGGGCGCGCTA	180				
Db	121	GGGATGACGCGGGCCCGGGAGCCATGCTCGCTTCGGGGACGAGCTGGGGCGCGCTA	180				
Qy	181	TGAGGCCCCGGCGGGAGCGGGCCCGGGCGCGCGCGCGCGGGGGGGGCC	240				
Db	181	TGAGGCCCCGGCGGGAGCGGGCCCGGGCGCGCGCGCGCGGGGGGGGCC	240				
Qy	241	GGGTCCCGGGGGCTGCACCCCGCGCGAGCGGGTCTCTACAGCAATCGATCGCGCAGC	300				
Db	241	GGGTCCCGGGGGCTGCACCCCGCGCGAGCGGGTCTCTACAGCAATCGATCGCGCAGC	300				
Qy	301	CGCGCGGACCATGGGCTGTACAACCCCATCCCGGTCAAGCAGAACTGCTTCAACGTC	360				
Db	301	CGCGCGGACCATGGGCTGTACAACCCCATCCCGGTCAAGCAGAACTGCTTCAACGTC	360				
Qy	361	CGGCTCGCTCTTCTTTCAGCGAGGACAACTGCTCGCGAAATACGGAAGCGCATCAC	420				
Db	361	CGGCTCGCTCTTCTTTCAGCGAGGACAACTGCTCGCGAAATACGGAAGCGCATCAC	420				
Qy	421	CGAGTGGCTCCATTCGAGTATATGATCTGTGCCACCATCATCGCAACTGCTCATGCTG	480				
Db	421	CGAGTGGCTCCATTCGAGTATATGATCTGTGCCACCATCATCGCAACTGCTCATGCTG	480				
Qy	481	GGCCCTGGAGGACGACCTCCCTGTGGGGAACAAACGCCCCATGTCGAGCGGCTGGAC	540				
Db	481	GGCCCTGGAGGACGACCTCCCTGTGGGGAACAAACGCCCCATGTCGAGCGGCTGGAC	540				
Qy	541	CACGAGGCGCTATTTTCATCGGATCTTTTGTCTCGGGAACGGCTGGAACTGATGACTTC	600				
Db	541	CACGAGGCGCTATTTTCATCGGATCTTTTGTCTCGGGAACGGCTGGAACTGATGACTTC	600				
Qy	601	GGGCTTTGCTTCCACAGGCTCTTACCTCGGGAACGGCTGGAACTGATGACTTCG	660				
Db	601	GGGCTTTGCTTCCACAGGCTCTTACCTCGGGAACGGCTGGAACTGATGACTTCG	660				
Qy	661	GGTGTCTCTCAGGGATCTTTCGACCGGCTGGAACTGATGACTTCGAACTTCG	720				
Db	661	GGTGTCTCTCAGGGATCTTTCGACCGGCTGGAACTGATGACTTCGAACTTCG	720				
Qy	721	GGCTGTGCTGTGAGGCGCCCTGAAGCTGTGCTGTGGGATTCGAAGTTTCAGGTGT	780				
Db	721	GGCTGTGCTGTGAGGCGCCCTGAAGCTGTGCTGTGGGATTCGAAGTTTCAGGTGT	780				
Qy	781	GCTCAAGTCCATCATGAAGCCATGGTTCACCTCTTCAGATTGGGCTGCTTCTTCTT	840				
Db	781	GCTCAAGTCCATCATGAAGCCATGGTTCACCTCTTCAGATTGGGCTGCTTCTTCTT	840				

Qy	841	TGCCATCTCTCATGTTTGCCATCATTTGGCCTGGAGTCTTACATATGGGCAAGTTCACCAAGGC	900
Db	841	TGCCATCTCTCATGTTTGCCATCATTTGGCCTGGAGTCTTACATATGGGCAAGTTCACCAAGGC	900
Qy	901	CTGTTTCCCAACAGCACAGATGCGGAGCCCGTGGGTGACTTCCCTGTGCAAGAGGC	960
Db	901	CTGTTTCCCAACAGCACAGATGCGGAGCCCGTGGGTGACTTCCCTGTGCAAGAGGC	960
Qy	961	CCGAGCCCGGCTGTGCGAGGGCGACACTGAGTGCAGGAGTACTGGCCACGACCCCACTT	1020
Db	961	CCGAGCCCGGCTGTGCGAGGGCGACACTGAGTGCAGGAGTACTGGCCACGACCCCACTT	1020
Qy	1021	TGGCATCACCAACTTTTGCAATATCTTGTGTCATCTTGACGCTGTTCCAGTGCATCAC	1080
Db	1021	TGGCATCACCAACTTTTGCAATATCTTGTGTCATCTTGACGCTGTTCCAGTGCATCAC	1080
Qy	1081	CATGAGGGCTGGACTGACATCTCTATATACAAACGATGCGGCCGGCAACCTTGGAA	1140
Db	1081	CATGAGGGCTGGACTGACATCTCTATATACAAACGATGCGGCCGGCAACCTTGGAA	1140
Qy	1141	CTGCTCTACTTCTCATCTCTCATCATCGGCTCTCTTCTCATGCTCAACCTGTGCT	1200
Db	1141	CTGCTCTACTTCTCATCTCTCATCATCGGCTCTCTTCTCATGCTCAACCTGTGCT	1200
Qy	1201	GGGCTGCTCTCGGGGAGTTTCCAAAGGAGGAGAGGGTGGAGAACCCGCGCGCTT	1260
Db	1201	GGGCTGCTCTCGGGGAGTTTCCAAAGGAGGAGAGGGTGGAGAACCCGCGCGCTT	1260
Qy	1261	CCTGAAGCTCGCGCGGAGCAGCAGATCGAGCAGAGCTCAGGGTACTTGGAGTGGAT	1320
Db	1261	CCTGAAGCTCGCGCGGAGCAGCAGATCGAGCAGAGCTCAGGGTACTTGGAGTGGAT	1320
Qy	1321	CTTCAAGGGGAGGAGTCACTGCTGCTGCTGGAGGACAGGAAATGACAGAGAGAAATGCC	1380
Db	1321	CTTCAAGGGGAGGAGTCACTGCTGCTGCTGGAGGACAGGAAATGACAGAGAGAAATGCC	1380
Qy	1381	TTTGGACGCTCTGAAGAGAGCGGCCAACAAAGAGAGCAAAATGACCTGATCCAGCAGA	1440
Db	1381	TTTGGACGCTCTGAAGAGAGCGGCCAACAAAGAGAGCAAAATGACCTGATCCAGCAGA	1440
Qy	1441	GGAGGAGAGGACCGGTTTGCAGATCTCTGCTGCTGTGGATCCCTTCGCGCGCCAG	1500
Db	1441	GGAGGAGAGGACCGGTTTGCAGATCTCTGCTGCTGTGGATCCCTTCGCGCGCCAG	1500
Qy	1501	CCTCAAGAGCGGGAAGACAGAGAGCTCGTCACTTCGAGGAGGAGGAGATGTTCCG	1560
Db	1501	CCTCAAGAGCGGGAAGACAGAGAGCTCGTCACTTCGAGGAGGAGGAGATGTTCCG	1560
Qy	1561	GTGTTTATCCGCGCATGCTGAAGGCTCAGAGCTTCTACTGGGTGGTGCCTGCGTGGT	1620
Db	1561	GTGTTTATCCGCGCATGCTGAAGGCTCAGAGCTTCTACTGGGTGGTGCCTGCGTGGT	1620
Qy	1621	GGCCCTGAACACACTGTGTGGCCATGGTGATTAACAACGCGCGCGCTTACCCAC	1680
Db	1621	GGCCCTGAACACACTGTGTGGCCATGGTGATTAACAACGCGCGCGCTTACCCAC	1680
Qy	1681	GACCTGTATTTTGCAGAGTTTGTGTTTCTTGGGTCTCTTCTCTCAGAGATGTCCCTGAA	1740
Db	1681	GACCTGTATTTTGCAGAGTTTGTGTTTCTTGGGTCTCTTCTCTCAGAGATGTCCCTGAA	1740
Qy	1741	GATGATGGCTTGGGGCCCGAGAGCTACTTCCGGTCTCTTCAACTGCTTCACTTGG	1800
Db	1741	GATGATGGCTTGGGGCCCGAGAGCTACTTCCGGTCTCTTCAACTGCTTCACTTGG	1800
Qy	1801	GCTCATCTGGGAGCGCTTTTGAAGTGGTCTGGCGGCCCATCAAGCGGGAAGCTCCTT	1860
Db	1801	GCTCATCTGGGAGCGCTTTTGAAGTGGTCTGGCGGCCCATCAAGCGGGAAGCTCCTT	1860
Qy	1861	TGGGATCAGTGTGCTGGCGGCCCTCCGCTCTCAGGATCTTCAAGTCTCAGAGTACTG	1920
Db	1861	TGGGATCAGTGTGCTGGCGGCCCTCCGCTCTCAGGATCTTCAAGTCTCAGAGTACTG	1920

Db 4081 TTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGGGGACTGCGAGGGGTCAAGTATTGGGA 4140
Qy 4141 TTATGAGAAGGAGAGTGGAGAGCTCAGCCCGAGGAGTGAAGAAATAAGACTTTCACTA 4200
Db 4141 TTATGAGAAGGAGAGTGGAGAGCTCAGCCCGAGGAGTGAAGAAATAAGACTTTCACTA 4200
Qy 4201 CGACAATGTGCTCTGGGCTCTGTGACGCTGTTTCAAGTGTCCACGGGAGAGGCTGGCC 4260
Db 4201 CGACAATGTGCTCTGGGCTCTGTGACGCTGTTTCAAGTGTCCACGGGAGAGGCTGGCC 4260
Qy 4261 CATGGTCTGAACACATCCCGTGAATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
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Qy 4621 GATGATGAAGTCTATGATGACCCCTATGAGTACGAGCTGATGCTGAATGCTGAACAT 4680
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Qy 4681 CGTGTTCATCATCATGTTCTCCATGGAATGCGTGTGAAGATCATCGCCTTTGGGGTGT 4740
Db 4681 CGTGTTCATCATCATGTTCTCCATGGAATGCGTGTGAAGATCATCGCCTTTGGGGTGT 4740
Qy 4741 GAACTATTTTCAAGATGCTGGAATGTCTTTGACTTTGTCACTGTGTTGGGAAGTATTAC 4800
Db 4741 GAACTATTTTCAAGATGCTGGAATGTCTTTGACTTTGTCACTGTGTTGGGAAGTATTAC 4800
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Qy 4861 CCTCTTTGAGCTGCGGGCTGATCAAGCTGCTCGCGAGGGCTACACCATCGCATCCT 4920
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Qy 5161 GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGCCCTACTTCTACTT 5220
Db 5161 GGCCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGCCCTACTTCTACTT 5220

Qy 5221 CGTCTCCTTCACTCTTCTGTCTCCTTTCTGATGTTGAACTCTTTGTGCTGTGATCAT 5280
Db 5221 CGTCTCCTTCACTCTTCTGTCTCCTTTCTGATGTTGAACTCTTTGTGCTGTGATCAT 5280
Qy 5281 GGAACAATTTTGAGTACCTTCAAGCGGGACTCTTCCATCCTAGGTCTTCACTTTGGATGA 5340
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Qy 5881 CCGGGTTTTCTTCACAGAAAGTTCACCTCCCTCAGCAATGGCGGGGCTCATACAAA 5940
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Qy 5941 CCAAGAGAGTGGCATCAAGAGTCTGTCTCTGGGGCACTCAAGAGACCCAGGATGCACC 6000
Db 5941 CCAAGAGAGTGGCATCAAGAGTCTGTCTCTGGGGCACTCAAGAGACCCAGGATGCACC 6000
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Db 6001 CATAGAGCCAGGCCACCCCTGGAGCTGGCCACTCCACAGAGATCCCTGTGGGCGGTC 6060
Qy 6061 AGGAGCACTGGCTGTGGAGCTTCAGATGAGAGATATCCCGAGGGGCTTGTATGGGA 6120
Db 6061 AGGAGCACTGGCTGTGGAGCTTCAGATGAGAGATATCCCGAGGGGCTTGTATGGGA 6120
Qy 6121 GCCCAGCCTGGGCTGGAGAGCCAGGGTTCAGAGCGGCTTCCATGCCCCGCTTGGCGCGGA 6180
Db 6121 GCCCAGCCTGGGCTGGAGAGCCAGGGTTCAGAGCGGCTTCCATGCCCCGCTTGGCGCGGA 6180
Qy 6181 GACTCAGCCCTCAGATGCGCCCATGAAGGCTTCATCTCCAGCTTGGCCACAGCG 6240
Db 6181 GACTCAGCCCTCAGATGCGCCCATGAAGGCTTCATCTCCAGCTTGGCCACAGCG 6240
Qy 6241 GCCCGTGGGACTCATCTTTTGCAGCACCAACCCCGGACCGCCACCCCTAGCCAGGCGTC 6300
Db 6241 GCCCGTGGGACTCATCTTTTGCAGCACCAACCCCGGACCGCCACCCCTAGCCAGGCGTC 6300

Qy	6301	GTGCGACCAACCAACACACCGCTGCGACACCGCGCAGAGGACAGAGAGTCCCTTGGA	6360
Db	6301	GTGCGACCAACCAACACACCGCTGCGACACCGCGCAGAGGACAGAGGTCCCTTGGA	6360
Qy	6361	GAAGGGGCCAGAGCCTGTCTGCCGATATGGATGGCGCACCAAGCAGTCTCTGTGGGGCCGGG	6420
Db	6361	GAAGGGGCCAGAGCCTGTCTGCCGATATGGATGGCGCACCAAGCAGTCTCTGTGGGGCCGGG	6420
Qy	6421	GCTGCCCCCGGAGAGGGGGCTTACAGGCTGCCTGGCGGGAAACGAGAGCGCCGGCAGGAGCG	6480
Db	6421	GCTGCCCCCGGAGAGGGGGCTTACAGGCTGCCTGGCGGGAAACGAGAGCGCCGGCAGGAGCG	6480
Qy	6481	GGGCGGTCCTCAGAGCGGAGCGACCCCTCATCTCTCTCTCGAGAAAGCAGAGCGCTTCTA	6540
Db	6481	GGGCGGTCCTCAGAGCGGAGCGACCCCTCATCTCTCTCTCGAGAAAGCAGAGCGCTTCTA	6540
Qy	6541	CTCTCTGGAGCGCTTTTGGGGGCGGTGAGCGCCCCCGAAGCCCAAGCCCTTCTCTCAGACGCCA	6600
Db	6541	CTCTCTGGAGCGCTTTTGGGGGCGGTGAGCGCCCCCGAAGCCCAAGCCCTTCTCTCAGACGCCA	6600
Qy	6601	CCCAACGTTCGCAACAGCTGCCAGGAGCGGGACCCCAACCCACAGGGCAGTGGTTCGGT	6660
Db	6601	CCCAACGTTCGCAACAGCTGCCAGGAGCGGGACCCCAACCCACAGGGCAGTGGTTCGGT	6660
Qy	6661	GAATGGAGGCCCTTGTGTCAACATCTGGTGTAGCAACCCCGGCGCGCGTGGGGCGGAG	6720
Db	6661	GAATGGAGGCCCTTGTGTCAACATCTGGTGTAGCAACCCCGGCGCGCGTGGGGCGGAG	6720
Qy	6721	GCAGCTCCCCAGACGCCCTTGACTCCCGGCCCGCAGCATCACCTACAAAGACGGCCAACTC	6780
Db	6721	GCAGCTCCCCAGACGCCCTTGACTCCCGGCCCGCAGCATCACCTACAAAGACGGCCAACTC	6780
Qy	6781	CTCACCATTCACATTCGCGGGGCTCAGACAGGCTCCCTGCCTTCTCCCAAGCCGGCT	6840
Db	6781	CTCACCATTCACATTCGCGGGGCTCAGACAGGCTCCCTGCCTTCTCCCAAGCCGGCT	6840
Qy	6841	CAGCCGTGGGCTTTCGAAACACAAACGCCCTGCTCAGAGAGACCCCTCAGCCAGGCCCT	6900
Db	6841	CAGCCGTGGGCTTTCGAAACACAAACGCCCTGCTCAGAGAGACCCCTCAGCCAGGCCCT	6900
Qy	6901	GGCCCCGTGGCTCTCGAATTGGCTCTGACCCCTTACCTGGGGCAGGGTCTGACAGTGAAGC	6960
Db	6901	GGCCCCGTGGCTCTCGAATTGGCTCTGACCCCTTACCTGGGGCAGGGTCTGACAGTGAAGC	6960
Qy	6961	CTCTGTCCAGCCCTGCTCAGGACACGCTCACATTTTCGAGAGGCTGTGGCCACCAACTC	7020
Db	6961	CTCTGTCCAGCCCTGCTCAGGACACGCTCACATTTTCGAGAGGCTGTGGCCACCAACTC	7020
Qy	7021	GGGCGGCTCTCCAGGACTTCTCTACGTGTCTCTCCCTGACCTCCACAGTCTCACCCCTCCG	7080
Db	7021	GGGCGGCTCTCCAGGACTTCTCTACGTGTCTCTCCCTGACCTCCACAGTCTCACCCCTCCG	7080
Qy	7081	CCGCGTGCCTAACCGTTACCTGCAACCTTGGGACTCAGCTCGGGTGGCGAGCAGCGCA	7140
Db	7081	CCGCGTGCCTAACCGTTACCTGCAACCTTGGGACTCAGCTCGGGTGGCGAGCAGCGCA	7140
Qy	7141	CAGCTACCAACCCCTGACCAAGACCACTGGTGTCTGCTGACCGTCAACCGCTCAGACGC	7200
Db	7141	CAGCTACCAACCCCTGACCAAGACCACTGGTGTCTGCTGACCGTCAACCGCTCAGACGC	7200
Qy	7201	CTGCATGCAGCAGCGGTGTGTTCCAGTGGATAGTGTATTCATCCACAGGGGCACTCGG	7260
Db	7201	CTGCATGCAGCAGCGGTGTGTTCCAGTGGATAGTGTATTCATCCACAGGGGCACTCGG	7260
Qy	7261	CCCTCGGGGAGGCCCTTGCACACTTGTGGTGAAGTCTCTGTGGGCCCTTCTCCGCCCTCT	7320
Db	7261	CCCTCGGGGAGGCCCTTGCACACTTGTGGTGAAGTCTCTGTGGGCCCTTCTCCGCCCTCT	7320
Qy	7321	CCCCCTCTTTTACTCTAGACGACGAATAAGCCCTTGTTGCTTGAGTGTACGTACCGC	7376
Db	7321	CCCCCTCTTTTACTCTAGACGACGAATAAGCCCTTGTTGCTTGAGTGTACGTACCGC	7376

RESULT 2
ABL65869
ID ABL65869 standard; DNA; 7364 BP.
XX AC
XX AC ABL65869;
XX DT
XX DT 15-MAY-2002 (first entry)
XX XX Lung cancer related gene sequence SEQ ID NO:4206.
XX KW Human; cancer; colon; breast; ovary; oesophagus;
XX KW stomach; lung; prostate; pancreas; carcinoma; ant
XX KW cytosaratic; gene therapy; anti-neoplastic; Wilm's
XX KW gene; ds.
XX OS
OS Homo sapiens.
XX PN
PX WO200194629-A2.
XX PD
PD 13-DEC-2001.
XX PF
PF 30-MAY-2001; 2001WO-US010838.
XX PR
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX PA
PA (AVAL-) AVALON PHARM.
XX PI
PI Young PE, Augustus M, Carter KC, Ebner R, End
PI Soppet DR., Weaver Zi;
XX DR
DR WPI; 2002-188264/24.
XX XX

PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PS in expression of a gene of a signature gene set.

PS Claim 1; SEQ ID NO 4206; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 847 sequences (given in ABL1664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
XX tumour

SQ Sequence 7364 BP; 1444 A; 2278 C; 2216 G; 1426 T; 0 U; 0 Other;

Query Match 99.5%; Score 7342; DB 6; Length 7364;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

QY	1	CGCGCGCGCGCTCGCGCGTGGCGCGCGCGAGGTCCGTGCGGTCCGCGCGGTCCCGT	60
DB	1	CGCGCGCGCGCTGCGCGGTGGCGCGCGCGAGGTCCGTGCGGTCCGCGCGGTCCCGT	60
QY	61	GCTGCTCCGCTGAGCGCTGCGCGCGCGCGCGCTCCCTCCGCGCGCGCGTGGCGG	120
DB	61	GCTGCTCCGCTGAGCGCTGCGCGCGCGCGCGCTCCCTCCGCGCGCGCGTGGCGG	120
QY	121	GGGATGCAACCGCGGCGCGCGCGATGCTGCGGTTCGGGGAGAGCTGGCGCGCGCTA	180
DB	121	GGGATGCAACCGCGGCGCGCGCGATGCTGCGGTTCGGGGAGAGCTGGCGCGCGCTA	180
QY	181	TGGAGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	240
DB	181	TGGAGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	240
QY	241	GGGTCCCGGGGCGCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	300
DB	241	GGGTCCCGGGGCGCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	300
QY	301	CGCGCGGACCATGGCGCTGTACACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	360
DB	301	CGCGCGGACCATGGCGCTGTACACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	360
QY	361	CGGCTCGCTCTTCGCTTTCAGCGAGCAAGCTGCTCGGCAACCATCGGCAACTGCTGCT	420
DB	361	CGGCTCGCTCTTCGCTTTCAGCGAGCAAGCTGCTCGGCAACCATCGGCAACTGCTGCT	420
QY	421	CGAGTGGGCTCAATTCGAGTATATGATCTCGGCAACCATCGGCAACTGCTGCTGCT	480
DB	421	CGAGTGGGCTCAATTCGAGTATATGATCTCGGCAACCATCGGCAACTGCTGCTGCT	480
QY	481	GGCCCTGGAGCAGACCTCCCTGATGGGGAACAAACGCGCCATGTCGAGCGGCTGGA	540
DB	481	GGCCCTGGAGCAGACCTCCCTGATGGGGAACAAACGCGCCATGTCGAGCGGCTGGA	540
QY	541	CACGAGCGCTATTTTCATCGGGATCTTTGCTTCGAGCGGGATCAAAATCATCGCTCT	600
DB	541	CACGAGCGCTATTTTCATCGGGATCTTTGCTTCGAGCGGGATCAAAATCATCGCTCT	600
QY	601	GGGCTTGTCTTCCAAAGGCTCTTACCTCGGAAACGCGTGGAAACGCTCATGACTTCGT	660
pb	601	GGGCTTGTCTTCCAAAGGCTCTTACCTCGGAAACGCGTGGAAACGCTCATGACTTCGT	660

QY 1741 GATGTATGGCTGGGGCCAGAGTACTTCCGGTCTCTTCAACTGCTTCGACTTTGG 1800
DB 1741 GATGTATGGCTGGGGCCAGAGTACTTCCGGTCTCTTCAACTGCTTCGACTTTGG 1800
QY 1801 GGTCAATCGTGGGAGCGTCTTTGAAGTGTCTGGCGGCCCATCAAGCCGGAGAGCTCCTT 1860
DB 1801 GGTCAATCGTGGGAGCGTCTTTGAAGTGTCTGGCGGCCCATCAAGCCGGAGAGCTCCTT 1860
QY 1861 TGGGATCAGTGTCTGGGGGCCCTCCGCTCTCTGAGGATCTTCAAAGTCAAGAGTACTG 1920
DB 1861 TGGGATCAGTGTCTGGGGGCCCTCCGCTCTCTGAGGATCTTCAAAGTCAAGAGTACTG 1920
QY 1921 GAGCTCCCTGGGAAACCTGTGTGTCTCTGCTGAACTCATGATGAAGTCCATCAGCCT 1980
DB 1921 GAGCTCCCTGGGAAACCTGTGTGTCTCTGCTGAACTCATGATGAAGTCCATCAGCCT 1980
QY 1981 GCTCTTCTTGTCTTCTCTGTTTCATTGTGTCTCTCGCCCTGTGGGATGCAAGCTGTTTGG 2040
DB 1981 GCTCTTCTTGTCTTCTCTGTTTCATTGTGTCTCTCGCCCTGTGGGATGCAAGCTGTTTGG 2040
QY 2041 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTTCGACACCTTCCCTGCGGC 2100
DB 2041 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTTCGACACCTTCCCTGCGGC 2100
QY 2101 CATCTCACTGTCTTCAGATCTCTGACGGAGAGGACTGGAAATGCAATGATATCAGG 2160
DB 2101 CATCTCACTGTCTTCAGATCTCTGACGGAGAGGACTGGAAATGCAATGATATCAGG 2160
QY 2161 GATCGAATCGCAAGCGCGTCAGCAAGGATGTTCTCGTCCCTTTTACTTTCATTTGCCCT 2220
DB 2161 GATCGAATCGCAAGCGCGTCAGCAAGGATGTTCTCGTCCCTTTTACTTTCATTTGCCCT 2220
QY 2221 GACACTGTTTCGAAACTACACTCTGCTGAATGTCTTTCTGGCCATCGTGTGGACAACCT 2280
DB 2221 GACACTGTTTCGAAACTACACTCTGCTGAATGTCTTTCTGGCCATCGTGTGGACAACCT 2280
QY 2281 GGCCAAAGCCCAAGAGTGCACCAAGGATGAAGAGGAGATGGAAGCAGCAATCAGAA 2340
DB 2281 GGCCAAAGCCCAAGAGTGCACCAAGGATGAAGAGGAGATGGAAGCAGCAATCAGAA 2340
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DB 2341 GCTTGTCTCTCAAAAGCCCAAGAGTGGCTGAAGTCAGCCCCCATGTCTCCCGGACAT 2400
QY 2401 CTCCATCGCCCGCAGGAGAGACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGGC 2460
DB 2401 CTCCATCGCCCGCAGGAGAGACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGGC 2460
QY 2461 CAGCCAGTACGGCTGCAGAACTCTGGGGCCAGCTGCGAGCGCTGTACAGCGAGATGGA 2520
DB 2461 CAGCCAGTACGGCTGCAGAACTCTGGGGCCAGCTGCGAGCGCTGTACAGCGAGATGGA 2520
QY 2521 CCCCGAGAGCGGTGCGCTTCGCCACTACGCGCCACTCGCGGCCGACATGAAGAGCGCA 2580
DB 2521 CCCCGAGAGCGGTGCGCTTCGCCACTACGCGCCACTCGCGGCCGACATGAAGAGCGCA 2580
QY 2581 CCTGGACCGGCGCTGTGTGTGAGCTGGGCGCGCAGCGCGCGGGCGCCGTGGGAGG 2640
DB 2581 CCTGGAACGGCGCTGTGTGTGAGCTGGGCGCGCAGCGCGGGCGCCGTGGGAGG 2640
QY 2641 CAAAGCCGACCTGAGGCTCGGAGGCCCCCGAGGGCGTGCACCTCCGCGCAGGACCA 2700
DB 2641 CAAAGCCGACCTGAGGCTCGGAGGCCCCCGAGGGCGTGCACCTCCGCGCAGGACCA 2700
QY 2701 CCGGCAACCGGACAGGACAGACCCCGCGCGGGGACAGGACCCGAGCAGGAGGCCCC 2760
DB 2701 CCGGCAACCGGACAGGACAGACCCCGCGCGGGGACAGGACCCGAGCAGGAGGCCCC 2760
QY 2761 GAAGCGGAGAGCGGGAGCCCGTGTCCCGGAGGAGCGGCGCGGCGCACCCGACCCA 2820
DB 2761 GAAGCGGAGAGCGGGAGCCCGTGTCCCGGAGGAGCGGCGCGGCGCACCCGACCCA 2820
QY 2821 CAGCAAGGAGCGCGGGGCCCCCGGAGGCGCGGAGCGAGCGCGGCCCGAGGCC 2880

DB 2821 CAGCAAGGAGCGCGGGGCCCCCGAGGCGCGAGCGAGCGCGGCCAGGCC 2880
QY 2881 CGAGGGCGGCGCGGCAACCAACCGGCGGCTCCCGGAGAGGCGGCGCGAGGAGCC 2940
DB 2881 CGAGGGCGGCGGCGGCAACCAACCGGCGGCTCCCGGAGAGGCGGCGCGAGGAGCC 2940
QY 2941 CCGACGCCACCGCGCGCACCGGCAACAGGATCCGAGCAAGAGTGTGCGCGCGCAAGGG 3000
DB 2941 CCGACGCCACCGCGCGCACCGGCAACAGGATCCGAGCAAGAGTGTGCGCGCGCAAGGG 3000
QY 3001 CGAGCGGCGCGGCGGCAACCGGCGGCCCCCGAGCGGGGCCCCCGGAGGCGGAGAGCGG 3060
DB 3001 CGAGCGGCGCGGCGGCAACCGGCGGCCCCCGAGCGGGGCCCCCGGAGGCGGAGAGCGG 3060
QY 3061 GGAAGGAGCGGCGGCGGCAACCGGCGGCCCCCGAGCGGCGGCAAGGAGTGTGCGCGCGCAAGGG 3120
DB 3061 GGAAGGAGCGGCGGCGGCGGCAACCGGCGGCCCCCGAGCGGCGGCAAGGAGTGTGCGCGCGCAAGGG 3120
QY 3121 GGAAGGAGGAGCGGCGGCGGCAACCGGCGGCCCCCGAGCGGCGGCAAGGAGTGTGCGCGCGCAAGGG 3180
DB 3121 GGAAGGAGGAGCGGCGGCGGCAACCGGCGGCCCCCGAGCGGCGGCAAGGAGTGTGCGCGCGCAAGGG 3180
QY 3181 CAAGGAAAGGAGCTCCGGAACCAACCGGCGGCCCCCGAGCGGCGGCAAGGAGTGTGCGCGCGCAAGGG 3240
DB 3181 CAAGGAAAGGAGCTCCGGAACCAACCGGCGGCCCCCGAGCGGCGGCAAGGAGTGTGCGCGCGCAAGGG 3240
QY 3241 TGGGACTGTGACCTGTGGTCCCATGACACACTGCCAGCACCTGTCTCCAGAGGTTGGA 3300
DB 3241 TGGGACTGTGACCTGTGGTCCCATGACACACTGCCAGCACCTGTCTCCAGAGGTTGGA 3300
QY 3301 GGAACGCGGAGGATGCGAGCAATCAGCGGAAACGTCACTCGCATGGGCGAGTCAGGCCCC 3360
DB 3301 GGAACGCGGAGGATGCGAGCAATCAGCGGAAACGTCACTCGCATGGGCGAGTCAGGCCCC 3360
QY 3361 AGACCGGAAACATTTGTATCATATCCAGTGTCTGAACGGGCGCTTCTGGGAGAGCCAC 3420
DB 3361 AGACCGGAAACATTTGTATCATATCCAGTGTCTGAACGGGCGCTTCTGGGAGAGCCAC 3420
QY 3421 GGTCTGTTCCAGTGTAAACGTGACCTTGGAAAGCCAGAGAGGGAAGAGGTTGGA 3480
DB 3421 GGTCTGTTCCAGTGTAAACGTGACCTTGGAAAGCCAGAGAGGGAAGAGGTTGGA 3480
QY 3481 AGCGGATGACGTCATGAGGAGCGGCCCCCGGCGCTATCGTCCCATACAGCTCCATGTTCTG 3540
DB 3481 AGCGGATGACGTCATGAGGAGCGGCCCCCGGCGCTATCGTCCCATACAGCTCCATGTTCTG 3540
QY 3541 TTTAAGCCCGACCAACCTGCTCCGCGCTTCTGCCACTACATCGTGAACCATGAGGTACTT 3600
DB 3541 TTTAAGCCCGACCAACCTGCTCCGCGCTTCTGCCACTACATCGTGAACCATGAGGTACTT 3600
QY 3601 CGAGGTGTCATTTCTCGTGTCTATCGCTTTGACGAGCATCGCTGCTGCTGAGGAGCC 3660
DB 3601 CGAGGTGTCATTTCTCGTGTCTATCGCTTTGACGAGCATCGCTGCTGCTGAGGAGCC 3660
QY 3661 AGTSCGACAGACTCGCCCAAGAAACGCTCTGAAATACCTGGATTACATTTTCACTGG 3720
DB 3661 AGTSCGACAGACTCGCCCAAGAAACGCTCTGAAATACCTGGATTACATTTTCACTGG 3720
QY 3721 TGTCTTTACCTTTGAGATGATGATAAGATGATGCACTTGGGACTGCTGCTTCACTCTGG 3780
DB 3721 TGTCTTTACCTTTGAGATGATGATAAGATGATGCACTTGGGACTGCTGCTTCACTCTGG 3780
QY 3781 AGCCTATTTCCGGGACTTGTGGAACTTCTGGACTTCTGAGTTCATTTGCTGAGTGGCCCTGGT 3840
DB 3781 AGCCTATTTCCGGGACTTGTGGAACTTCTGGACTTCTGAGTTCATTTGCTGAGTGGCCCTGGT 3840
QY 3841 GGGCTTTGCTTCTC-----AGGATCCAAAGGGAAGAGCATCAATACCATCAA 3900
DB 3841 GGGCTTTGCTTCTC-----AGGATCCAAAGGGAAGAGCATCAATACCATCAA 3900
QY 3901 GTCTCTGAGAGTCTTCTGCTGCTGCGGCCCTTCAAGACCATCAACCGGCTGCCAAGCT 3960

QY 6121 GCCCAGCGTGGGTGAGAGCCAGGGTCTGAGCGGCTCCATGCCCCCGCTTGGCGCCGA 6180
DB 6109 GCCCAGCGTGGGTGAGAGCCAGGGTCTGAGCGGCTCCATGCCCCCGCTTGGCGCCGA 6168
QY 6181 GACTCAGCCGTCACAGATGCCACCATGAAGCGTCCATCTCCACGCTGGCCCGCAGCG 6240
DB 6169 GACTCAGCCGTCACAGATGCCACCATGAAGCGTCCATCTCCACGCTGGCCCGCAGCG 6228
QY 6241 GCCCGTGGGACTCATCTTTGACGACACACCCCGGACCGCCCTAGCCAGGCGTC 6300
DB 6229 GCCCGTGGGACTCATCTTTGACGACACACCCCGGACCGCCCTAGCCAGGCGTC 6288
QY 6301 GTCCACACACACACACCGCTGCCACCGCGGACGAGACGAGAGTCCCTGGA 6360
DB 6289 GTCCACACACACACACCGCTGCCACCGCGGACGAGAGTCCCTGGA 6348
QY 6361 GAAGGGGCCAGCGCTGTCTGCCGATATGGATGGCGCACCAAGCAGTGTCTGTGGGCGCGG 6420
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QY 6421 GCTGCCCGCGGAGAGGGGCTTACAGGCTGCCGGCGGGAACGAGAGCGCGCGGAGAGCG 6480
DB 6409 GCTGCCCGCGGAGAGGGGCTTACAGGCTGCCGGCGGGAACGAGAGCGCGCGGAGAGCG 6468
QY 6481 GGGCGGTCCAGGAGGAGGAGCGCTCATCTCTCTCTCGAGAGAGAGCGCTTCTA 6540
DB 6469 GGGCGGTCCAGGAGGAGGAGCGCTCATCTCTCTCTCGAGAGAGAGCGCTTCTA 6528
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DB 6529 CTCCTGGACCGCTTTGGGGGCGGTGAGCGCCCGAAGCCCAAGCCCTCCCTCAGCAGCCA 6588
QY 6601 CCCAACGTCGCAACAGTGGCCAGGAGCGGGACCCCAACGAGGGCAGTGTTCCT 6660
DB 6589 CCCAACGTCGCAACAGTGGCCAGGAGCGGGACCCCAACGAGGGCAGTGTTCCT 6648
QY 6661 GAATGGAGGCCCTTGTGTCAACATCTGTGTAGCACCCCGCGCGGTGGGCGGAG 6720
DB 6649 GAATGGAGGCCCTTGTGTCAACATCTGTGTAGCACCCCGCGCGGTGGGCGGAG 6708
QY 6721 GCAGCTCCCGCAGAGCGCCCTGACTCCCGCGCCAGCATCACTACAGAGCGGCAACTC 6780
DB 6709 GCAGCTCCCGCAGAGCGCCCTGACTCCCGCGCCAGCATCACTACAGAGCGGCAACTC 6768
QY 6781 CTCACCCATCCACTTCGCGGGGCTCAGACAGAGCTCTCCGCTTCTCCCGCAGCGGCT 6840
DB 6769 CTCACCCATCCACTTCGCGGGGCTCAGACAGAGCTCTCCGCTTCTCCCGCAGCGGCT 6828
QY 6841 CAGCGTGGGCTTTCCGAACAAACGCGCTGTCTGAGAGAGACCCCTCAGCCAGCGCCCT 6900
DB 6829 CAGCGTGGGCTTTCCGAACAAACGCGCTGTCTGAGAGAGACCCCTCAGCCAGCGCCCT 6888
QY 6901 GGCCCTGGCTCTGAAATGGCTCTGACCTTACTTGGGCGAGCGTCTGGACAGTGAAGC 6960
DB 6889 GGCCCTGGCTCTGAAATGGCTCTGACCTTACTTGGGCGAGCGTCTGGACAGTGAAGC 6948
QY 6961 CTCCTGTCCAGCCCTGCTGAGGACAGGCTCACTTTTCGAGAGAGCTGTGGCCACCAACTC 7020
DB 6949 CTCCTGTCCAGCCCTGCTGAGGACAGGCTCACTTTTCGAGAGAGCTGTGGCCACCAACTC 7008
QY 7021 GGGCGGTCTCAGAGATCTCTAGTGTCTCTCCCTGAGCTCCAGTCTCACTCTCCG 7080
DB 7009 GGGCGGTCTCAGAGATCTCTAGTGTCTCTCCCTGAGCTCCAGTCTCACTCTCCG 7068
QY 7081 CCGGTGCCAACGGTTACCACTCCACCTCGGACTCAGCTCGGGTGGCGGACCGGCA 7140
DB 7069 CCGGTGCCAACGGTTACCACTCCACCTCGGACTCAGCTCGGGTGGCGGACCGGCA 7128
QY 7141 CAGCTACCAACCCCTGACCAAGACCACTGTGTGTAGCTGACCGTCAACGCTCAGACGC 7200
DB 7129 CAGCTACCAACCCCTGACCAAGACCACTGTGTGTAGCTGACCGTCAACGCTCAGACGC 7188
QY 7201 CTGCATGACAGGCGGTGTGTTCAGTGGATAGTATTTATATCCACACGCGGCGAGTCGG 7260

DB 7189 CTGCATGACAGGCGGTGTTCAGTGGATAGTATTTATCATCCACACGCGGCGAGTCGG 7248
QY 7261 CCCTCGGGGAGAGCGCTTGGCCACCTTGGTGAGGCTCTGTGGCCCTCCCTCCCTCCCTCT 7320
DB 7249 CCCTCGGGGAGAGCGCTTGGCCACCTTGGTGAGGCTCTGTGGCCCTCCCTCCCTCTCT 7308
QY 7321 CCCTCTTTTACTCTCTAGACGACGAATAAAGCCCTGTGTGTGAGTGTACGTACCGC 7376
DB 7309 CCCTCTTTTACTCTCTAGACGACGAATAAAGCCCTGTGTGTGAGTGTACGTACCGC 7364

RESULT 3
ABZ58366
ID ABZ58366 standard; cDNA; 7364 BP.
XX AC ABZ58366;
XX AC ABZ58366;
DT 28-APR-2003 (first entry)
XX Human N-type calcium channel alpha-1B subunit coding sequence.
XX Human; calcium channel; voltage-gated ion channel; splice variant; gene;
XX ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 146..7165
XX FT /*tag= a
XX FT /product= "Human calcium channel, alpha-1B subunit"
XX PN WO2003006103-A2.
XX XX
XX PD 23-JAN-2003.
XX PF 12-JUL-2002; 2002WO-US022161.
XX XX
XX PR 12-JUL-2001; 2001US-0304955P.
XX XX
XX (MERI) MERCK & CO INC.
XX Augustine PR, Bennett PB, Bugianesi RM, Garyantes TA, Imredy JP;
PI Kath GS, Mcmanus OB;
XX WPI: 2003-221676/21.
XX P-PSDB; ABP72255.
XX
PT Identifying modulators of the activity of a voltage-gated ion channel,
PT comprises altering the transmembrane potential of a portion of the cell
PT membrane expressing the voltage-gated ion channel by electric field
PT stimulation.
XX
PS Disclosure; Fig 20A-C; 188pp; English.
XX
CC The present sequence is the coding sequence for a splice variant of the
CC alpha-1B subunit of the human T-type calcium channel. The invention
CC provides methods of identifying activators and inhibitors of voltage-
CC gated ion channels (VC). The methods use electrical field stimulation of
CC calls via extracellular electrodes to manipulate the open/close state
CC transitions of the VCs. This allows for more convenient, more precise
CC manipulation of these transitions and, coupled with efficient methods of
CC detecting ion flux or membrane potential, results in methods that are
CC especially suitable for high-throughput screening of compounds as
CC potential activators and inhibitors of VCs. The VC may be a sodium,
CC potassium calcium channel. The cells are e.g. HEK293 (ATCC 1573) cells
CC transfected with DNA encoding the VC, and may contain a fluorescent
CC indicator compound. Defective sodium, calcium and potassium VCs have been
CC implicated in a variety of disorders including long QT syndrome, ataxia,
CC migraine, muscle paralysis, deafness, and cardiac conduction
CC diseases
XX
SQ Sequence 7364 BP; 1444 A; 2278 C; 2216 G; 1426 T; 0 U; 0 Other;

Query Match 99.5%; Score 7342; DB 7; Length 7364;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;									
QY	1	CGCGCGCGGCTCGGCGGTGGGGCGGGCGAGGTCCGCTGCGGTCCCGCGCGCTCCGCG	60						
DB	1	CGCGCGCGGCTCGGCGGTGGGGCGGGCGAGGTCCGCTGCGGTCCCGCGCGCTCCGCG	60						
QY	61	GCTGCTCCGCTCTGAGCGCTGAGCGCCCGCGCCCGCCCTCCCTGCGCGGGCGCGCTGGGCG	120						
DB	61	GCTGCTCCGCTCTGAGCGCTGAGCGCCCGCGCCCGCCCTCCCTGCGCGGGCGCGCTGGGCG	120						
QY	121	GGGATGCACCGGGGCCGGGAGCCATGCTCCGCTTCGGGAGCGAGCTGGGCGCGCTTA	180						
DB	121	GGGATGCACCGGGGCCGGGAGCCATGCTCCGCTTCGGGAGCGAGCTGGGCGCGCTTA	180						
QY	181	TGAGGCCCCGGCGGAGAGCGGCGCGGGCGCGGGCGCGGGCGGGCGGGCGG	240						
DB	181	TGAGGCCCCGGCGGAGAGCGGCGCGGGCGCGGGCGCGGGCGGGCGGGCGG	240						
QY	241	GGGTCCCGGGGGCTGCAGCCCGCGCAGCGGGTCTCTACAAGCAATCGATCGCGCAGCG	300						
DB	241	GGGTCCCGGGGGCTGCAGCCCGCGCAGCGGGTCTCTACAAGCAATCGATCGCGCAGCG	300						
QY	301	CGCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACGTC	360						
DB	301	CGCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACGTC	360						
QY	361	CGCTCGCTCTGCTTTCAGCGAGGACAACTGTCGCGCAACATCGCATCGTCT	420						
DB	361	CGCTCGCTCTGCTTTCAGCGAGGACAACTGTCGCGCAACATCGCATCGTCT	420						
QY	421	CGAGTGGCTCCATTCAGTATATGATCTGCGCAACATCATCGCAACTGATCGTCT	480						
DB	421	CGAGTGGCTCCATTCAGTATATGATCTGCGCAACATCATCGCAACTGATCGTCT	480						
QY	481	GGCCCTGGAGCAGACCTCCCTGATGGGCAAAAACGCCCATGTCCGACCGGCTGGACGA	540						
DB	481	GGCCCTGGAGCAGACCTCCCTGATGGGCAAAAACGCCCATGTCCGACCGGCTGGACGA	540						
QY	541	CACGAGCCCTATTTTCATCGGATCTTTTGTCTCGAGCGAGGATCAAAATCATCGCTCT	600						
DB	541	CACGAGCCCTATTTTCATCGGATCTTTTGTCTCGAGCGAGGATCAAAATCATCGCTCT	600						
QY	601	GGGCTTTGCTTCCAAAGGGCTCTTACCTGCGGAACGGCTGGAACTGATCGTCT	660						
DB	601	GGGCTTTGCTTCCAAAGGGCTCTTACCTGCGGAACGGCTGGAACTGATCGTCT	660						
QY	661	GCTGCTCTCAGGGATCTTGCACGGCTGGAACTGATCGACCTTGGAACTGAG	720						
DB	661	GCTGCTCTCAGGGATCTTGCACGGCTGGAACTGATCGACCTTGGAACTGAG	720						
QY	721	GGCTGTGCTGTGCTGAGGCCCTGAAAGTGTGTCTGGGATTCGAAGTTTGCAGGTGGT	780						
DB	721	GGCTGTGCTGTGCTGAGGCCCTGAAAGTGTGTCTGGGATTCGAAGTTTGCAGGTGGT	780						
QY	781	GCTCAAGTCCATCATGAAGGCCCATGGTTCCATCTCTGCAGATTGGGCTGCTTCTTCTT	840						
DB	781	GCTCAAGTCCATCATGAAGGCCCATGGTTCCATCTCTGCAGATTGGGCTGCTTCTTCTT	840						
QY	841	TGCCATCTCATGTTTGCATATGGCTGGAGTTCTACATGGGCAAGTTTCCAAAGGC	900						
DB	841	TGCCATCTCATGTTTGCATATGGCTGGAGTTCTACATGGGCAAGTTTCCAAAGGC	900						
QY	901	CTGTTTCCCAACAGCACAGATGCGGAGCCGCTGGGTGACTTCCCTGTGGCAAGGAGGC	960						
DB	901	CTGTTTCCCAACAGCACAGATGCGGAGCCGCTGGGTGACTTCCCTGTGGCAAGGAGGC	960						
QY	961	CCAGCCCGGCTGTGCGAGGGGACACTGATGTCGGGAGTACTGGCCAGGACCCAACTT	1020						
DB	961	CCAGCCCGGCTGTGCGAGGGGACACTGATGTCGGGAGTACTGGCCAGGACCCAACTT	1020						
QY	1021	TGGCATCAACCAACTTTGACATATCCCTGTTTGGCCATCTTGACGGTGTTCAGTCATCAC	1080						
DB	1021	TGGCATCAACCAACTTTGACATATCCCTGTTTGGCCATCTTGACGGTGTTCAGTCATCAC	1080						
QY	1081	CATGAGGGCTTGGACTGACATCTCTATAATAACAAGATGCGGCCCGGCAACACTTGGAA	1140						
DB	1081	CATGAGGGCTTGGACTGACATCTCTATAATAACAAGATGCGGCCCGGCAACACTTGGAA	1140						
QY	1141	CTGCTCTACTTCTCATCTCTCATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1200						
DB	1141	CTGCTCTACTTCTCATCTCTCATCATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1200						
QY	1201	GGGCGTCTCTCGGGGAGTTTGCACAGGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGG	1260						
DB	1201	GGGCGTCTCTCGGGGAGTTTGCACAGGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGG	1260						
QY	1261	CCTGAAAGCTGCGCGGCGCAGCAGATCGAGCGAGAGCTCAACGGGTACCTGGAGTGGAT	1320						
DB	1261	CCTGAAAGCTGCGCGGCGCAGCAGATCGAGCGAGAGCTCAACGGGTACCTGGAGTGGAT	1320						
QY	1321	CTTCAAGCGCGGAGGAGTCTGCTGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1380						
DB	1321	CTTCAAGCGCGGAGGAGTCTGCTGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1380						
QY	1381	TTTGGACGCTGCTGAAGAGAGCGGCCCAAGAGAGCAGAAATGACCTGTTCACGCGAGA	1440						
DB	1381	TTTGGACGCTGCTGAAGAGAGCGGCCCAAGAGAGCAGAAATGACCTGTTCACGCGAGA	1440						
QY	1441	GGAGGAGAGGACCGGTTTGCAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1500						
DB	1441	GGAGGAGAGGACCGGTTTGCAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1500						
QY	1501	CCTCAAGCGCGGAGGAGCAGAGAGCTGTCATCTCTGCTGTGTGTGTGTGTGTGTGTGT	1560						
DB	1501	CCTCAAGCGCGGAGGAGCAGAGAGCTGTCATCTCTGCTGTGTGTGTGTGTGTGTGTGT	1560						
QY	1561	GTTTTTTATCCGCGCATGCTGAGGCTCAGAGCTTCTACTGGGTGTGTGTGTGTGTGTGT	1620						
DB	1561	GTTTTTTATCCGCGCATGCTGAGGCTCAGAGCTTCTACTGGGTGTGTGTGTGTGTGTGT	1620						
QY	1621	GGCCCTGMAACACTGT	1680						
DB	1621	GGCCCTGMAACACTGT	1680						
QY	1681	GACCTGTATTTTGCAGAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1740						
DB	1681	GACCTGTATTTTGCAGAGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1740						
QY	1741	GATGTATGGCTGGGCCCGCAGAGCTACTTCCGGTCTCTCTTCAACTGTCTTCGACTTTGG	1800						
DB	1741	GATGTATGGCTGGGCCCGCAGAGCTACTTCCGGTCTCTCTTCAACTGTCTTCGACTTTGG	1800						
QY	1801	GGTCATCGTGGGAGGCTTTTGAAGTGTCTGGGGGGCCATCAAGCCGGGAAAGCTTCTT	1860						
DB	1801	GGTCATCGTGGGAGGCTTTTGAAGTGTCTGGGGGGCCATCAAGCCGGGAAAGCTTCTT	1860						
QY	1861	TGGGATCAGTGTGCTCGGGGCCCTCCGCTCTGTGAGGATCTTCAAAGTCAAGAGTACTG	1920						
DB	1861	TGGGATCAGTGTGCTCGGGGCCCTCCGCTCTGTGAGGATCTTCAAAGTCAAGAGTACTG	1920						
QY	1921	GAGCTCCCTCGGAACTGGT	1980						
DB	1921	GAGCTCCCTCGGAACTGGT	1980						
QY	1981	GCTCTTCTTGTCTTCT	2040						
DB	1981	GCTCTTCTTGTCTTCT	2040						
QY	2041	GGGACAGTTTCAACTTCCAGGATGAGACTCCCAACCAACTTTCGACACCTTCCCTGCCCG	2100						
DB	2041	GGGACAGTTTCAACTTCCAGGATGAGACTCCCAACCAACTTTCGACACCTTCCCTGCCCG	2100						
QY	2101	CATCTCTACTGTCTTCCAGATCCTGACGGGAGGAGGACTGGAAATGCAATGATNTACGG	2160						

[illegible]

3181	CAAGGAAAGAGAGCTTCGAGAACACACAGACCCCGGAGGCCACACTGTGACCTTGGAGACCAG	3240
3241	TGGGACTGTGACTGTGGGTCCCATGCAACAACCTGCCAGCACCTGTCTCCAGAAAGGTGGA	3300
3241	TGGGACTGTGACTGTGGGTCCCATGCAACAACCTGCCAGCACCTGTCTCCAGAAAGGTGGA	3300
3301	GGAAACGCCAGAGGATGCAGACAATCAGCGGAACGTCTCTCCATGGGAGTCAAGCCCC	3360
3301	GGAAACGCCAGAGGATGCAGACAATCAGCGGAACGTCTCTCCATGGGAGTCAAGCCCC	3360
3361	AGACCCGGAACACTATTGTGACATATCCACAGTGATCTGACGGGCCCTCTTTGGGGAAGCCAC	3420
3361	AGACCCGGAACACTATTGTGACATATCCACAGTGATCTGACGGGCCCTCTTTGGGGAAGCCAC	3420
3421	GGTGTGTTCCAGTGGTAAACGTGGACCTTGGAAAGCCAAAGCAGAGGGGAAAGAGGAGTGGGA	3480
3421	GGTGTGTTCCAGTGGTAAACGTGGACCTTGGAAAGCCAAAGCAGAGGGGAAAGAGGAGTGGGA	3480
3481	AGCGGATGACGTGATGAGGAGCGGCCCTCCGGCCCTATCTGTCCTACATACAGTCCATGTTCTG	3540
3481	AGCGGATGACGTGATGAGGAGCGGCCCTCCGGCCCTATCTGTCCTACATACAGTCCATGTTCTG	3540
3541	TTTAAAGCCCAACCAACCTGCTCGCGCTTCTGCGCATACATCTGTCGACCATGAGGTACTT	3600
3541	TTTAAAGCCCAACCAACCTGCTCGCGCTTCTGCGCATACATCTGTCGACCATGAGGTACTT	3600
3601	CGAGGTGGTCAATCTCTGTGGTGCATCGCCTTGACAGCATCGCCCTGCTGAGGACCC	3660
3601	CGAGGTGGTCAATCTCTGTGGTGCATCGCCTTGACAGCATCGCCCTGCTGAGGACCC	3660
3661	AGTGGCGCACAGACTCGCCCAAGGAACACGCTCTGAAATACCTGGAATACATTTTCACTGG	3720
3661	AGTGGCGCACAGACTCGCCCAAGGAACACGCTCTGAAATACCTGGAATACATTTTCACTGG	3720
3721	TGCTCTTACCTTTGAGATGGTGATTAAGATGATCGACTTGGGACCTGCTCTCAACCTGG	3780
3721	TGCTCTTACCTTTGAGATGGTGATTAAGATGATCGACTTGGGACCTGCTCTCAACCTGG	3780
3781	AGCCTATTTCCGGGACTTGTGGAACATTTCTGGACTTCATTGTGGTCACTGGCGCCCTGGT	3840
3781	AGCCTATTTCCGGGACTTGTGGAACATTTCTGGACTTCATTGTGGTCACTGGCGCCCTGGT	3840
3841	GGCGTTTGTCTTCGAGCTTCGTGGGAGGATCCAAAGGGAAGACATCAATACCATCAA	3900
3841	GGCGTTTGTCTTCGAGCTTCGTGGGAGGATCCAAAGGGAAGACATCAATACCATCAA	3888
3901	GTCTCTGAGAGTCTTGTGTGTCCTGGGCCCTCAAGACCATCAAAACGGCTGCCCAAGCT	3960
3889	GTCTCTGAGAGTCTTGTGTGTCCTGGGCCCTCAAGACCATCAAAACGGCTGCCCAAGCT	3948
3961	CAAGGCTGTGTTTGACTGTGTGGTGAATCCCTCGAAGAATGTCCTCAACATCTTGATTGT	4020
3949	CAAGGCTGTGTTTGACTGTGTGGTGAATCCCTCGAAGAATGTCCTCAACATCTTGATTGT	4008
4021	CTACATGCTCTTCATGTTTCATATTGCGGTCAATGCGGTGCAGCTCTTCAAAGGGAAGTT	4080
4009	CTACATGCTCTTCATGTTTCATATTGCGGTCAATGCGGTGCAGCTCTTCAAAGGGAAGTT	4068
4081	TTTCTACTGCAAGATGAAATCAAGAGAGTGGAGAGGAGCTCAGGGGTCAAGTATTTGGA	4140
4069	TTTCTACTGCAAGATGAAATCAAGAGAGTGGAGAGGAGCTCAGGGGTCAAGTATTTGGA	4128
4141	TTATGAGAGGAGGAGTGGGAAGCTCAGCCCAAGGCGAGTGGGAAGAATAACGACTTTTCACTA	4200
4129	TTATGAGAGGAGGAGTGGGAAGCTCAGCCCAAGGCGAGTGGGAAGAATAACGACTTTTCACTA	4188
4201	CGACAATGTGCTCTGGGCTCTGCTGAGCGTGTTCAGTGTCCAGGGAGAGGCTGGCC	4260
4189	CGACAATGTGCTCTGGGCTCTGCTGAGCGTGTTCAGTGTCCAGGGAGAGGCTGGCC	4248
4261	CATGTGTGTGAAACAACCTCGTGGATGTCACCTATGAGAGAGCAGGGTCCAGCCCTGGGTA	4320
4249	CATGTGTGTGAAACAACCTCGTGGATGTCACCTATGAGAGAGGAGGGTCCAGCCCTGGGTA	4308

Db 6469 GGGCCGCTCCAGAGCGGAGCGCCCTCATCTCTCTCGGAGAAGCAGCGCTTCTA 6528
Qy 6541 CTCCTGCGACCGCTTTGGGGCGCGTGAAGCCCCCGAAGCCCAAGCCCTCCCTCAGCAGCCCA 6600
Db 6529 CTCCTGCGACCGCTTTGGGGCGCGTGAAGCCCCCGAAGCCCAAGCCCTCCCTCAGCAGCCCA 6588
Qy 6601 CCCAACGTCGCCCAACAGCTGCGCCAGGAGCGGAGCCCAAGCCCAAGGCGCAGTGTCCGT 6660
Db 6589 CCCAACGTCGCCCAACAGCTGCGCCAGGAGCGGAGCCCAAGCCCAAGGCGCAGTGTCCGT 6648
Qy 6661 GAATGGAGCGCCCTTGCTCAACATCTGGTGTAGCACCCTCCGCGCGCGTGGCGGAG 6720
Db 6649 GAATGGAGCGCCCTTGCTCAACATCTGGTGTAGCACCCTCCGCGCGCGTGGCGGAG 6708
Qy 6721 GCAGCTCCCCCAGACGCGCCCTGACTCCCGCGCCCGCAGCATCACTTACAAAGCGGCCAACTC 6780
Db 6709 GCAGCTCCCCCAGACGCGCCCTGACTCCCGCGCCCGCAGCATCACTTACAAAGCGGCCAACTC 6768
Qy 6781 CTCACCCATCCACTTCCCGGGGCTCAGACAGCCTCCCTGCTTCTCCCAAGCGCGGCT 6840
Db 6769 CTCACCCATCCACTTCCCGGGGCTCAGACAGCCTCCCTGCTTCTCCCAAGCGCGGCT 6828
Qy 6841 CAGCGTGGGCTTCCGAAACACACGCGCTGCTGCAGAGACCCCTCAGCCAGCCCT 6900
Db 6829 CAGCGTGGGCTTCCGAAACACACGCGCTGCTGCAGAGACCCCTCAGCCAGCCCT 6888
Qy 6901 GGCCCTGGCTCTGAAATGGCTCTGACCTTACTGGGCGAGCGTCTGACAGTGAAGC 6960
Db 6889 GGCCCTGGCTCTGAAATGGCTCTGACCTTACTGGGCGAGCGTCTGACAGTGAAGC 6948
Qy 6961 CTCTGTCCACGCGCTGCTGAGGACAGCTCACTTTCAGGAGCGTGTGCCCAACCACTC 7020
Db 6949 CTCTGTCCACGCGCTGCTGAGGACAGCTCACTTTCAGGAGCGTGTGCCCAACCACTC 7008
Qy 7021 GGGCGGCTCTCAGGATCTTCTACGTTCTCTCCCTGACCTCCAGTCTCACCTCTCCG 7080
Db 7009 GGGCGGCTCTCAGGATCTTCTACGTTCTCTCCCTGACCTCCAGTCTCACCTCTCCG 7068
Qy 7081 CCGGCTGCCCAACGCTTACCACTGCACCTCGGAGTCACTCGGTTGGCGGAGCAGCGCA 7140
Db 7069 CCGGCTGCCCAACGCTTACCACTGCACCTCGGAGTCACTCGGTTGGCGGAGCAGCGCA 7128
Qy 7141 CAGTACCAACCACTGACCAAGACCACTGCTAGCTGACCGTCAACCGTCAAGACGC 7200
Db 7129 CAGTACCAACCACTGACCAAGACCACTGCTAGCTGACCGTCAACCGTCAAGACGC 7188
Qy 7201 CTGATCGACGAGCGTGTGTTCCAGTGGATGAGTTTATCATCCACACGGGCGAGTCCG 7260
Db 7189 CTGATCGACGAGCGTGTGTTCCAGTGGATGAGTTTATCATCCACACGGGCGAGTCCG 7248
Qy 7261 CCCTCGGGGAGGCGTTGCCACCTTGGTGAAGGCTCTGTGGCCCTTCCCTCCCTCCCT 7320
Db 7249 CCCTCGGGGAGGCGTTGCCACCTTGGTGAAGGCTCTGTGGCCCTTCCCTCCCTCCCT 7308
Qy 7321 CCCCTCTTTTACTCTAGACGACGAATAAGCCCTGTTGTTGAGTGTACGTACCGC 7376
Db 7309 CCCCTCTTTTACTCTAGACGACGAATAAGCCCTGTTGTTGAGTGTACGTACCGC 7364

RESULT 4

AAV42685

ID AAV42685 standard; DNA; 7362 BP.

XX AC AAV42685;

XX DT 25-MAR-2003 (revised)

DT 12-OCT-1998 (first entry)

XX DE DNA encoding human calcium channel alpha-1B-1 subunit.

XX KW Alpha-1B subunit; human; calcium channel; assay; detection;

XX characterisation; Lambert Eaton Syndrome; LES; diagnosis; da.

XX OS Homo sapiens.
XX FH 5'UTR Location/Qualifiers
FT 1. .143 /tag= a
FT CDS 144. .7163 /tag= b
FT 3'UTR 7161. .7362 /tag= c
XX US5792846-A.
XX 11-AUG-1998.
XX 31-MAY-1995; 95US-00455543.
XX 04-APR-1988; 88US-00176899.
XX 04-APR-1989; 89WO-US001408.
XX 20-FEB-1990; 90US-00482384.
XX 08-NOV-1990; 90US-00603751.
XX 30-NOV-1990; 90US-00620250.
XX 15-AUG-1991; 91US-00745206.
XX 04-APR-1994; 94US-00223305.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Brenner R, Ellis SB, Williams ME, Feldman DH, Mccue AF;
PI Harpold MM;
XX WPI; 1998-456192/39.
XX P-PSDB; AAW63141.
XX DNA encoding human calcium channel alpha 1B subunit protein - useful for
XX recombinant production of the channel for screening of its modulators,
XX and diagnosis of Lambert Eaton Syndrome.
XX Claim 1; Col 75-92; 166pp; English.
XX The present sequence encodes the alpha-1B subunit of a human calcium
XX channel. Calcium channels are membrane-spanning, multi-subunit proteins
XX that allow controlled entry of calcium ions into cells. This leads to
XX depolarisation events required for muscle contraction. The recombinant
XX subunit, when expressed with nucleic acids encoding the complete calcium
XX channel, can be used in assays for the detection and characterisation of
XX compounds that modulate the channel. The DNA encoding the subunits can be
XX alternatively spliced when transcribed, giving more than one form of the
XX protein from the same transcript, each having slightly different
XX properties. In addition, the reactivity of the alpha 1 subunit with IgG
XX molecules from the serum of an individual with Lambert Eaton Syndrome
XX (LES) can be used as a diagnostic for the disease. (Updated on 25-MAR-
XX 2003 to correct PR field.)
XX SQ Sequence 7362 BP; 1445 A; 2277 C; 2215 G; 1425 T; 0 U; 0 Other;
Query Match 99.2%; Score 7316.4; DB 2; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;
Qy 1 GCGGCGCGCGCTCGCGCGGTGGGGCCGGGCGAGGTCCGTCGGTCCCGCGGCTCCGTG 60
Db 1 GCGGCGCGCGCTCGCGCGGTGGGGCCGGGCGAGGTCCG-TGCGGTCCCGCGGCTCCGTG 59
Qy 61 GCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCGGCGCTCCCTCCCGGGGCGCGTGGGCGG 120
Db 60 GCTGCTCCGCTCTGAGCGCTT-GCGGCGCCCGCGGCGCTCCCTCCCGGGGCGCGTGGGCGG 118
Qy 121 GGGATGCACGCGGGGCCCGGAGCCATGTTGTCGCTTTCGGGGACGAGCTGGCGCGCCGCTA 180
Db 119 GGGATGCACGCGGGGCCCGGAGCCATGTTGTCGCTTTCGGGGACGAGCTGGCGCGCCGCTA 178
Qy 181 TGGAGGCGCGCGCGGCGGAGAGCGGCGCCCGGGCGCGCGCGCGCGGGGGGGGGCCCC 240

Db 179 TGGAGGCCCCGGGGGGAGAGCGGGCCCGGGGCGGGGCGGGGGGGCC 238
Qy 241 GGGTCCCGGGGGGTGTCAGAGCCCGGCGAGCGGGTCCCTTACAGCAATCATCGCGAGCG 300
Db 239 GGGTCCCGGGGGGTGTCAGAGCCCGGCGAGCGGGTCCCTTACAGCAATCATCGCGAGCG 298
Qy 301 CGCGCGAACCATGGCGCTGTACAAACCCCATCCGGTCAAGCAGAACTGCTTACCGTCAA 360
Db 299 CGCGCGAACCATGGCGCTGTACAAACCCCATCCGGTCAAGCAGAACTGCTTACCGTCAA 358
Qy 361 CGCGTGGCTTCCCTTTCAGCGAGAGCAACAGTGTCCGCAATATCGCGAGCGCATCAC 420
Db 359 CGCGTGGCTTCCCTTTCAGCGAGAGCAACAGTGTCCGCAATATCGCGAGCGCATCAC 418
Qy 421 CGAGTGGCTTCCCTTTCAGAGATATGATCCTGGCCACCATCATCGCCAACTGATCGTGT 480
Db 419 CGAGTGGCTTCCCTTTCAGAGATATGATCCTGGCCACCATCATCGCCAACTGATCGTGT 478
Qy 481 GGGCTTGGAGAGCACTCCCTGTATGGGGAACAAAGCCCATGTCCGAGCGCTGGACGA 540
Db 479 GGGCTTGGAGAGCACTCCCTGTATGGGGAACAAAGCCCATGTCCGAGCGCTGGACGA 538
Qy 541 CAGGAGCCCTATTTTCATCGGGATCTTTTTCGCTTTCGAGCGAGGATCAAAATCATCGCT 600
Db 539 CAGGAGCCCTATTTTCATCGGGATCTTTTTCGCTTTCGAGCGAGGATCAAAATCATCGCT 598
Qy 601 GGGCTTGTCTTCCCAAGAGGGCTCTTACCTCGGGGAACGGCTGGAACGTATGGACTTCGT 660
Db 599 GGGCTTGTCTTCCCAAGAGGGCTCTTACCTCGGGGAACGGCTGGAACGTATGGACTTCGT 658
Qy 661 GGTGTCTTCAGAGGATCTTGCACCGCTGGAACTGACTTTCGACCTGCGAACAACCTGAG 720
Db 659 GGTGTCTTCAGAGGATCTTGCACCGCTGGAACTGACTTTCGACCTGCGAACAACCTGAG 718
Qy 721 GGTGTGTGTGTGTCAGAGCCCTTGAAGCTGTGTCTGGATTCGAAGTTCGAGGTGGT 780
Db 719 GGTGTGTGTGTGTCAGAGCCCTTGAAGCTGTGTCTGGATTCGAAGTTCGAGGTGGT 778
Qy 781 GGTCAAGTCCATCATGAAGGCCATGGTCCCATCTCTGAGATTTGGGCTGTCTTCTTCT 840
Db 779 GGTCAAGTCCATCATGAAGGCCATGGTCCCATCTCTGAGATTTGGGCTGTCTTCTTCTT 838
Qy 841 TGCCATCTCATGTTTGGCATATTTGGCTGGAGTTCATATGGCAAGTTTCBAAGGC 900
Db 839 TGCCATCTCATGTTTGGCATATTTGGCTGGAGTTCATATGGCAAGTTTCBAAGGC 898
Qy 901 CTGTTTCCCCAAACAGCACAGATGCGAGCCCGTGGTGCATTTCCCTGTGTGCAAGGAGGC 960
Db 899 CTGTTTCCCCAAACAGCACAGATGCGAGCCCGTGGTGCATTTCCCTGTGTGCAAGGAGGC 958
Qy 961 CCCAGCCGGTGTGCGAGGGGACACTGAGTGCAGGAGTACTTGGCCAGGACCCAACTT 1020
Db 959 CCCAGCCGGTGTGCGAGGGGACACTGAGTGCAGGAGTACTTGGCCAGGACCCAACTT 1018
Qy 1021 TGGCATCACCAACTTGGATATCTCTTTGGCATCTTGGCATCTTGGCATCTTGGCATCTAC 1080
Db 1019 TGGCATCACCAACTTGGATATCTCTTTGGCATCTTGGCATCTTGGCATCTTGGCATCTAC 1078
Qy 1081 CATGAGGGGCTGGAATGATCATCTCTTATAATAACAAACGATCGCGCCGCGCAACCTGGAA 1140
Db 1079 CATGAGGGGCTGGAATGATCATCTCTTATAATAACAAACGATCGCGCCGCGCAACCTGGAA 1138
Qy 1141 CTGGCTCTACTTCTTCTCTCATCATCATCGGTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
Db 1139 CTGGCTCTACTTCTTCTCTCATCATCATCGGTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1198
Qy 1201 GGGCTGTCTCTCGGGGAGTTTGCAGAGCGAGAGGGTGGAGAACCGCGCGCTT 1260
Db 1199 GGGCTGTCTCTCGGGGAGTTTGCAGAGCGAGAGGGTGGAGAACCGCGCGCTT 1258
Qy 1261 CCTGAAGCTGCGCGGACGACAGATCGAGCGAGAGCTCAACGGGTACCTTGGAGTGGAT 1320
Db 1259 CCTGAAGCTGCGCGGACGACAGATCGAGCGAGAGCTCAACGGGTACCTTGGAGTGGAT 1318

Qy 1321 CTTCAAGCGCGAGGAAGTCATGCTGGCGGAGGAGGACAGGAATCCAGAGAGGAAGTCCCC 1380
Db 1319 CTTCAAGCGCGAGGAAGTCATGCTGGCGGAGGAGGACAGGAATCCAGAGAGGAAGTCCCC 1378
Qy 1381 TTTTGAAGCTGTGAAGAGAGCGGCACCAAGAGAGCAGAAATGACCTGATCCACGAGAGA 1440
Db 1379 TTTTGAAGCTGTGAAGAGAGCGGCACCAAGAGAGCAGAAATGACCTGATCCACGAGAGA 1438
Qy 1441 GGAAGGAGAGAACCGGTTTCAGATCTCTGTGTGTGTGGATCCCTTTCGCCCGCGCCAG 1500
Db 1439 GGAAGGAGAGAACCGGTTTCAGATCTCTGTGTGTGTGGATCCCTTTCGCCCGCGCCAG 1498
Qy 1501 CCTCAAGAGCGGAGAGACAGAGAGCTCGTATCTTCCGAGGAGAGAGATGTTCCG 1560
Db 1499 CCTCAAGAGCGGAGAGACAGAGAGCTCGTATCTTCCGAGGAGAGAGATGTTCCG 1558
Qy 1561 GTTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGTCGTGGT 1620
Db 1559 GTTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGTCGTGGT 1618
Qy 1621 GGCCTGAAACACTGTGTGTGGCCATGTGTCATTAACAACGCGCGCGCTTACCAC 1680
Db 1619 GGCCTGAAACACTGTGTGTGGCCATGTGTCATTAACAACGCGCGCGCTTACCAC 1678
Qy 1681 GACCTGTATTTTGCAGAGTTTCTTCTGGGTCTTCTTCTTCAACAGAGATGTCCTGAA 1740
Db 1679 GACCTGTATTTTGCAGAGTTTCTTCTGGGTCTTCTTCTTCAACAGAGATGTCCTGAA 1738
Qy 1741 GATGTATGGCTTGGGCCCCAGAAAGTACTTTCGGGTCTCTTCTTCAACTGTCTTGG 1800
Db 1739 GATGTATGGCTTGGGCCCCAGAAAGTACTTTCGGGTCTCTTCTTCAACTGTCTTGG 1798
Qy 1801 GGTCTATGTTGGGAGAGCTCTTTGAAGTGTCTGGGCGGCCATCAAGCGGGAAGTCTCTT 1860
Db 1799 GGTCTATGTTGGGAGAGCTCTTTGAAGTGTCTGGGCGGCCATCAAGCGGGAAGTCTCTT 1858
Qy 1861 TGGGATCAGTGTCTCGGGCCCTCCGCTGTGTGAGGATCTTCAAAAGTCAAGAGTACTG 1920
Db 1859 TGGGATCAGTGTCTCGGGCCCTCCGCTGTGTGAGGATCTTCAAAAGTCAAGAGTACTG 1918
Qy 1921 GAGTCTCTTGGGAACTCTGGTGTGTCTTCTGTGTAACTCCATGAAGTCAATCATAGCCT 1980
Db 1919 GAGTCTCTTGGGAACTCTGGTGTGTCTTCTGTGTAACTCCATGAAGTCAATCATAGCCT 1978
Qy 1981 GCTCTTCTTGTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2040
Db 1979 GCTCTTCTTGTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2038
Qy 2041 GGGACAGTTTCACTTCCAGGATGAGACTCCCAACCAACTTCCGACACCTTCCCTGCCGC 2100
Db 2039 GGGACAGTTTCACTTCCAGGATGAGACTCCCAACCAACTTCCGACACCTTCCCTGCCGC 2098
Qy 2101 CATCTCTACTGTCTTCCAGATCTTGAAGGAGGACTGGAATGCAAGTCAATCATACCG 2160
Db 2099 CATCTCTACTGTCTTCCAGATCTTGAAGGAGGACTGGAATGCAAGTCAATCATACCG 2158
Qy 2161 GATCGAATCGAAGCGGCTCAGCAAGGAGTGTCTGTCTTCTTCTTCTTCTTCTTCTTCT 2220
Db 2159 GATCGAATCGAAGCGGCTCAGCAAGGAGTGTCTGTCTTCTTCTTCTTCTTCTTCTTCT 2218
Qy 2221 GACACTGTTTCCGAACTACACTCTGTGAATGTCTTCTTGGCCATCGCTGTGGAACCT 2280
Db 2219 GACACTGTTCCGAACTACACTCTGTGAATGTCTTCTTGGCCATCGCTGTGGAACCT 2278
Qy 2281 GGGCAACGCCCAAGAGCTGACCAAGATGAAGAGAGATGGAAGAGAGAGTCAATCAGAA 2340
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Qy 2341 GCTTGTCTTCAAAAGGGCCAAAGAGTGTGCTGAAGTGTGCTGAGAGTGTGCTGAGAGT 2400
Db 2339 GCTTGTCTTCAAAAGGGCCAAAGAGTGTGCTGAAGTGTGCTGAGAGTGTGCTGAGAGT 2398

Db	4547	GGTCTCCCGCCCTTTGAAATATCTTCAATCATGGCCATGATAGCCCTCAACACATGTGGTGCT	4606	QY	5701	GATGACAGTGGGAAGGTTTATGACAGCTCTCATGATATTTCACTTCTACAGCAACAA	5760
QY	4621	GATGATGAAGTTCTATGATGACCCCTATGATGACGAGCTGATGCTGAATGACCTGACAT	4680	Db	5687	GATGACAGTGGGAAGGTTTATGACAGCTCTCATGATATTTCACTTCTACAGCAACAA	5746
Db	4607	GATGATGAAGTTCTATGATGACCCCTATGATGACGAGCTGATGCTGAATGCTGGAACAT	4666	QY	5761	AACCAACAGAGACACAGATGACAGCAGGCTCTGAGGAGCTCTCCAGATGGGTCTGTGTC	5820
QY	4681	CGTGTTCATATCCATGTTCTCCATGGAATGCGTCTGAAAGATCATCGCCTTTGGGGTGCT	4740	Db	5747	AACCAACAGAGACACAGATGACAGCAGGCTCTGAGGAGCTCTCCAGATGGGTCTGTGTC	5806
Db	4667	CGTGTTCATATCCATGTTCTCCATGGAATGCGTCTGAAAGATCATCGCCTTTGGGGTGCT	4726	QY	5821	CCTGTTCCACCTCTGAAGGCCACCTTGGAGCAGACACAGCCGCTGTGCTCCAGGAGC	5880
QY	4741	GAACTATTTGAGAGATGCTGGAATGCTTTGACTTTGTCACATGTTGGGAAGTATTAC	4800	Db	5807	CCTGTTCCACCTCTGAAGGCCACCTTGGAGCAGACACAGCCGCTGTGCTCCAGGAGC	5866
Db	4727	GAACTATTTGAGAGATGCTGGAATGCTTTGACTTTGTCACATGTTGGGAAGTATTAC	4786	QY	5881	CGGGTTTTCTTTCGACAGAAAGATTCCACTCCTCAGCAATGGCGGGCCATACAAAA	5940
QY	4801	TGATATTTTAAAGAGATGCGGAACGAAATTTTCACTCAACCTCAGCTTCTCTCG	4860	Db	5867	CGGGTTTTCTTTCGACAGAAAGATTCCACTCCTCAGCAATGGCGGGCCATACAAAA	5926
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QY	4921	GCTGTGAGCTTTGTCCAGTCTTTCAAGGCCCTGCGCTAGCTGCTGCTCATTTGCCAT	4980	Db	5987	CCATGAGGCCAGGCCACCCCTGGAGCGTGCCACTCCACAGAGATCCTCTGTGGGCGGTC	6046
Db	4907	GCTGTGAGCTTTGTCCAGTCTTTCAAGGCCCTGCGCTAGCTGCTGCTCATTTGCCAT	4966	QY	6061	AGGAGCACTGCTGTGAGCGTTCAGATGACAGCATTAACCGGAGGGCCCTCATTGGGGA	6120
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QY	5161	GGCCTGTGATGACAGGCCAATGCCACCGAGTGTGGAGTGACTTTTGCTACTTCTACTT	5220	Db	6227	GCCCCGTGGGACTCATCTTTGACAGCACCCCGGACCGCCACCGGACCGCCCTTAGCGGCGTC	6286
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QY	5221	CGTCTCCTTTCATCTTCTGCTGCTCTTCTGATGTTGAACCTTTTGGCTGTGATCAT	5280	Db	6287	GTGCGACCAACCAACCGCTGCCACCGCGCAGGGAAGCAAGAGAGAGAGTCTCTGGA	6346
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QY	5401	CATGTTTGAATGCTGAACACATGCTCCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460	Db	6467	GGGCGGCTCCAGAGCGGAGGAGCGCTCTCATCTCTCTCGGAGAGAGAGCGCTTCTA	6526
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QY	5461	TCGAGTTGCTTAAAGCGCTGGTTGCGATGAACATGCCATCTCCAAACGAGGACATGAC	5520	Db	6527	CTCCTCGACCGCTTTGGGGCCCTGAGCCCGGAGCCCAAGCCCTCCCTCAGCAGCA	6586
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Db	5567	CCAGCTGGGCAAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGAGATTTCCGTTGT	5626	QY	6721	GCAGTCTCCCGCAGAGCGCCCTGACTCTCCCGGCCAGCATCACCTACAGAGCGGCCAATCTC	6780
QY	5641	GTGGGCCAATCTGCCAGAGACTTTGGACTTGTGCTATCCACCCCATTAAGCCTGATGA	5700	Db	6707	GCAGTCTCCCGCAGAGCGCCCTGACTCTCCCGGCCAGCATCACCTACAGAGCGGCCAATCTC	6766
Db	5627	GTGGGCCAATCTGCCAGAGACTTTGGACTTGTGCTATCCACCCCATTAAGCCTGATGA	5686				

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Db 7187 CTGCATCAGCAGCGGTGTGTTCCAGTGGATGAGTTTATCATCCACAGGGGAGTCCG 7246
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RESULT 5
ID AAA71703
XX AAA71703 standard; DNA; 7362 BP.
AC AAA71703;
XX
XX 22-DEC-2000 (first entry)
XX
XX Human calcium channel alphaB-1 subunit encoding DNA.
XX
XX Human; calcium channel; calcium channel subunit; diagnosis;
XX Lambert Eaton Syndrome; calcium channel subunit alphaB-1; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 144..7163
XX /*tag= a
XX /product= "calcium channel alphaB-1 subunit"
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XX
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XX
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XX 02-FEB-1990; 90US-00482384.
XX 08-NOV-1990; 90US-00603751.
XX 30-NOV-1990; 90US-00620250.
XX 15-AUG-1991; 91US-00745206.
XX 10-APR-1992; 92US-00868354.
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PR 13-JUL-1992; 92US-00914231.
PR 11-AUG-1993; 93US-00105536.
PR 05-NOV-1993; 93US-00149097.
PR 07-FEB-1994; 94US-00193078.
PR 04-APR-1994; 94US-00223305.
PR 11-AUG-1994; 94US-00290012.
PR 23-SEP-1994; 94US-00311363.
PR 28-SEP-1994; 94US-00314083.
PR 07-NOV-1994; 94US-00336257.
PR 13-MAR-1995; 95US-00404950.
XX
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX
XX Ellis SB, Williams ME, Mccue AF, Harpold MM;
XX P-PSDB; AAB10572.
XX
XX WPI; 2000-548230/50.
XX
XX Human calcium channel beta subunit polynucleotides, useful for producing
XX recombinant eukaryotic cells and for diagnosing Lambert Eaton Syndrome.
XX
XX Example II; Col 97-112; 153pp; English.
XX
XX This invention describes a novel isolated DNA molecule (I) comprising a
XX sequence encoding a beta3-1 subunit of a human calcium channel. Nucleic
XX acid probes comprising 14-30 contiguous nucleotides of beta 3 subunit
XX encoding DNA are useful for isolation and cloning of calcium channel
XX subunit-encoding DNA. Recombinant eukaryotic cells that express
XX heterologous calcium channel are useful for identifying compounds that
XX modulate calcium channel activity and in assays for identifying agonists
XX and antagonists of calcium channel activity in humans. Human calcium
XX channel subunit or eukaryotic cells expressing the channel are useful for
XX diagnosing Lambert Eaton Syndrome (LES) in a human. This sequence encodes
XX the human calcium channel alphaB-1 subunit which is described in the
XX method of the invention
XX
XX SQ Sequence 7362 BP; 1445 A; 2277 C; 2215 G; 1425 T; 0 U; 0 Other;
XX
XX Query Match 99.2%; Score 7316.4; DB 3; Length 7362;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;
Qy 1 GCGGCGCGGCTCGCGCGTGGGCGCGGCGAGGTTCGGTCCGTCGCCGCGGCTCCGCGT 60
Db 1 GCGGCGCGGCTCGCGCGTGGGCGCGGCGAGGTTCGGTCCGTCGCCGCGGCTCCGCGT 59
Qy 61 GCTGCTCCGCTCTGAGCGCTGCGCGCCCGCGCCCTCCCTGCGCGGCGGCTGGGCGG 120
Db 60 GCTGCTCCGCTCTGAGCGCTT-GCGGCGCCCGCGCCCTCCCTGCGGCGGCGCTGGGCGG 118
Qy 121 GGGATGCACGCGGCGCGCGGAGCCATGGTCCGCTTCGGGAGCAGAGCTGGGCGCGCTA 180
Db 119 GGGATGCACGCGGCGCGCGGAGCCATGGTCCGCTTCGGGAGCAGAGCTGGGCGCGCTA 178
Qy 181 TGGAGGCGCGCGCGGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 240
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Db 419 CGAGTGGCTTCCATTCGAGTATATGATCCTGGGCCACCATCATCGCAACTGCTGCTGT 478
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Db 479 GGCCCTGGAGCAGCACCTCCTGATGGGACAAAAAGCCCAATGTCGAGCGGCTGACGA 538
QY 541 CACGAGCCCTATTTCATCGGGAATCTTTGCTCGAGGCAAGGATCAAAATCATCGCTCT 600
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QY 601 GGGCTTTGCTCTCCACAAGGGCTCTTACCTGCGGAACGGCTGAAAGTCAATGAGACTTCGT 660
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QY 661 GGTGCTCCTCACAGGATCTTGCACAGGCTGAACTGACTTCGACTCGCAACACTGAG 720
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QY 721 GGTGCTGCTGCTGAGGCCCCCTGAGCTGGTGTCTGGGATTCGAAGTTTGAGGTGT 780
Db 719 GGTGCTGCTGCTGAGGCCCCCTGAGCTGGTGTCTGGGATTCGAAGTTTGAGGTGT 778
QY 781 GCTCAAGTCCATCATGAAGGCCATGTTCCACTCTCGCAGATTGGGCTGCTCTCTCTT 840
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QY 841 TGGCATCCTCATGTTTGCACATCATTTGGCTTGAGTTCTACATGGGCAAGTTCCACAAGGC 900
Db 839 TGGCATCCTCATGTTTGCACATCATTTGGCTTGAGTTCTACATGGGCAAGTTCCACAAGGC 898
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Db 899 CTGTTTCCCCAACAGCACAGATCGGAGCCCGTGGGTGACTTCCCTGTTGGCAAGGAGC 958
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QY 1501 CTTCAAGAGCGGAGAGCAGAGACTCGTCTACTCTTCGGAGGAGAGAGATGTTCCG 1560
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QY 1561 GTTTTATTATCCGGCCATGGTGAAGGCTCAGAGCTTCTACTGGGTGGTGCTGTGGGTGGT 1620
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Db 3301 GGAAACGCCAGGAGATCAGACATCAGCGGAACGTCACTCGCATGGGAGTCAAGCCCC 3360
Qy |||||
Db 3299 GGAAACGCCAGGAGATCAGACATCAGCGGAACGTCACTCGCATGGGAGTCAAGCCCC 3358
Qy |||||
Db 3361 AGACCCGAAACACTATTGTATATATCCAGTGTGCTGACGGGCCCTCTTGGGNAAGCCAC 3420
Qy |||||
Db 3359 AGACCCGAAACACTATTGTATATATCCAGTGTGCTGACGGGCCCTCTTGGGNAAGCCAC 3418
Qy |||||
Db 3421 GGTCTGTTCCAGTGTAACTGGACCTGGAAGCCAAAGCAGAGGGGAAGAGGTGGA 3480
Qy |||||
Db 3419 GGTCTGTTCCAGTGTAACTGGACCTGGAAGCCAAAGCAGAGGGGAAGAGGTGGA 3478
Qy |||||
Db 3481 AGCGGATGACGTGATGAGGAGCGGCCCGCGCCTATCGTCCCATACAGCTCCATGTTCTG 3540
Qy |||||
Db 3479 AGCGGATGACGTGATGAGGAGCGGCCCGCGCCTATCGTCCCATACAGCTCCATGTTCTG 3538
Qy |||||
Db 3541 TTTAAGCCCCACCAACCTGCTCCGCGCTTCTGCACTACATCGTGACCATGAGGTACTT 3600
Qy |||||
Db 3539 TTTAAGCCCCACCAACCTGCTCCGCGCTTCTGCACTACATCGTGACCATGAGGTACTT 3598
Qy |||||
Db 3601 CGAGGTGTCATCTCTGTGTCATCGCTTGAGCAGCATCGCCCTGCTCTGAGGACCC 3660
Qy |||||
Db 3599 CGAGGTGTCATCTCTGTGTCATCGCTTGAGCAGCATCGCCCTGCTCTGAGGACCC 3658
Qy |||||
Db 3661 AGTGCACACAGACTCGCCCGAGAAACAACGCTCTGAATACTCGGATTACATTTTCACTGG 3720
Qy |||||
Db 3659 AGTGCACACAGACTCGCCCGAGAAACAACGCTCTGAATACTCGGATTACATTTTCACTGG 3718
Qy |||||
Db 3721 TGTCTTTACCTTTGAGATGTTGATAAAGATGATCGATTGGGACTGCTTCACTCCCTCG 3780
Qy |||||

Db 3719 TGTCTTTACCTTTGAGATGTTGATAAAGATGATCGACTTGGGACTGCTGCTTCACTCCCTGG 3778
Qy |||||
Db 3781 AGCTATTTTCCGGGACTTGTGGAAACATTTCTGGACTTCAATTGTGGTCAAGTGGCGCCCTGGT 3840
Qy |||||
Db 3779 AGCTATTTTCCGGGACTTGTGGAAACATTTCTGGACTTCAATTGTGGTCAAGTGGCGCCCTGGT 3838
Qy |||||
Db 3841 GCGTGTGCTTTCTCGAGCTTCTGGGAGGATCCAAAGGGAAAAGACATCAATACCATCAA 3900
Qy |||||
Db 3839 GCGTGTGCTTTCTC-----AGGATCCAAAGGGAAAAGACATCAATACCATCAA 3886
Qy |||||
Db 3901 GTCTCTGAGAGTCTTCTGTGCTCGGGCCCCCAAGACCATCAAAAGCGCTGCCCAAGCT 3960
Qy |||||
Db 3887 GTCTCTGAGAGTCTTCTGTGCTCGGGCCCCCAAGACCATCAAAAGCGCTGCCCAAGCT 3946
Qy |||||
Db 3961 CAAGGCTGTGTTTGACTGTGTGTGAACCTCCCTGGAAGAAATGTCTCAACATCTTGATTTGT 4020
Qy |||||
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Qy |||||
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Qy |||||
Db 4007 CTACATGCTCTTCATGTTCAATTTTGCCTCATTTGGGTGTCAGCTCTTCAAGGGAGTT 4066
Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
Db 4201 CGACAATGTGCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCAAGGGAGAGGCTGGCC 4260
Qy |||||
Db 4187 CGACAATGTGCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCAAGGGAGAGGCTGGCC 4246
Qy |||||
Db 4261 CATGGTGTGAACACTCCGTGGATGCCACTATGAGGAGCGGCTCCAGGCGCTGGGA 4320
Qy |||||
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Qy |||||
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Db 4367 CAACATCTTTTGTGGCTTTGATCATCATCTTCCAGGAGCAGGGGACAAGGTGATGTC 4426
Qy |||||
Db 4441 TGAATCAGCCTCGAGAGAAACGAGAGGCTTCATTTGACTTCGCCATCAGCGCCAAACC 4500
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Db 4427 TGAATCAGCCTCGAGAGAAACGAGAGGCTTCATTTGACTTCGCCATCAGCGCCAAACC 4486
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Qy |||||
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Qy |||||
Db 4561 GGTCTCCCGCCCTTTGAATACATTTTCATGTCATGTCATGATAGCCCTCAACACTGTGTGCT 4620
Qy |||||
Db 4547 GGTCTCCCGCCCTTTGAATACATTTTCATGTCATGTCATGATAGCCCTCAACACTGTGTGCT 4606
Qy |||||
Db 4621 GATGATGAGTTCATGATGACCCCTATGATGACGAGCTGATGCTGAAATGCTGGAACAT 4680
Qy |||||
Db 4607 GATGATGAGTTCATGATGACCCCTATGATGACGAGCTGATGCTGAAATGCTGGAACAT 4666
Qy |||||
Db 4681 CGTGTTCACATCCATGTTCTCCATGGAATCGCTGCTGAAGATCATCGCCCTTTGGGGTGTCT 4740
Qy |||||
Db 4667 CGTGTTCACATCCATGTTCTCCATGGAATCGCTGCTGAAGATCATCGCCCTTTGGGGTGTCT 4726
Qy |||||
Db 4741 GAACTATTTACAGAGATGCTCGGAATGCTTTGACTGTGCTGCTGTTGGGAAGTATTAC 4800
Qy |||||
Db 4727 GAACTATTTACAGAGATGCTCGGAATGCTTTGACTGTGCTGCTGTTGGGAAGTATTAC 4786
Qy |||||
Db 4801 TGATATTTTAGTAAACAGAGTTCCGGAAACGAAATTTTCACTCAACCTCAGCTTCTCCG 4860
Qy |||||
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Qy |||||

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QY 6061 AGGAGCACTGGCTGTGGACGTTAGATGACAGAGATAACCCGGAGGGGCTCTGATGGGGA 6120
DB AGGAGCACTGGCTGTGGACGTTAGATGACAGAGATAACCCGGAGGGGCTCTGATGGGGA 6106
QY 6121 GCCCCAGCTGGGCTGGAGAGCCAGGCTGAGCGGCTTCATGCCCCCGCTTTGGCGCGGA 6180
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DB GACTCAGCCGCTACAGATGCCAGCCCATGAAAGCGCTTCCATCTTCCACGCTTGGGCCACGC 6226
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QY 6661 GAATGGGAGCCCTTGTCTGTCAACATCTGTGTAGCAACCCCGCGCGGTGGGCGGAG 6720
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QY 7021 GGGCGCTCTCTCCAGGACTTCTCTAGTGTCTCTCCCTGACCTCCAGCTCTCACCTCTCG 7080

Db 7007 GGGCGGCTCTCCAGGACTTCTACGTTGCTCTCCCTGACCTCCAGTCTCACCCCTCTCCG 7066
Qy 7081 CCGGTCGCCCAACGGTTTACCACTGCACCTCGGACTCAGCTCGGGTGGCGGAGCAGCGCA 7140
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Qy 7201 CTGCATGCAGACGCGTGTCTTCAGTGGATGAGTTTATCATCCACACGGGAGTCGG 7260
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Qy 7261 CCCTCGGGGAGGCTTGGCCACCTTGGTGAAGTCTCTGGGCGCCCTCCCTCCCTCCCT 7320
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Db 7307 CCCTCTTTTACTCTAGACGACGAATAAGCCCTGTGTTGTTGAGTGATGATACCGC 7362

RESULT 6
AAD39955
ID AAD39955 standard; DNA; 7362 BP.
AC AAD39955;
XX 22-OCT-2002 (first entry)
XX Human calcium channel alpha 1B-1 protein encoding DNA.
XX Human; calcium channel protein; therapeutic; autoimmune disease;
KW diagnosis; Lambert Eaton Syndrome; alpha 1B-1 protein; splice variant;
KW gene; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT 5'UTR 1..143
FT /*tag= a
FT CDS 144..7163
FT /*tag= b
FT /product= "Human calcium channel alpha 1B-1 protein"
FT 3'UTR 7164..7362
FT /*tag= c

XX US6387696-B1.
XX
XX 14-MAY-2002.
XX
XX 25-MAY-1995; 95US-00450272.
XX
XX 04-APR-1989; 89WO-US001408.
XX 02-FEB-1990; 90US-00482384.
XX 08-NOV-1990; 90US-00603751.
XX 30-NOV-1990; 90US-00620250.
XX 15-AUG-1991; 91US-00745206.
XX 13-JUL-1992; 92US-00914231.
XX 14-AUG-1992; 92WO-US006903.
XX 11-AUG-1993; 93US-00105536.
XX 05-NOV-1993; 93US-00149097.
XX 07-FEB-1994; 94US-00193078.
XX 04-APR-1994; 94US-00223305.
XX 11-AUG-1994; 94US-00290012.
XX 23-SEP-1994; 94US-00311363.
XX 07-NOV-1994; 94US-00336257.
XX 15-FEB-1995; 95US-00404354.
XX (MERI) MERCK & CO INC.

PI Harpold MM, Ellis SB, Williams ME, Mccue AF;
XX WPI; 2002-470318/50.
DR P-PSDB; AAE24785.
XX
PT Eukaryotic cells expressing a functional heterologous human calcium
channel and encoding nucleic acid isolated from human cerebellum for drug
design and to diagnose Lambert Eaton Syndrome.
XX
PS Example 2; Col 97-114; 154pp; English.
XX
CC The present invention relates to novel human calcium channel proteins and
polynucleotides encoding such proteins. The invention also relates to
eukaryotic cells expressing a functional heterologous human calcium
channel alpha 1, alpha 2, beta and gamma subunits. The eukaryotic cells
are useful for screening for potential calcium channel antagonists or
agonists to select compounds that have potential as disease or tissue-
specific therapeutic agents. The subunits may be used in diagnostic
assays for the autoimmune disease Lambert Eaton Syndrome. The present
sequence is a DNA encoding human calcium channel alpha 1B subunit splice
variant, alpha 1B-1 protein
XX
SQ Sequence 7362 BP; 1445 A; 2277 C; 2215 G; 1425 T; 0 U; 0 Other;
Query Match 99.2%; Score 7316.4; DB 6; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;
Qy 1 GCGGCGGCGGCTGCGGCGGTGGGGCGGGAGGTCCGGTCCGGTCCCGGCGGCGCGCG 60
Db 1 GCGGCGGCGGCTGCGGCGGTGGGGCGGGAGGTCCG--TGCGGTCCCGGCGGCTCCGTG 59
Qy 61 GCTGCTCCGCTCTGAGCGCTTGGCGGCGCCCGCGGCGCTTCCCTCCCGGGCGGCTGGCCG 120
Db 60 GCTGCTCCGCTCTGAGGCGCT--GCGGCGCCCGCGGCGCTTCCCTCCCGGGCGGCTGGCCG 118
Qy 121 GGGATGACGCGGGGCGCGGAGCCATGTGTCCGCTTCGGGGACGAGTGGGCGGCGCGCTA 180
Db 119 GGGATGACGCGGGGCGCGGAGCCATGTGTCCGCTTCGGGGACGAGTGGGCGGCGCGCTA 178
Qy 181 TGGAGGCGCGGCGGAGAGCGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGCC 240
Db 179 TGGAGGCGCGGCGGCGGAGAGCGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGCC 238
Qy 241 GGGTCCCGGGGGCTGCAGCCCGCGGCGGCGGCTCTCTACAAGCAATTCGATCCGCGAGCG 300
Db 239 GGGTCCCGGGGGCTGCAGCCCGCGGCGGCGGCTCTCTACAAGCAATTCGATCCGCGAGCG 298
Qy 301 CGCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGTCTTCAACCGTCAA 360
Db 299 CGCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGTCTTCAACCGTCAA 358
Qy 361 CGGCTCGCTTTCGCTTTCAGCGAGGACCAACGTCGTCGCGCAATACGGAAGCGCATCAC 420
Db 359 CGGCTCGCTTTCGCTTTCAGCGAGGACCAACGTCGTCGCGCAATACGGAAGCGCATCAC 418
Qy 421 CGAGTGGCTTCCATTTCGAGTATATGATCTTGGGCCACCATCATCGCCAATTCGATTCGTCT 480
Db 419 CGAGTGGCTTCCATTTCGAGTATATGATCTTGGGCCACCATCATCGCCAATTCGATTCGTCT 478
Qy 481 GGCCCTGGAGCAGACCTCCCTGATGGGACAAAACGCCCATGTCCGAGCGGTGAGACGA 540
Db 479 GGCCCTGGAGCAGACCTCCCTGATGGGACAAAACGCCCATGTCCGAGCGGTGAGACGA 538
Qy 541 CAGGAGCCCTATTTTCATCGGATCTTTTTCGAGGCGAGGATCAAAATCATCGCTCT 600
Db 539 CAGGAGCCCTATTTTCATCGGATCTTTTTCGAGGCGAGGATCAAAATCATCGCTCT 598
Qy 601 GGGCTTTGTCTTCCAAAGGGCTTTTACCTGCGGAACGGCTGGAAAGCTCATGACTTCGT 660
Db 599 GGGCTTTGTCTTCCAAAGGGCTTTTACCTGCGGAACGGCTGGAAAGCTCATGACTTCGT 658
Qy 661 GGTCTGCTCTACAGGATCCTTGGCCACGGCTGGAACTGACTTTCGAACTGCGAACAACCTGAG 720

Db	659	GGTGTCTCTCAGGGATCCCTTGGCCACGGCTGGAACTGACTTCGACCTGCGAACACTGG	718
Qy	721	GGCTGTGGGTGTCTGAGGCCCTTGAAGCTGGTGTCTGGGATTCGAAGTTTTCAGAGTGGT	780
Db	719	GGCTGTGGGTGTCTGAGGCCCTTGAAGCTGGTGTCTGGGATTCGAAGTTTTCAGAGTGGT	778
Qy	781	GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCTCTGCAGATGGGCTGTCTTCTTCTT	840
Db	779	GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCTCTGCAGATGGGCTGTCTTCTTCTT	838
Qy	841	TGCCATCTCATGTTTGGCCATTCATGGCTCGAGATTCTACATGGCAAGTTTCCACAAGGC	900
Db	839	TGCCATCTCATGTTTGGCCATTCATGGCTCGAGATTCTACATGGCAAGTTTCCACAAGGC	898
Qy	901	CTGTTTCCCAACACGACAGATCGGAGCCCGTGGTGAATTCCTCTGTGSCAAGAGGC	960
Db	899	CTGTTTCCCAACACGACAGATCGGAGCCCGTGGTGAATTCCTCTGTGSCAAGAGGC	958
Qy	961	CCAGCCCGGTGTGCGAGGCGACACTGAGTGC GGAGTACTGSCCAGGACCCACTT	1020
Db	959	CCAGCCCGGTGTGCGAGGCGACACTGAGTGC GGAGTACTGSCCAGGACCCACTT	1018
Qy	1021	TGGCATCAACAACTTGCATAATCTCTGTTTGGCATCTTGACGGTGTTCAGTGCATCAC	1080
Db	1019	TGGCATCAACAACTTGCATAATCTCTGTTTGGCATCTTGACGGTGTTCAGTGCATCAC	1078
Qy	1081	CATGAGGCTGGACTGACATCTCTATATACAAAGATCGCGCGGCAACCTGGAA	1140
Db	1079	CATGAGGCTGGACTGACATCTCTATATACAAAGATCGCGCGGCAACCTGGAA	1138
Qy	1141	CTGCTCTTACTTCACTCCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGT	1200
Db	1139	CTGCTCTTACTTCACTCCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGT	1198
Qy	1201	GGGCGTGTCTCGGGGAGTTTGC AAGGACGAGAGAGGGTGGAGAACCGCCGCGCTT	1260
Db	1199	GGGCGTGTCTCGGGGAGTTTGC AAGGACGAGAGAGGGTGGAGAACCGCCGCGCTT	1258
Qy	1261	CCTGAAGCTGCGCGGACGACAGAGATCGACGAGAGCTCAA CGGGTACCTCGAGTGGAT	1320
Db	1259	CCTGAAGCTGCGCGGACGACAGATCGACGAGAGCTCAA CGGGTACCTCGAGTGGAT	1318
Qy	1321	CTTCAAGCGGAGGAAGTCACTGTGCGCGAGGAGCACAGGAATCGAGAGAGTCCCC	1380
Db	1319	CTTCAAGCGGAGGAAGTCACTGTGCGCGAGGAGCACAGGAATCGAGAGAGTCCCC	1378
Qy	1381	TTTGGACGTGCTGAAGAGAGCGGCCCAAGAGAGCAGAAATGACTGATCAACCGACA	1440
Db	1379	TTTGGACGTGCTGAAGAGAGCGGCCCAAGAGAGCAGAAATGACTGATCAACCGACA	1438
Qy	1441	GGAGGAGAGAACCGGTTTGACATCTCTGTGTTGGATCCCCCTTCCCGCGCGCCAG	1500
Db	1439	GGAGGAGAGAACCGGTTTGACATCTCTGTGTTGGATCCCCCTTCCCGCGCGCCAG	1498
Qy	1501	CCTCAAGCGGGAAGACAGAGAGCTGCTCATACTTCCGAGAGAGAGATGTTCCG	1560
Db	1499	CCTCAAGCGGGAAGACAGAGAGCTGCTCATACTTCCGAGAGAGAGATGTTCCG	1558
Qy	1561	GTTTTTTATCCGCGCATGGTGAAGGCTCAGAGCTTCTACTGCGGTGGTGTCTGCTGGT	1620
Db	1559	GTTTTTTATCCGCGCATGGTGAAGGCTCAGAGCTTCTACTGCGGTGGTGTCTGCTGGT	1618
Qy	1621	GGCCCTGAACACACTGTGTGCGCATGGTGCAATTACACAGCCGCGGGCTTACCAAC	1680
Db	1619	GGCCCTGAACACACTGTGTGCGCATGGTGCAATTACACAGCCGCGGGCTTACCAAC	1678
Qy	1681	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTCCTCACAGAGATGTCCTGAA	1740
Db	1679	GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTCCTCACAGAGATGTCCTGAA	1738
Qy	1741	GATGTATGGCCTGGGCCCAGAGACTACTTCGGTCTCTCTCAACTGCTTCGACTTGG	1800

Db 5027 TGACACAGCATCAACCGCCACAACAATTCGCGAGTTTTTTCGAAAGCCCTGATGCTGCT 5086
QY GTTCAGAGAGCCCAACGGGGAGCCCTGGCAGAGATCATGCTGTCTGCTGCTGAGCAACCA 5160
Db 5087 GTTCAGAGAGCCCAACGGGGAGCCCTGGCAGAGATCATGCTGTCTGCTGCTGAGCAACCA 5146
QY GGCTGTGTATGAGCAGGCCAAATGCCACCGAGTGTGGAAGTGACTTTGGCCTACTTCTACTTT 5220
Db 5147 GGCTGTGTATGAGCAGGCCAAATGCCACCGAGTGTGGAAGTGACTTTGGCCTACTTCTACTTT 5206
QY CGTCTCCTTCATCTTCTGTGTCTCTTTCTGTATGATTTGAACCTCTTTGTGGCTGTATCAT 5221
Db 5207 CGTCTCCTTCATCTTCTGTGTCTCTTTCTGTATGATTTGAACCTCTTTGTGGCTGTATCAT 5266
QY GGACAAATTTTGTAGTACTCTACGGGGGACTCTTCCATCTTAGTCTCCACCACTTGGATGA 5340
Db 5267 GGACAAATTTTGTAGTACTCTACGGGGGACTCTTCCATCTTAGTCTCCACCACTTGGATGA 5326
QY GTTCATCCGGGTCTGGGCTGAATACGACCCGGCTGCTGTGGCGCATCAGTTACAATGA 5400
Db 5327 GTTCATCCGGGTCTGGGCTGAATACGACCCGGCTGCTGTGGCGCATCAGTTACAATGA 5386
QY CATGTTTGTAGATGCTGAACACATGTCCCGGCTCTGGGGCTGGGGAAGAAATGCCCTGC 5460
Db 5387 CATGTTTGTAGATGCTGAACACATGTCCCGGCTCTGGGGCTGGGGAAGAAATGCCCTGC 5446
QY TCGAGTTGCTTACAAGCGCTGTTTCGCATGAACATGCCCATCTCCAACGAGGACATGAC 5520
Db 5447 TCGAGTTGCTTACAAGCGCTGTTTCGCATGAACATGCCCATCTCCAACGAGGACATGAC 5506
QY TGTTCATCTTCAGTCCACGCTGATGCCCTCATCCGACGGCACTGGAGATCAAGCTGCG 5580
Db 5507 TGTTCATCTTCAGTCCACGCTGATGCCCTCATCCGACGGCACTGGAGATCAAGCTGCG 5566
QY CCCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGAGATTCGGTTGT 5640
Db 5567 CCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGAGATTCGGTTGT 5626
QY GTGGGCCAATTCGCCCCAGAAACTTTGGACTTGCTGGTACCACCCCATAGCCCTGATGA 5700
Db 5627 GTGGGCCAATTCGCCCCAGAACTTTGGACTTGCTGGTACCACCCCATAGCCCTGATGA 5686
QY GATGACAGTGGGGAAGGTTTATGACGCTGTGATGATATTTGACTTCTACAAGACGAAACAA 5760
Db 5687 GATGACAGTGGGGAAGGTTTATGACGCTGTGATGATATTTGACTTCTACAAGACGAAACAA 5746
QY AACCACAGAGACAGATGACAGGCTCCTGGAGGCTCCTCCAGAGTGGGTCCCTGTGTC 5820
Db 5747 AACCACAGAGACAGATGACAGGCTCCTGGAGGCTCCTCCAGATGGGTCCCTGTGTC 5806
QY CTTGTTTCCACCTCTGAAGGCCACCTGGAGCAGACACAGCCGGCTGTGCTCCGAGGAGC 5880
Db 5807 CTTGTTTCCACCTCTGAAGGCCACCTGGAGCAGACACAGCCGGCTGTGCTCCGAGGAGC 5866
QY CCGGGTTTTCTTCACAGAGAGGTTTCAACCTCCTCAGCAATGGCGGGCCATACAAAA 5940
Db 5867 CCGGGTTTTCTTCACAGAGAGGTTTCAACCTCCTCAGCAATGGCGGGCCATACAAAA 5926
QY CCAAGAGAGTGGCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC 6000
Db 5927 CCAAGAGAGTGGCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC 5986
QY CCATAGAGCCAGGCCACCCCTGGAGCGTGGCCAATCCACAGAGATCCTGTGGGGCGGTC 6060
Db 5987 CCATAGAGCCAGGCCACCCCTGGAGCGTGGCCAATCCACAGAGATCCTGTGGGGCGGTC 6046
QY AGGACACTGTGTGGACGTTTCAGATGACAGATCAACCCGAGGGCCCTGTATGGGA 6120
Db 6047 AGGACACTGTGTGGACGTTTCAGATGACAGATCAACCCGAGGGCCCTGTATGGGA 6106
QY GCCCCAGCTGGGCTGGAGAGCCAGGCTCAGACGGGCTCCATGCCCGCCCTTGGCGCCGA 6180

Db 6107 GCCCCAGCTGGGCTGGAGAGCCAGGCTCAGACGGCTCCTCATGCCCGCCCTTTCGGCGCGA 6166
QY GACTCAGCCCGTCTCAGATGCCAGCCCATGAAGCGTTCATCTTCCACGCTGGGCCACGCG 6240
Db 6167 GACTCAGCCCGTCTCAGATGCCAGCCCATGAAGCGTTCATCTTCCACGCTGGGCCACGCG 6226
QY GCCCCGTGGGACTCATCTTTTGCAGCACACCCCGGACCGGCCACCCCTTAGCCAGGCGTC 6300
Db 6227 GCCCCGTGGGACTCATCTTTTGCAGCACACCCCGGACCGGCCACCCCTTAGCCAGGCGTC 6286
QY GTGCACACCAACCAACCAACCGCTGCCACCGCGCAGGGAACAGGAAGCAGAGGTCCTTGGGA 6360
Db 6287 GTGCACACCAACCAACCAACCGCTGCCACCGCGCAGGGAACAGGAAGCAGAGGTCCTTGGGA 6346
QY GAAGGGGCCAGGCTGTCTGCCGATATGATGGGGCAACGAAGCATGCTGTGGGGCCGGG 6420
Db 6347 GAAGGGGCCAGGCTGTCTGCCGATATGATGGGGCAACGAAGCATGCTGTGGGGCCGGG 6406
QY GCTGCCCGCGGAGAGGGGCTTACAGGCTCCCGCGGGAACGAGAGCGCGCGGAGAGCG 6480
Db 6407 GCTGCCCGCGGAGAGGGGCTTACAGGCTCCCGCGGGAACGAGAGCGCGCGGAGAGCG 6466
QY GGGCGGCTCCAGAGCGAGGAGCGGCTCATCTCTCTCGGAGAGCAGGCGCTTCTA 6540
Db 6467 GGGCGGCTCCAGAGCGAGGAGCGGCTCATCTCTCTCGGAGAGCAGGCGCTTCTA 6526
QY CTCTCGGACCGCTTTGGGGCGCTGAGCCCCCGAAGCCCCAAGCCCTTCTCAGCAGCCCA 6600
Db 6527 CTCCTCGGACCGCTTTGGGGCGCTGAGCCCCCGAAGCCCCAAGCCCTTCTCAGCAGCCCA 6586
QY CCCAAAGCTGCCAAACAGCTGGCCAGAGCGGGAACCCACACAGGGCACTGGTTCCGT 6660
Db 6587 CCCAAAGCTGCCAAACAGCTGGCCAGAGCGGGAACCCACACAGGGCACTGGTTCCGT 6646
QY GAATGGAGAGCCCTTGTGTCTGTCATCTGTCATGAGACCCCGCGCGGCTGGGGCGGAG 6720
Db 6647 GAATGGAGAGCCCTTGTGTCTGTCATCTGTCATGAGACCCCGCGCGGCTGGGGCGGAG 6706
QY GCAGCTCCCCCAGACGCCCTGACTCCCCCGCCAGCATCCTTACAGACGCGCAACTC 6780
Db 6707 GCAGCTCCCCCAGACGCCCTGACTCCCCCGCCAGCATCCTTACAGACGCGCAACTC 6766
QY CTCACCCATCTCACTTCGCCGGGCTCAGACAGCCCTTCTGCTTCTCCCTCAGGCCCGGCT 6840
Db 6767 CTCACCCATCTCACTTCGCCGGGCTCAGACAGCCCTTCTGCTTCTCCCTCAGGCCCGGCT 6826
QY CAGCGCTGGGCTTTCCGAACACACCGCCCTGTGACAGAGAGACCCCTCAGCAGGCCCT 6900
Db 6827 CAGCGCTGGGCTTTCCGAACACACCGCCCTGTGTCAGAGAGACCCCTCAGCAGGCCCT 6886
QY GGCCCCCTGGCTTCGAAATTTGGGCTCTGACCCCTTACCTGGGGCAGCGTCTGGAACAGTGAGGC 6960
Db 6887 GGCCCCCTGGCTTCGAAATTTGGGCTCTGACCCCTTACCTGGGGCAGCGTCTGGAACAGTGAGGC 6946
QY CTTGTCTCAGGCCCTGCTGAGGACACGCTCACTTTTCGAGGAGGCTGTGGCCACCAACTC 7020
Db 6947 CTTGTCTCAGGCCCTGCTGAGGACACGCTCACTTTTCGAGGAGGCTGTGGCCACCAACTC 7006
QY GGSCCGCTCCTCCAGGACTTCCTAGTGTCTCCTCGACTCCCTCAGTCTCCTCTCCG 7080
Db 7007 GGSCCGCTCCTCCAGGACTTCCTAGTGTCTCCTCGACTCCCTCAGTCTCCTCTCCG 7066
QY CCGCGTGGCCAAACGGGTTTACACTGCACCCCTGGGACTCAGCTCGGGTGGCCAGCAGCGCA 7140
Db 7067 CCGCGTGGCCAAACGGGTTTACACTGCACCCCTGGGACTCAGCTCGGGTGGCCAGCAGCGCA 7126
QY CAGCTACCAACCAACCTGACCAAGACCACTGTGTGTAGTGTGACACCGTGAACCTCAGAGCGC 7200
Db 7127 CAGCTACCAACCAACCTGACCAAGACCACTGTGTGTAGTGTGACACCGTGAACCTCAGAGCGC 7186
QY CTTGCATGACGAGGCGTGTTCAGTGGATGAGTTTTATCATCCACGCGGCGAGTGG 7260
Db 7187 CTTGCATGACGAGGCGTGTTCAGTGGATGAGTTTTATCATCCACGCGGCGAGTGG 7246

Qy 7261 CCCTCGGGAGGCTTCCACCTTGCTGAGGCTCCCTGCTGCGCCCTCCCTCCCTCCCTCCCT 7320
Db 7247 CCCTCGGGAGGCTTCCACCTTGCTGAGGCTCCCTGCTGCGCCCTCCCTCCCTCCCTCCCT 7306
Qy 7321 CCCCTCTTTACTTAGACGAGCAATAAAGCCCTTGTGCTTGAGTGTACGTACCGC 7376
Db 7307 CCCCTCTTTACTTAGACGAGCAATAAAGCCCTTGTGCTTGAGTGTACGTACCGC 7362
RESULT 7
AAQ84657
ID AAQ84657 standard; DNA; 7362 BP.
XX AC AAQ84657;
XX
DT 25-MAR-2003 (revised)
DT 01-DEC-1995 (first entry)
XX
DE Human neuronal calcium channel subunit alpha 1B-1.
XX
KW Calcium channel subunit; antagonist; agonist; diagnosis;
KW Lambert Eaton Syndrome; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 144..7163 /*tag= a
FT misc_difference 6633..6819 /*tag= b
FT /label= additional exon wrt alpha 1B-2
FT misc_feature 6820..7362 /*tag= c
FT /*tag= c
FT /note= "identical to alpha 1B-2"
XX
PN W09504822-A1.
XX
PD 16-FEB-1995.
XX
PF 11-AUG-1994; 94WO-US009230.
XX
PR 11-AUG-1993; 93US-00105536.
PR 05-NOV-1993; 93US-00149097.
XX
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
PI Harpold WM, Ellis SB, Williams ME, Mccue AF, Gillespie A;
XX
DR WPI; 1995-090900/12.
DR P-PSDB; AAR71005.
XX
PT DNA encoding human calcium channel sub-unit(s) - used for developing
PT prods. for studying calcium channels, e.g. for obtaining agonists and
PT antagonists.
XX
PS Disclosure; Page 138-149; 285pp; English.
XX
CC DNA encoding the alpha 1B subunit was isolated by screening a human basal
CC ganglia cDNA library with fragments of the rabbit skeletal muscle calcium
CC channel alpha 1 subunit-encoding cDNA. A portion of one of the positive
CC clones was used to screen an IMR32 cell cDNA library. Clones that
CC hybridised to the basal ganglia probe were used to further screen an
CC IMR32 cell cDNA library to identify overlapping clones that in turn were
CC used to screen a human hippocampus cDNA library. A series of clones to
CC span nearly the entire length of the nt. sequence encoding the human
CC alpha 1B subunit was obt'd. Nucleic acid amplification of specific regions
CC of the IMR32 cell alpha 1B mRNA yielded additional segments of the alpha
CC 1B coding sequence. A full- length alpha 1B DNA clone was constructed by
CC ligating portions of the partial cDNA clones. Nucleic acid amplification
CC analysis of IMR32 cell RNA and genomic DNA using oligo primers corresp.
CC to sequences located 5' and 3' of the stop codon of the DNA encoding the
CC alpha 1B subunit revealed an alternatively spliced alpha 1B-encoding mRNA

CC in IMR32 cells. This second mRNA product is the result of differential
CC splicing of the alpha 1B subunit transcript to include another exon that
CC is not present in the mRNA corresp. to the other 3' alpha 1B cDNA
CC sequence that was initially isolated. The alpha 1B subunit encoded by a
CC DNA sequence contg. an additional exon is referred to as alpha 1B-1 and
CC given in AAQ84657/R71005, whereas the other form is referred to as alpha
CC 1B-2 and is given in AAQ84658/R71006. Following the sequence of the
CC additional exon in alpha 1B-1 the alpha 1B-1 and alpha 1B-2 sequences are
CC identical. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 7362 BP; 1445 A; 2278 C; 2214 G; 1425 T; 0 U; 0 Other;
Query Match 99.2%; Score 7314.8; DB 2; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7360; Conservative 0; Mismatches 2; Indels 14; Gaps 3;
Qy 1 GCGGCGCGGCTGCGGCGTGGGGCGGGGCGGCGTCCGCTGCGTCCCGCGGCTCCGTG 60
Db 1 GCGGCGCGGCTGCGGCGTGGGGCGGGGCGGCGTCCG-TGCCGTCCCGCGGCTCCGTG 59
Qy 61 GCTGCTCCGCTCTGAGCGCTGCGGCGCCCGCGGCGCTCCCTGCGGGGCGGCTGGGCGG 120
Db 60 GCTGCTCCGCTCTGAGCGCTT-GCGGCGCCCGCGGCGCTCCCTGCGGGGCGGCTGGGCGG 118
Qy 121 GGGATGACGCGGGGCGCGGAGCGATGCTGCTGGGGAGCAGAGTGGGGCGGCGCTA 180
Db 119 GGGATGACGCGGGGCGCGGAGCGATGCTGCTGGGGAGCAGAGTGGGGCGGCGCTA 178
Qy 181 TGGAGCGCGCGGCGGAGAGCGGCGCGGGGCGGGGCGGGGCGGGGCGGGGCGG 240
Db 179 TGGAGCGCGCGGCGGAGAGCGGCGCGGGGCGGGGCGGGGCGGGGCGGGGCGG 238
Qy 241 GGGTCCCGGGGGGCTGCAGCCCGCGCGGCGGCTCTTACAAGCAATCGATCGCGACGC 300
Db 239 GGGTCCCGGGGGGCTGCAGCCCGCGCGGCGGCTCTTACAAGCAATCGATCGCGACGC 298
Qy 301 GCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGTCTACCGTCAA 360
Db 299 GCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGTCTACCGTCAA 358
Qy 361 CCGCTGCTCTTCTTTCAGCGAGGACACGCTGCTCCGCAATACGCGAGCGCATCAC 420
Db 359 CCGCTGCTCTTCTTTCAGCGAGGACACGCTGCTCCGCAATACGCGAGCGCATCAC 418
Qy 421 CGAGTGGCTCCATTCGAGTATATGATCTTGGCCACCATCATCGCCAACTGCTGCT 480
Db 419 CGAGTGGCTCCATTCGAGTATATGATCTTGGCCACCATCATCGCCAACTGCTGCT 478
Qy 481 GGGCTGGAGCAGCAGCTCCCTGATGGGGACAAAACGCCCATGTCCGAGCGGCTGGACGA 540
Db 479 GGGCTGGAGCAGCAGCTCCCTGATGGGGACAAAACGCCCATGTCCGAGCGGCTGGACGA 538
Qy 541 CAGGAGCGCTATTTTCATCGGGATCTTTGCTTCGAGGCGAGGATCAAAATCATCGCTCT 600
Db 539 CAGGAGCGCTATTTTCATCGGGATCTTTGCTTCGAGGCGAGGATCAAAATCATCGCTCT 598
Qy 601 GGGCTTTGTCTTCCACAAGGGCTCTTACCTGCGGAACGGTGGAAAGTTCATGGACTTCGT 660
Db 599 GGGCTTTGTCTTCCACAAGGGCTCTTACCTGCGGAACGGTGGAAAGTTCATGGACTTCGT 658
Qy 661 GGTGCTCTCACAAGGATCTTCCCAAGGCTGGAACCTGACCTCGAAACACTGTAG 720
Db 659 GGTGCTCTCACAAGGATCTTCCCAAGGCTGGAACCTGACCTCGAAACACTGTAG 718
Qy 721 GGTGCTGCTGCTGAGGCGGCTGAGCTGGTGTCTGGGATTCGAAGTTTTCAGGTTGT 780
Db 719 GGTGCTGCTGCTGAGGCGGCTGAGCTGGTGTCTGGGATTCGAAGTTTTCAGGTTGT 778
Qy 781 GCTCAAGTTCATCATGAAGGCCCATGGTTCACCTCTGCGAGATTTGGGCTGCTCTTCTT 840
Db 779 GCTCAAGTTCATCATGAAGGCCCATGGTTCACCTCTGCGAGATTTGGGCTGCTCTTCTT 838
Qy 841 TGCCATCTCTCATGTTTGGCCATCATTTGCCCTGGAGTTCTTACATGGGCAAGTTCCACAGGC 900

QY	3061	GGAGAGCCGCGCGGGCAACCGGGCCCGGCAACAAGCGCAGCCTGCTCACGAGGCTGT	3120
DB	3059	GGAGAGCCGCGCGGGCAACCGGGCCCGGCAACAAGCGCAGCCTGCTCACGAGGCTGT	3118
QY	3121	GGAGAAGAGACCAACGAGAGAGAGGCGCAACGAGAGAGGCTGAGATAGTGGAGCCGA	3180
DB	3119	GGAGAAGAGACCAACGAGAGAGAGGCGCAACGAGAGAGGCTGAGATAGTGGAGCCGA	3178
QY	3181	CAAGGAAAAGAGCTCCGGAACCAACAGCCCGGAGCCACACTGTGACCTGGAGACCA	3240
DB	3179	CAAGGAAAAGAGCTCCGGAACCAACAGCCCGGAGCCACACTGTGACCTGGAGACCA	3238
QY	3241	TGGGACTGTGACTGTGGGTCCCATGCAACACTGCCAGCACCTGTCTCCAGAAAGTGGA	3300
DB	3239	TGGGACTGTGACTGTGGGTCCCATGCAACACTGCCAGCACCTGTCTCCAGAAAGTGGA	3298
QY	3301	GGAAACGACAGAGATGAGCAACATCAGCGGAACGTCCTCGATGGGCGAGTCAGCCCC	3360
DB	3299	GGAAACGACAGAGATGAGCAACATCAGCGGAACGTCCTCGATGGGCGAGTCAGCCCC	3358
QY	3361	AGACCCGAAACACTATTGTACATATCCAGATGCTGACGGGCCCTCTTGGGGAAGCCAC	3420
DB	3359	AGACCCGAAACACTATTGTACATATCCAGATGCTGACGGGCCCTCTTGGGGAAGCCAC	3418
QY	3421	GGTCGTTCCAGTGGTAAACGTTGACCTGGAAAGCCAAAGAGAGGGGAAGAGGTGGA	3480
DB	3419	GGTCGTTCCAGTGGTAAACGTTGACCTGGAAAGCCAAAGAGAGGGGAAGAGGTGGA	3478
QY	3481	AGCGGATGACGTATGAGGAGCGGCCCGGCCCTATCGTCCCATACAGCTCCATGTTCTG	3540
DB	3479	AGCGGATGACGTATGAGGAGCGGCCCGGCCCTATCGTCCCATACAGCTCCATGTTCTG	3538
QY	3541	TTTAAAGCCCAACCAACTGCTCGCCGCTTCTGCACTTACATCGTGACCATGAGGTACTT	3600
DB	3539	TTTAAAGCCCAACCAACTGCTCGCCGCTTCTGCACTTACATCGTGACCATGAGGTACTT	3598
QY	3601	CGAGGTGGTCAATTCCTGTGTGTCATCGCCTTGAGCAGCATCGCCCTGCTGAGGACCC	3660
DB	3599	CGAGGTGGTCAATTCCTGTGTGTCATCGCCTTGAGCAGCATCGCCCTGCTGAGGACCC	3658
QY	3661	AGTCGGCACAGACTCGCCCGAGGAACAACGCTCTGAAATACCTGATACATTTCACTGG	3720
DB	3659	AGTCGGCACAGACTCGCCCGAGGAACAACGCTCTGAAATACCTGATACATTTCACTGG	3718
QY	3721	TGCTTTTACCTTTGAGATGGTGAATAAGATGATCGACTTGGGACTGTGCTTCAACCTGG	3780
DB	3719	TGCTTTTACCTTTGAGATGGTGAATAAGATGATCGACTTGGGACTGTGCTTCAACCTGG	3778
QY	3781	AGCCTATTTCCGGGACTTGTGGAAACATTTGGACTTCATTTGTGTCAAGTGGCGCCCTGGT	3840
DB	3779	AGCCTATTTCCGGGACTTGTGGAAACATTTGGACTTCATTTGTGTCAAGTGGCGCCCTGGT	3838
QY	3841	GGCGTTTGTCTTTCGAGCTTCGTGGAGAGTCAAAAGGGGAAGACATCAATACCATCAA	3900
DB	3839	GGCGTTTGTCTTTCGAGCTTCGTGGAGAGTCAAAAGGGGAAGACATCAATACCATCAA	3886
QY	3901	GTCTCTGAGAGTCCCTGCTGTCGCGGCCCTCAAGACCATCAACCGGCTGCCCAAGCT	3960
DB	3887	GTCTCTGAGAGTCCCTGCTGTCGCGGCCCTCAAGACCATCAACCGGCTGCCCAAGCT	3946
QY	3961	CAAGGCTGTGTTGACTGTGTGTGAACCTCCCTGAAGAAATGCTCAACATCTTGATTGT	4020
DB	3947	CAAGGCTGTGTTGACTGTGTGTGAACCTCCCTGAAGAAATGCTCAACATCTTGATTGT	4006
QY	4021	CTACATGCTCTTCAATGTTTCAATTTGGCGTCAATTTGGCGTGAGGCTCTTCAAGGGAAGTT	4080
DB	4007	CTACATGCTCTTCAATGTTTCAATTTGGCGTCAATTTGGCGTGAGGCTCTTCAAGGGAAGTT	4066
QY	4081	TTTTCTACTGCACAGATGAATCCAGGAGCTGGAGAGGACTGACAGGGGTGAGTATTTGGA	4140
DB	4067	TTTTCTACTGCACAGATGAATCCAGGAGCTGGAGAGGACTGACAGGGGTGAGTATTTGGA	4126

QY	4141	TTATGAGAGGAGGAAGTGGAAAGCTCAGCCACGGCAGTGGAAAGAAATACGACTTTTCACTA	4200
DB	4127	TTATGAGAGGAGGAAGTGGAAAGCTCAGCCACGGCAGTGGAAAGAAATACGACTTTTCACTA	4186
QY	4201	CGAATATGTCTCTGGGCTCTGTCAGCTGTTCACAGTGTCCACGGGGAAGGCTGGCC	4260
DB	4187	CGAATATGTCTCTGGGCTCTGTCAGCTGTTCACAGTGTCCACGGGGAAGGCTGGCC	4246
QY	4261	CATGSGTCTGAAACACTCCGTTGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA	4320
DB	4247	CATGSGTCTGAAACACTCCGTTGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA	4306
QY	4321	CCGATGAGAGCTCTCAATCTTCTACGTGTCCTATTTGTGGTCTTTCCCTCTTCTTTCGT	4380
DB	4307	CCGATGAGAGCTCTCAATCTTCTACGTGTCCTATTTGTGGTCTTTCCCTCTTCTTTCGT	4366
QY	4381	CAACATCTTTGTGGCTTTGATCATCATCATCTTCCAGGAGCAGGGGACAAGGTGATGTC	4440
DB	4367	CAACATCTTTGTGGCTTTGATCATCATCATCTTCCAGGAGCAGGGGACAAGGTGATGTC	4426
QY	4441	TGAATGCAGCTCGGAGAAAGAACGAGAGGCTTGCAATTGACTTCGCCATCAGCGCCAAACC	4500
DB	4427	TGAATGCAGCTCGGAGAAAGAACGAGAGGCTTGCAATTGACTTCGCCATCAGCGCCAAACC	4486
QY	4501	CCTGACACGGTACATGCCCCAAACCGGCGAGTCGTTCAGTATGAAGCTGGACATTTGT	4560
DB	4487	CCTGACACGGTACATGCCCCAAACCGGCGAGTCGTTCAGTATGAAGCTGGACATTTGT	4546
QY	4561	GGTCTCCCGCCCTTTGAAATACCTTCAATGAGTACGAGCTGATCTGAAATGCCCTGAACAT	4620
DB	4547	GGTCTCCCGCCCTTTGAAATACCTTCAATGAGTACGAGCTGATCTGAAATGCCCTGAACAT	4606
QY	4621	GATGATGAAGTCTTATGATGACCTTATGATGACGAGCTGATCTGAAATGCCCTGAACAT	4680
DB	4607	GATGATGAAGTCTTATGATGACCTTATGATGACGAGCTGATCTGAAATGCCCTGAACAT	4666
QY	4681	CGTGTTCACATCATGTTCTCCATGGAATGCGTGTGGAAGATCATCGCTTTGGGGTGTCT	4740
DB	4667	CGTGTTCACATCATGTTCTCCATGGAATGCGTGTGGAAGATCATCGCTTTGGGGTGTCT	4726
QY	4741	GAACTATTTTCAGAGATGCGTGGAAATGCTTTGACTTTGTACCTGTGTGTTGGGAAGTATTAC	4800
DB	4727	GAACTATTTTCAGAGATGCGTGGAAATGCTTTGACTTTGTACCTGTGTGTTGGGAAGTATTAC	4786
QY	4801	TGATATTTTATGATAACAGAGATTCGGAAACGAAACAAATTTTCACTCAGCTTCTCCCG	4860
DB	4787	TGATATTTTATGATAACAGAGATTCGGAAACGAAACAAATTTTCACTCAGCTTCTCCCG	4846
QY	4861	CCTCTTTTCGAGCTGCGCGCTGATCAAGCTGTCCGCGCAGGGCTACACCATCCGCACTCT	4920
DB	4847	CCTCTTTTCGAGCTGCGCGCTGATCAAGCTGTCCGCGCAGGGCTACACCATCCGCACTCT	4906
QY	4921	GCTGTGGAACCTTTGTCCAGTCTTCAAGGCCCTCCCTCAGTGTGCTGCTCATTTGCCAT	4980
DB	4907	GCTGTGGAACCTTTGTCCAGTCTTCAAGGCCCTCCCTCAGTGTGCTGCTCATTTGCCAT	4966
QY	4981	GCTGTTTCTTTCATCTAGCCCATCATCGGCATGCAAGTGTGTTGGGAATATTTGCCCTGATGA	5040
DB	4967	GCTGTTTCTTTCATCTAGCCCATCATCGGCATGCAAGTGTGTTGGGAATATTTGCCCTGATGA	5026
QY	5041	TGACACAGCATCAACCGGCACAACTTCCGAGCGTGTTCGAGCGTGTTCGAGCCCTGATGTCT	5100
DB	5027	TGACACAGCATCAACCGGCACAACTTCCGAGCGTGTTCGAGCGTGTTCGAGCCCTGATGTCT	5086
QY	5101	GTTTCAGAGCGCCACGGGGAGGCGCTGGCAGGAGATCATGCTGCTGCTGAGCAACCA	5160
DB	5087	GTTTCAGAGCGCCACGGGGAGGCGCTGGCAGGAGATCATGCTGCTGCTGAGCAACCA	5146
QY	5161	GGCTGTGATGAGCAGGCGCAATGCCACCGAGTGTGGAAGTGAATTTTGCCTTACTTCTT	5220
DB	5147	GGCTGTGATGAGCAGGCGCAATGCCACCGAGTGTGGAAGTGAATTTTGCCTTACTTCTT	5206
QY	5221	CGTCTCCTTCATCTTCTGTGCTCTTTCTGATGTTGAAACCTCTTTTGTGGCTGTGATCAT	5280

[illegible]

ID AAQ37817 standard; cDNA; 7362 BP.
XX
AC AAQ37817;
XX
XX 25-MAR-2003 (revised)
DT 30-JUN-1993 (first entry)
XX
XX Sequence encoding the alpha 1B-1 human calcium channel subunit.
DE
XX Human calcium channel subunit; diagnosis; agonist; antagonist;
KW Lambert Eaton syndrome; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 144..7163
FT /*tag= a
XX
XX W09304083-A1.
XX
XX 04-MAR-1993.
XX
XX 14-AUG-1992; 92WO-US006903.
XX
XX 15-AUG-1991; 91US-00745206.
XX 10-APR-1992; 92US-00868354.
XX
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX
XX Harpold MM, Ellis SB, Williams ME, Feldman DH, Mecue AF;
PI Brenner R;
XX
XX WPI; 1993-093936/11.
XX P-PSDB; AAR33549.
XX
XX DNA encoding specific human calcium channel sub-units - used for
PT identifying calcium channel agonists and antagonists and diagnosing
PT Lambert Eaton syndrome.
XX
XX Disclosure; Page 111-120; 150pp; English.
XX
XX DNA encoding the alpha 1B subunit was isolated by screening a human basal
CC ganglia cDNA library with fragments of the rabbit skeletal muscle calcium
CC channel alpha 1 subunit-encoding cDNA. A portion of one of the positive
CC clones was used to screen an IMR32 cell cDNA library. Clones that
CC hybridized to the basal ganglia DNA probe were used to further screen an
CC IMR32 cell cDNA library to identify overlapping clones that in turn were
CC used to screen a human hippocampus cDNA library. In this way, a
CC sufficient series of clones to span nearly the entire length of the
CC nucleotide sequence encoding the human alpha 1B subunit was obtained. PCR
CC amplification of specific regions of the IMR32 cell alpha 1B mRNA yielded
CC additional segments of the alpha 1B coding sequence. A full-length alpha
CC 1B DNA clone was constructed by ligating portions of the partial cDNA
CC clones (see AAQ37817, AAQ37818). Alpha 1B-1 and alpha 1B-2 are derived by
CC alternative splicing of the alpha 1B subunit transcript. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 7362 BP; 1446 A; 2276 C; 2214 G; 1426 T; 0 U; 0 Other;

Query Match 99.1%; Score 7313.2; DB 2; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7359; Conservative 0; Mismatches 3; Indels 14; Gaps 3;

QY 1 GCGGCGCGGCTGCGGGTGGGCGCGGAGGTCCGCTGCGTCCCGGGCGGCTCCGTG 60
DB 1 GCGGCGCGGCTGCGGGTGGGCGCGGAGGTCCG-TGCGGTCCCGGGCTCCGTG 59

QY 61 GCTGCTCGGCTCTGAGCGCTTGGGCGCGCCGCGCCCTCCCTGCGGCGCGCTGGGCGG 120
DB 60 GCTGCTCGGCTCTGAGCGCTT-GCGGCGCGCGCGCCCTCCCTGCGGCGCGCTGGGCGG 118

QY 121 GGGATGACGCGGGCGCGGAGGCATGTCCGCTTGCGGACAGCTGGGCGCGCGCTA 180
|||||

Db 119 GGGATGACGCGGGGCGCGGAGGCATGTCCGCTTGGGGAGACAGCTGGGCGCGCGCTA 178
QY 181 TGGAGCCCCCGCGCGGAGAGCGGCCCCGGGCGCGGCGCGGCGCGGCGCGCGCGCC 240
|||||
Db 179 TGGAGCCCCCGCGCGGAGAGCGGCCCCGGGCGCGGCGCGGCGCGGCGCGCGCGCC 238
|||||
QY 241 GGGTCCCGGGGGCTGCAGCCCGGCCAGCGGGTCTCTACAAAGCAATCGATCGGCGAGCG 300
|||||
Db 239 GGGTCCCGGGGGCTGCAGCCCGGCCAGCGGGTCTCTACAAAGCAATCGATCGGCGAGCG 298
|||||
QY 301 CGCGCGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAA 360
|||||
Db 299 CGCGCGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAA 358
|||||
QY 361 CGGCTCGCTTTCGTTTCAGCGAGGACAAAGTGTGTCGCGCAATAACGCGAAGCGCATCAC 420
|||||
Db 359 CGGCTCGCTTTCGTTTCAGCGAGGACAAAGTGTGTCGCGCAATAACGCGAAGCGCATCAC 418
|||||
QY 421 CGAGTGGCTTCATTCGAGTATATGATCTTGGGCCACCATCATGCCAACTGCTATCGTCT 480
|||||
Db 419 CGAGTGGCTTCATTCGAGTATATGATCTTGGGCCACCATCATGCCAACTGCTATCGTCT 478
|||||
QY 481 GGGCTTGGAGCAGCACTCCCTGATGSGGACAAAAAGCCCATGTCCGAGCGGCTGGACGA 540
|||||
Db 479 GGGCTTGGAGCAGCACTCCCTGATGSGGACAAAAAGCCCATGTCCGAGCGGCTGGACGA 538
|||||
QY 541 CACGAGCCCTATTTTCATCGGGATCTTTTGTCTTCGAGCGAGGAGATCAAAATCATCGCTCT 600
|||||
Db 539 CACGAGCCCTATTTTCATCGGGATCTTTTGTCTTCGAGCGAGGAGATCAAAATCATCGCTCT 598
|||||
QY 601 GGGCTTGTCTTCCACAGGGCTTTTACCTGCGGAACGGCTGGAACTCATGAGACTTCGT 660
|||||
Db 599 GGGCTTGTCTTCCACAGGGCTTTTACCTGCGGAACGGCTGGAACTCATGAGACTTCGT 658
|||||
QY 661 GGTGCTCTCACAGGATCTTCCACGGCTGGAACTGACTTCGACTCTGCGAACTGAG 720
|||||
Db 659 GGTGCTCTCACAGGATCTTCCACGGCTGGAACTGACTTCGACTCTGCGAACTGAG 718
|||||
QY 721 GGTGTCGCTGCTCAGGCCCCCTGAAAGTGTGTCTGGGATTCGAAGTTTCAGGTGGT 780
|||||
Db 719 GGTGTCGCTGCTCAGGCCCCCTGAAAGTGTGTCTGGGATTCGAAGTTTCAGGTGGT 778
|||||
QY 781 GCTCAAGTCCATCATGAGGCCATGTTCACCTCTGCAGATTTGGGCTGCTTCTTCTT 840
|||||
Db 779 GCTCAAGTCCATCATGAGGCCATGTTCACCTCTGCAGATTTGGGCTGCTTCTTCTT 838
|||||
QY 841 TGCATCTCTCATCTTTGCCATCATTTGCCCTGGAAGTTCTACATGGCAAGTTCCACAAGGC 900
|||||
Db 839 TGCATCTCTCATCTTTGCCATCATTTGCCCTGGAAGTTCTACATGGCAAGTTCCACAAGGC 898
|||||
QY 901 CTGTTTTCCCCAACAGCACAGATCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC 960
|||||
Db 899 CTGTTTTCCCCAACAGCACAGATCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC 958
|||||
QY 961 CCAGCCCGGCTGTGCGAGGGCGACATGAGTCCCGGAGTACTGGCCAGACCCAACTT 1020
|||||
Db 959 CCAGCCCGGCTGTGCGAGGGCGACATGAGTCCCGGAGTACTGGCCAGACCCAACTT 1018
|||||
QY 1021 TGGCATCAACCACTTTGACAATATCTGTTTGCATCTTTCAGCGTGTTCAGTGCATCAC 1080
|||||
Db 1019 TGGCATCAACCACTTTGACAATATCTGTTTGCATCTTTCAGCGTGTTCAGTGCATCAC 1078
|||||
QY 1081 CATGGAGGGCTGAGCATGACATCTCTATAATAAACAAGATGCGGCCCGGCAACACCTGGAA 1140
|||||
Db 1079 CATGGAGGGCTGAGCATGACATCTCTATAATAAACAAGATGCGGCCCGGCAACACCTGGAA 1138
|||||
QY 1141 CTGGCTCTACTTTCATCCCTCATCATCATCGGCTCTTCTTTCATGCTCAACCTGGTCT 1200
|||||
Db 1139 CTGGCTCTACTTTCATCCCTCATCATCATCGGCTCTTCTTTCATGCTCAACCTGGTCT 1198
|||||
QY 1201 GGGCGTCTCTCGGGGAGTTTTCGAAGGAGCGAGAGAGGTGGAGAACCGCCGCGGCTT 1260
|||||
Db 1199 GGGCGTCTCTCGGGGAGTTTTCGAAGGAGCGAGAGAGGTGGAGAACCGCCGCGGCTT 1258
|||||

QY	1261	CCTGAAGCTCGCGGAGCAGCAGATCGAGCGAGCTCAACGGGTACTCTGGAGTGAT	1320
Db	1259	CCTGAAGCTCGCGGAGCAGCAGATCGAGCGAGCTCAACGGGTACTCTGGAGTGAT	1318
QY	1321	CTTCAAGCGGAGAAAGTCACTGTGCGCGAGGAGGACAGAAATGCAGAGGAAAGTCCCC	1380
Db	1319	CTTCAAGCGGAGAAAGTCACTGTGCGCGAGGAGGACAGAAATGCAGAGGAAAGTCCCC	1378
QY	1381	TTTGGAGCTGCTCAAGAGAGCGCCACCAAGAGAGCAGAAATGACCTGATCCAGCAGA	1440
Db	1379	TTTGGAGCTGCTCAAGAGAGCGCCACCAAGAGAGCAGAAATGACCTGATCCAGCAGA	1438
QY	1441	GGAGGAGAGGACCGGTTTGCAGATCTCTGTGTGTGTGATCCCCCTTCGCCCGGCCAG	1500
Db	1439	GGAGGAGAGGACCGGTTTGCAGATCTCTGTGTGTGTGATCCCCCTTCGCCCGGCCAG	1498
QY	1501	CCTCAAGCGGAGAAAGCAGAGAGCTCGTCATCTTCCGAGGAAAGGAAAGATGTTCCG	1560
Db	1499	CCTCAAGCGGAGAAAGCAGAGAGCTCGTCATCTTCCGAGGAAAGGAAAGATGTTCCG	1558
QY	1561	GTTTTTTATCCGCGCATGCTGAAGCTCAGAGCTTCTACTGGGTGCTGTGCGTGGT	1620
Db	1559	GTTTTTTATCCGCGCATGCTGAAGCTCAGAGCTTCTACTGGGTGCTGTGCGTGGT	1618
QY	1621	GGCCCTGAACACACTGTGTGTGCGCATGTGTGCAATTAACACCGCGCGCGCTTACCAC	1680
Db	1619	GGCCCTGAACACACTGTGTGTGCGCATGTGTGCAATTAACACCGCGCGCGCTTACCAC	1678
QY	1681	GACCTGTATTTTCAGAGTTGTTTTCTGGGTCTCTTCTCA CAGAGATGTCCTGAA	1740
Db	1679	GACCTGTATTTTCAGAGTTGTTTTCTGGGTCTCTTCTCA CAGAGATGTCCTGAA	1738
QY	1741	GATGTATGCTTGGGCGCCAGAGCTACTTTCGGTCTCTTCAACTGCTTCGACTTTGG	1800
Db	1739	GATGTATGCTTGGGCGCCAGAGCTACTTTCGGTCTCTTCAACTGCTTCGACTTTGG	1798
QY	1801	GGTCATGCTGGGAGCGCTTTTGAAGTGTCTGGCGGCGCATCAAGCGGGAAGCTCCTT	1860
Db	1799	GGTCATGCTGGGAGCGCTTTTGAAGTGTCTGGCGGCGCATCAAGCGGGAAGCTCCTT	1858
QY	1861	TGGGATCAGTGTCTGGGCGCCTCGGCTGTGAGGATCTTCAAGTCAGAGTACTG	1920
Db	1859	TGGGATCAGTGTCTGGGCGCCTCGGCTGTGAGGATCTTCAAGTCAGAGTACTG	1918
QY	1921	GAGCTCCCTGCGGAACCTGGTGTCTCTGCTGAACCTCCATGAAGTCCATCATCAGCT	1980
Db	1919	GAGCTCCCTGCGGAACCTGGTGTCTCTGCTGAACCTCCATGAAGTCCATCATCAGCT	1978
QY	1981	GCTCTTCTGCTTCTTCTGTTCAATTGTGGTCTTCCGCTGTGGGATGCAAGCTTTGG	2040
Db	1979	GCTCTTCTGCTTCTTCTGTTCAATTGTGGTCTTCCGCTGTGGGATGCAAGCTTTGG	2038
QY	2041	GGGACAGTTCAACTTCCAGGATGAGCTCCACAAACAACTTCGACACCTTCCCTGCGC	2100
Db	2039	GGGACAGTTCAACTTCCAGGATGAGCTCCACAAACAACTTCGACACCTTCCCTGCGC	2098
QY	2101	CATCTCACTGTCTTCCAGATCTTGAAGGAGGACTTGAATGCAAGTGTATACAGG	2160
Db	2099	CATCTCACTGTCTTCCAGATCTTGAAGGAGGACTTGAATGCAAGTGTATACAGG	2158
QY	2161	GATCAAAATCGAAGCGGCGTCAAGAAAGGATGTTCTGCTCTTTTACTTTCATGTCT	2220
Db	2159	GATCAAAATCGAAGCGGCGTCAAGAAAGGATGTTCTGCTCTTTTACTTTCATGTCT	2218
QY	2221	GACACTGTTCGAAACTACACTCTGTAAGTGTCTTCTGGCCATCGCTGGACACCT	2280
Db	2219	GACACTGTTCGAAACTACACTCTGTAAGTGTCTTCTGGCCATCGCTGGACACCT	2278
QY	2281	GGCCAAACCCCAAGAGCTGACAAAGGATGAAGAGGATGAAGAGCAGCAGCAGAA	2340
Db	2279	GGCCAAACCCCAAGAGCTGACAAAGGATGAAGAGGATGAAGAGCAGCAGCAGAA	2338

QY	2341	GCTTGCTCTGCAAAAGGCCAAAGATTGGCTGAAGTCAAGCCCCATGTCTGCCGGAACAT	2400
Db	2339	GCTTGCTCTGCAAAAGGCCAAAGATTGGCTGAAGTCAAGCCCCATGTCTGCCGGAACAT	2398
QY	2401	CTCCATCGCCGCCAGGACAGAACTCGGCCCAAGCGCGCTCGGTGTGGAGCAGCGGC	2460
Db	2399	CTCCATCGCCGCCAGGACAGAACTCGGCCCAAGCGCGCTCGGTGTGGAGCAGCGGC	2458
QY	2461	CAGCAGCTACGGTGTGAGAACTTCGCGGCGCAGCTGCGAGGCGCTGTACAGCAGATGGA	2520
Db	2459	CAGCAGCTACGGTGTGAGAACTTCGCGGCGCAGCTGCGAGGCGCTGTACAGCAGATGGA	2518
QY	2521	CCCCGAGGAGCGCTCGCTTCGCCACTACGCCCACTTCGGGCCCCACATGAAGAGCCA	2580
Db	2519	CCCCGAGGAGCGCTCGCTTCGCCACTACGCCCACTTCGGGCCCCACATGAAGAGCCA	2578
QY	2581	CCTGGAACCGGCGCTGTGTGTGTGAGCTTGGGCGCGCAGCGCGCGGGGCGCCGTGGGAGG	2640
Db	2579	CCTGGAACCGGCGCTGTGTGTGTGAGCTTGGGCGCGCAGCGCGGGGCGCCGTGGGAGG	2638
QY	2641	CAAAAGCCGACCTGAGGCTCGGAGGCGCCCGAGGGCGTCAACCTCCGCGCAGGACCA	2700
Db	2639	CAAAAGCCGACCTGAGGCTCGGAGGCGCCCGAGGGCGTCAACCTCCGCGCAGGACCA	2698
QY	2701	CCGGCACCGCAGCAAGGACAAGACCCCGCGCGGGGACAGGACCGAGCAGAGGCCCC	2760
Db	2699	CCGGCACCGCAGCAAGGACAAGACCCCGCGCGGGGACAGGACCGAGCAGAGGCCCC	2758
QY	2761	GAAAGCGAGAGCGGGAGCCCGGTGTCGCCGGAGGAGCGCGCGCGCCAGCCAGAGCCA	2820
Db	2759	GAAAGCGAGAGCGGGAGCCCGGTGTCGCCGGAGGAGCGCGCGCGCCAGCCAGAGCCA	2818
QY	2821	CAGCAGGAGCGCGGGGCGCCCGAGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCC	2880
Db	2819	CAGCAGGAGCGCGGGGCGCCCGAGGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCC	2878
QY	2881	CGAGGCG	2940
Db	2879	CGAGGCG	2938
QY	2941	CCGACGCGACCGCGCGCACCGGCAACAGGATCCGAGCAAGGAGTGCCTCGCCCAAGGG	3000
Db	2939	CCGACGCGACCGCGCGCACCGGCAACAGGATCCGAGCAAGGAGTGCCTCGCCCAAGGG	2998
QY	3001	CGAGCG	3060
Db	2999	CGAGCG	3058
QY	3061	GGAGGAGCGCGCGCGCGCGCACCGGCGCGCGCACAAAGCGCGAGCTGTCTCAAGAGCTGT	3120
Db	3059	GGAGGAGCGCGCGCGCGCGCACCGGCGCGCGCACAAAGCGCGAGCTGTCTCAAGAGCTGT	3118
QY	3121	GGAGAGGAGACCAAGGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	3180
Db	3119	GGAGAGGAGACCAAGGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	3178
QY	3181	CAAGGAAAAGGAGCTCCGGAAACACAGCGCGCGGAGCCACACTGTGACCTGGAGACCA	3240
Db	3179	CAAGGAAAAGGAGCTCCGGAAACACAGCGCGCGGAGCCACACTGTGACCTGGAGACCA	3238
QY	3241	TGGGACTGTGACTGTGGTCCCATGCACACTGCGCCAGACCTGTCTCCAGAGGTGGA	3300
Db	3239	TGGGACTGTGACTGTGGTCCCATGCACACTGCGCCAGACCTGTCTCCAGAGGTGGA	3298
QY	3301	GGACAGCCAGAGGATGCAGAACTCAGCGGAACTGCTACTCGCATGGGCACTCAGCGCCC	3360
Db	3299	GGACAGCCAGAGGATGCAGAACTCAGCGGAACTGCTACTCGCATGGGCACTCAGCGCCC	3358
QY	3361	AGACCCGGAACACTATTTGTACATATCCAGTGTGTGAGCGGCGCTCTTGGGGAGGCCAC	3420
Db	3359	AGACCCGGAACACTATTTGTACATATCCAGTGTGTGAGCGGCGCTCTTGGGGAGGCCAC	3418
QY	3421	GGTGTCTCCAGTGTAAAGTGGACCTGGAAAGCAAGCAAGGAGGAGGAGGAGGTGGA	3480

Db 3419 GGTGTTCCCAAGTGGTAACTGGGACCTGGAAAGCAAGCAGAGGGGAAAGAGGTGGA 3478
Qy 3481 AGCCGATGACGTGATGAGGAGCGGCCCGCCCTATCGTCCCAACACAGCTCCATGTTCTG 3540
Db 3479 AGCGATGACGTGATGAGGAGCGGCCCGCCCTATCGTCCCAACACAGCTCCATGTTCTG 3538
Qy 3541 TTTAAGGCCCAACCACTGCTCCGCGCTCTGCGCACTACATCGTGACCAAGGTACTT 3600
Db 3539 TTTAAGGCCCAACCACTGCTCCGCGCTCTGCGCACTACATCGTGACCAAGGTACTT 3598
Qy 3601 CGAGGTGCTCATCTCGTGGTCACTCGCTTGAGCAGCATCGCCCTGCTGAGGACCC 3660
Db 3599 CGAGGTGCTCATCTCGTGGTCACTCGCTTGAGCAGCATCGCCCTGCTGAGGACCC 3658
Qy 3661 AGTCGCGACAGACTCGCCCAAGAAACAACGCTCTGAATACCTGGATTACATTTCACTGG 3720
Db 3659 AGTCGCGACAGACTCGCCCAAGAAACAACGCTCTGAATACCTGGATTACATTTCACTGG 3718
Qy 3721 TGTCTTTACCTTTGAGATGGTGATAAAGATGATCGACTTGGGACTGCTGTCAACCTCG 3780
Db 3719 TGTCTTTACCTTTGAGATGGTGATAAAGATGATCGACTTGGGACTGCTGTCAACCTCG 3778
Qy 3781 AGCCTATTTCCGGACTTGTGGACATTTCTGACTTCATTTGTGTCACTGGCGCCCTGCT 3840
Db 3779 AGCCTATTTCCGGACTTGTGGACATTTCTGACTTCATTTGTGTCACTGGCGCCCTGCT 3838
Qy 3841 GGCCTTTGCTTTCTCGAGCTTCGTGGGAGATCCAAAGGGAAGACATCAATACCATCAA 3900
Db 3839 GGCCTTTGCTTTCTC-----AGATCCAAAGGGAAGACATCAATACCATCAA 3886
Qy 3901 GTCTCTGAGAGTCTTCTGCTCTCGCGCCCTCAAGACCATCAACCGCTGCCCAAGCT 3960
Db 3887 GTCTCTGAGAGTCTTCTGCTCTCGCGCCCTCAAGACCATCAACCGCTGCCCAAGCT 3946
Qy 3961 CAAGGCTGTTTGAACGTGTGGTGAACCTCGCTGAAGAAATGTCCTCAACATCTTGATTGT 4020
Db 3947 CAAGGCTGTTTGAACGTGTGGTGAACCTCGCTGAAGAAATGTCCTCAACATCTTGATTGT 4006
Qy 4021 CTACATGCTCTTCAATGTTCAATTTGCGCTCATTTGCGGTGCAGCTCTTCAAGGGAAGTT 4080
Db 4007 CTACATGCTCTTCAATGTTCAATTTGCGGTGCAGCTCTTCAAGGGAAGTT 4066
Qy 4081 TTTCTACTGCACAGATGAATCCAAAGAGCTGGAGAGGACTGCAAGGGTCAAGTATTTGGA 4140
Db 4067 TTTCTACTGCACAGATGAATCCAAAGAGCTGGAGAGGACTGCAAGGGTCAAGTATTTGGA 4126
Qy 4141 TTATGAGAGGGAAGTGGNAGCTCAGCCAGCAGTGGNAGAAATACGACTTTCACTA 4200
Db 4127 TTATGAGAGGGAAGTGGNAGCTCAGCCAGCAGTGGNAGAAATACGACTTTCACTA 4186
Qy 4201 CGACAAATGTGCTCTGGGCTCTGCTGAGCTGTTCAACAGTGTCCACGGGAGAGGCTGGCC 4260
Db 4187 CGACAAATGTGCTCTGGGCTCTGCTGAGCTGTTCAACAGTGTCCACGGGAGAGGCTGGCC 4246
Qy 4261 CATGGTCTGAAACACTCCGTTGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
Db 4247 CATGGTCTGAAACACTCCGTTGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4306
Qy 4321 CCGCATGGAGCTGTCATCTTCTAGTGGTCTACTTTGTGTTCTTCCCTTCTTCTCGT 4380
Db 4307 CCGCATGGAGCTGTCATCTTCTAGTGGTCTACTTTGTGTTCTTCCCTTCTTCTCGT 4366
Qy 4381 CAACATCTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGACAAGGTGATGTC 4440
Db 4367 CAACATCTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGACAAGGTGATGTC 4426
Qy 4441 TGAATGAGCTGAGAGGAACGAGAGGGCTTGCAATTTGACTTCCGCACTCAGCGCCAAACC 4500
Db 4427 TGAATGAGCTGAGAGGAACGAGAGGGCTTGCAATTTGACTTCCGCACTCAGCGCCAAACC 4486
Qy 4501 CCTGACAGGTACATGCCCCAAACCAGGAGTCTTCCAGTATTAAGACGTGGACATTTGT 4560

Db 4487 CCTGACACAGGTACATGCCCCAAAACCGCGAGTCTGTTCCAGTATAAGACGTGGACATTTGT 4546
Qy 4561 GGTCTCCCCGCCCTTTGAATACCTTTCATCATGGCCATGATAGCCCTCAACACTGTGGTGTCT 4620
Db 4547 GGTCTCCCCGCCCTTTGAATACCTTTCATCATGGCCATGATAGCCCTCAACACTGTGGTGTCT 4606
Qy 4621 GATGATGAAGTCTTATGATGACCCCTATGATGATGAGGTAGAGCTGATGTAATGCTTGAACAT 4680
Db 4607 GATGATGAAGTCTTATGATGACCCCTATGATGATGAGGTAGAGCTGATGTAATGCTTGAACAT 4666
Qy 4681 CGTGTTCACATCATCTTCTCAATGGAATCGCTGGAAGATCATCGCTTTCGGGGTGTCT 4740
Db 4667 CGTGTTCACATCATCTTCTCAATGGAATCGCTGGAAGATCATCGCTTTCGGGGTGTCT 4726
Qy 4741 GAACTATTTTCAGAGATGCTTGGAAATGCTTTTGACTTTGTCACTGTGTGGAAAGTATTAC 4800
Db 4727 GAACTATTTTCAGAGATGCTTGGAAATGCTTTTGACTTTGTCACTGTGTGGAAAGTATTAC 4786
Qy 4801 TGATATTTTAGTAAACAGAGATTGCGGAACGAACAAATTTTCATCAACCTCAGCTTCCTCCG 4860
Db 4787 TGATATTTTAGTAAACAGAGATTGCGGAACGAACAAATTTTCATCAACCTCAGCTTCCTCCG 4846
Qy 4861 CCTCTTTCGAGCTGCGCGCTGATCAAGCTGCTCCGCCAGGGCTACACCATCCGCAATCCT 4920
Db 4847 CCTCTTTCGAGCTGCGCGCTGATCAAGCTGCTCCGCCAGGGCTACACCATCCGCAATCCT 4906
Qy 4921 GCTGTGGACCTTTGTCCAGTCTTCAAGGCCCTGCCCCCTACGTGTGTCTCATTTGCCAT 4980
Db 4907 GCTGTGGACCTTTGTCCAGTCTTCAAGGCCCTGCCCCCTACGTGTGTCTCATTTGCCAT 4966
Qy 4981 GCTGTCTTTCATCTACGCCATCATTCGGCATGCAAGGTGTTTGGGAATATTGCCCTGAGTGA 5040
Db 4967 GCTGTCTTTCATCTACGCCATCATTCGGCATGCAAGGTGTTTGGGAATATTGCCCTGAGTGA 5026
Qy 5041 TGACACAGCATCAACCGCCACAACTTCCGGAGCTTTTTCGAAGCCCTGATGCTGTCT 5100
Db 5027 TGACACAGCATCAACCGCCACAACTTCCGGAGCTTTTTCGAAGCCCTGATGCTGTCT 5086
Qy 5101 GTTCAGGAGCGCCACCGGGGAGGCTTGGCACGAGATCATGCTGTCTGCTGAGCAACCA 5160
Db 5087 GTTCAGGAGCGCCACCGGGGAGGCTTGGCACGAGATCATGCTGTCTGCTGAGCAACCA 5146
Qy 5161 GGCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGCGCTACTTCTACTT 5220
Db 5147 GGCTGTGATGAGCAGGCCAATGCCACCGAGTGTGGAAGTGACTTTGCGCTACTTCTACTT 5206
Qy 5221 CGTCTCTTTCATCTTCTGTGCTCTTCTGATGTTGAACTCTTGTGCTGTGATCAT 5280
Db 5207 CGTCTCTTTCATCTTCTGTGCTCTTCTGATGTTGAACTCTTGTGCTGTGATCAT 5266
Qy 5281 GGAACAATTTTGATACCTCACCGGGAGCTTTCATCTCTAGGTCTTCACACATTTGATGA 5340
Db 5267 GGAACAATTTTGATACCTCACCGGGAGCTTTCATCTCTAGGTCTTCACACATTTGATGA 5326
Qy 5341 GTTCATCCGGGTCTGGGCTGAATAACGACCGGTGCTGTGGGCGCATCAGTTTACAATGA 5400
Db 5327 GTTCATCCGGGTCTGGGCTGAATAACGACCGGTGCTGTGGGCGCATCAGTTTACAATGA 5386
Qy 5401 CATGTTTGATGCTCAAAACATGTCCTCGCTCTGCGGCTGCGGAGGAATAAGCCCTGC 5460
Db 5387 CATGTTTGATGCTCAAAACATGTCCTCGCTCTGCGGCTGCGGAGGAATAAGCCCTGC 5446
Qy 5461 TCCAGTTGCTTACAAGCGCTGCTTCGATGAACATGCCCCATCTCCAAACGAGGACATGAC 5520
Db 5447 TCCAGTTGCTTACAAGCGCTGCTTCGATGAACATGCCCCATCTCCAAACGAGGACATGAC 5506
Qy 5521 TGTTCACTTCACTGTCACGCTGATGCGCTCATTCGGAACGCGCATCGGATCAAGCTGGC 5580
Db 5507 TGTTCACTTCACTGTCACGCTGATGCGCTCATTCGGAACGCGCATCGGATCAAGCTGGC 5566
Qy 5581 CCCAGCTGGGACAAACAGCATCAGTGTGACGGGAGTTGAGGAAGAGATTTTCCCTGT 5640
Db 5567 CCCAGCTGGGACAAACAGCATCAGTGTGACGGGAGTTGAGGAAGAGATTTTCCCTGT 5626

QY	5641	GTGGCCCAATCTGCCCAGAGACTTTTGGACTTGTGTACCAACCCCATTAAGCCTGATGA	5700
Db	5627	GTGGCCCAATCTGCCCAGAGACTTTTGGACTTGTGTACCAACCCCATTAAGCCTGATGA	5686
QY	5701	GATGACAGTGGGGAAGTTTATGACGCTCTGATGATATTTGACTTTTCAAGCAGAACAA	5760
Db	5687	TATGACAGTGGGGAAGTTTATGACGCTCTGATGATATTTGACTTTTCAAGCAGAACAA	5746
QY	5761	AACCAACAGAGACAGATGACAGAGGCTCTGTGAGAGCCTCTCCAGATGGTCTGTGTGC	5820
Db	5747	AACCAACAGAGACAGATGACAGAGGCTCTGTGAGAGCCTCTCCAGATGGTCTGTGTGC	5806
QY	5821	CTGTGTTCCACCTCTGAAGGCCACCTTGGAGCAGACACAGCCGCTGTGTCTCCAGAGGC	5880
Db	5807	CCTGTGTTCCACCTCTGAAGGCCACCTTGGAGCAGACACAGCCGCTGTGTCTCCAGAGGC	5866
QY	5881	CCGGTGTCTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGCGGGCCATACAAA	5940
Db	5867	CCGGTGTCTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGCGGGCCATACAAA	5926
QY	5941	CCAAGAGAGTGGCATCAAGAGTCTGTCTCTGGGCACTCAAGAGACCCAGATGCACC	6000
Db	5927	CCAAGAGAGTGGCATCAAGAGTCTGTCTCTGGGCACTCAAGAGACCCAGATGCACC	5986
QY	6001	CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6060
Db	5987	CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6046
QY	6061	AGGAGCACTGGCTGTGGAGCTTCAGATGACAGAGCATTAACCCGAGGGCCCTGATGGGA	6120
Db	6047	AGGAGCACTGGCTGTGGAGCTTCAGATGACAGAGCATTAACCCGAGGGCCCTGATGGGA	6106
QY	6121	GCCCCAGCTGGCTGGAGAGCCAGGGTCGAGGGCTCCATGCCCGGCTTGGCGGCGA	6180
Db	6107	GCCCCAGCTGGCTGGAGAGCCAGGGTCGAGGGCTCCATGCCCGGCTTGGCGGCGA	6166
QY	6181	GACTAGCCGCTCAGATGCCAGCCCATGAAGCGCTCCATCTCCAGCTGGGCCAGCG	6240
Db	6167	GACTAGCCGCTCAGATGCCAGCCCATGAAGCGCTCCATCTCCAGCTGGGCCAGCG	6226
QY	6241	GCCCCGTGGGACTCATCTTTGACAGACCAACCCCGGACCGCCACCCCTAGCCAGGGGTC	6300
Db	6227	GCCCCGTGGGACTCATCTTTGACAGACCAACCCCGGACCGCCACCCCTAGCCAGGGGTC	6286
QY	6301	GTGCAACCAACACACCGCTGCCACCGCGCAGGACAGGAAGCAGAGGTCCCTGGA	6360
Db	6287	GTGCAACCAACACACCGCTGCCACCGCGCAGGACAGGAAGCAGAGGTCCCTGGA	6346
QY	6361	GAAGGGCCAGCCTGTCTGCGGATATGGATGGCGCACCAAGCAGTGTGTGGGGCCGG	6420
Db	6347	GAAGGGCCAGCCTGTCTGCGGATATGGATGGCGCACCAAGCAGTGTGTGGGGCCGG	6406
QY	6421	GCTGCCCCCGGAGAGGGCCTTACAGGCTGCGCGGGGAACGAGAGCCCGCAGGAGCG	6480
Db	6407	GCTGCCCCCGGAGAGGGCCTTACAGGCTGCGCGGGGAACGAGAGCCCGCAGGAGCG	6466
QY	6481	GGGCGGTCTCCAGGAGCGGAGCGCCTCATCTCTCTCGAGAGCAGCGCTTCTA	6540
Db	6467	GGGCGGTCTCCAGGAGCGGAGCGCCTCATCTCTCTCGAGAGCAGCGCTTCTA	6526
QY	6541	CTCTCTCGACCGCTTTGGGGCCGTTGAGCCCGGAGCCCAAGCCCTCCCTCAGACCCA	6600
Db	6527	CTCTCTCGACCGCTTTGGGGCCGTTGAGCCCGGAGCCCAAGCCCTCCCTCAGACCCA	6586
QY	6601	CCCAACGTGGCCAAACAGCTGCCAGGAGCCCGGAGCCCAACCAAGGGCAGTGTCCGT	6660
Db	6587	CCCAACGTGGCCAAACAGCTGCCAGGAGCCCGGAGCCCAACCAAGGGCAGTGTCCGT	6646
QY	6661	GAATGGGAGCCCTTGTCTCAACATCTGGTCTAGCACCCCGGCGCGGTGGCGGAG	6720
Db	6647	GAATGGGAGCCCTTGTCTCAACATCTGGTCTAGCACCCCGGCGCGGTGGCGGAG	6706

QY	6721	GCAGTCCCCAGAGCCCTTGA	6780
Db	6707	GCAGTCCCCAGAGCCCTTGA	6766
QY	6781	CTACCCATCCACTTTCGCGGGGCTCAGACAGGCTCCCTGCTTCTCCAGGCGCGCT	6840
Db	6767	CTACCCATCCACTTTCGCGGGGCTCAGACAGGCTCCCTGCTTCTCCAGGCGCGCT	6826
QY	6841	CAGCGTGGGCTTTCGAAACAAACAGCGCTGCTCAGAGAGACCCCTCAGCCAGCCCT	6900
Db	6827	CAGCGTGGGCTTTCGAAACAAACAGCGCTGCTCAGAGAGACCCCTCAGCCAGCCCT	6886
QY	6901	GCCCGCTGGCTCTCGAATTGGCTCTGACCTTACCTGGGCGAGGCTTGACAGTGAAGC	6960
Db	6887	GCCCGCTGGCTCTCGAATTGGCTCTGACCTTACCTGGGCGAGGCTTGACAGTGAAGC	6946
QY	6961	CTCTGTCCAGCGCTTTCGAGGACAGCTCACTTTTCGAGAGGCTGTGCGCACCAACTC	7020
Db	6947	CTCTGTCCAGCGCTTTCGAGGACAGCTCACTTTTCGAGAGGCTGTGCGCACCAACTC	7006
QY	7021	GGGCGGCTCTCAGAGACTTCTCAGTGTCTCTCCCTGACCTCCOAGTCTCACCTCTCCG	7080
Db	7007	GGGCGGCTCTCAGAGACTTCTCAGTGTCTCTCCCTGACCTCCOAGTCTCACCTCTCCG	7066
QY	7081	CCGGTGGCCAAACGGTTTACCACTGCACCTGGGACTCAGCTCGGGTGGCGAGCAGGCA	7140
Db	7067	CCGGTGGCCAAACGGTTTACCACTGCACCTGGGACTCAGCTCGGGTGGCGAGCAGGCA	7126
QY	7141	CAGTACCAACCCCTGAGACCAAGACCACTGGTGTCTAGCTGACCCGTGACCCCTCAGACGC	7200
Db	7127	CAGTACCAACCCCTGAGACCAAGACCACTGGTGTCTAGCTGACCCGTGACCCCTCAGACGC	7186
QY	7201	CTCATGACAGCAGCGTGTGTTCCAGTGGATGATTTTATCATCCACAGCGGCACTCGG	7260
Db	7187	CTCATGACAGCAGCGTGTGTTCCAGTGGATGATTTTATCATCCACAGCGGCACTCGG	7246
QY	7261	CCCTCGGGGAGCGCTTGGCCACCTTGGTGGGCTCTCTGGGCGCCCTCCCTCCCGCTCT	7320
Db	7247	CCCTCGGGGAGCGCTTGGCCACCTTGGTGGGCTCTCTGGGCGCCCTCCCTCCCGCTCT	7306
QY	7321	CCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTGCTTGAGTGTAGTACGTAACGC	7376
Db	7307	CCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTGCTTGAGTGTAGTACGTAACGC	7362

RESULT 9
AAV29059

ID AAV29059 standard; cDNA; 7266 BP.

XX AAV29059;

AC AAV29059;

XX 28-AUG-1998 (first entry)

DT 28-AUG-1998 (first entry)

XX Human calcium channel a1B subunit cDNA.

DE Calcium channel; human; central nervous system disorder;

XX Lambert-Eaton syndrome; diagnosis; therapy; ds.

OS Homo sapiens.

XX Key

PH Location/Qualifiers

FT CDS

FT 92..7105

FT /*tag= a

XX WO9811131-A2.

XX 19-MAR-1998.

XX 11-SEP-1997; 97WO-US016146.

XX 16-SEP-1996; 96US-00713118.

XX (AMHP) AMERICAN HOME PROD CORP.

XX PI Franco R, Chen ARS, Shuey DJ;
XX WPI; 1998-207325/18.
XX DR P-PSDB; AAW37878.
XX PT DNA encoding human neuronal calcium channel subunit(s) - useful for
XX diagnosis of and treatment of central nervous system disorders, e.g.
XX Lambert-Eaton syndrome.
XX PS Claim 18; Fig 1; 89pp; English.
XX CC This cDNA clone codes for the $\alpha 1B$ subunit (see AAW37878) of the human
XX neuronal calcium channel. cDNA clones encoding the $\alpha 1B$ subunit, the $\alpha 2D$
XX subunit (see AAW29060) and a $\beta 3$ subunit (see AAW29061) have been
XX isolated. These have been inserted into expression vectors and are stably
XX expressed in transformed cell lines. The transformed cells show omega-
XX conotoxin GVIA binding activity, and omega-conotoxin GVIA toxin sensitive
XX potassium-stimulated calcium uptake, indicating that the proteins
XX expressed by the clones are capable of forming a functioning calcium
XX channel. Nucleic acids encoding the 3 subunits, as well as vectors, host
XX cells and methods of isolating nucleic acids encoding related calcium
XX channels are disclosed. Subunit proteins (see AAW37878-60), fusion
XX proteins, antibodies, as well as assays to identify agents that modulate
XX calcium channel activity are also provided. Such agents can be used to
XX treat certain central nervous system disorders by altering calcium
XX channel activity. Methods of diagnosing diseases associated with
XX particular calcium channels, such as Lambert-Eaton syndrome, are
XX disclosed
SQ Sequence 7266 BP; 1433 A; 2249 C; 2173 G; 1411 T; 0 U; 0 Other;
Query Match 97.9%; Score 7223.2; DB 2; Length 7266;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7263; Conservative 0; Mismatches 3; Indels 18; Gaps 2;
Qy 55 TCCGTGCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCGCGCTTCCCTGCGGGGCGCT 114
Db 1 TCCGTGCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCGCGCTTCCCTGCGGGGCGCT 60
Qy 115 GGGCGGGGATGACGCGGGGCGCGGAGCCATCGTCCGTTGGGACGAGCTGGGCGG 174
Db 61 GGGCGGGGATGACGCGGGGCGCGGAGCCATCGTCCGTTGGGACGAGCTGGGCGG 120
Qy 175 CCGCTATGAGGCGCCCGCGCGGAGAGCGGGCCCGGGCGCGCGCGCGGGCGG 234
Db 121 CCGCTATGAGGCGCCCGCGCGGAGAGCGGGCCCGGGCGCGCGCGGGCGG 180
Qy 235 GGGCGCGGTCCTGGGGGCTGACGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 294
Db 181 GGGCGCGGTCCTGGGGGCTGACGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Qy 295 GCAGCGCGCGGACCAATGGGCTGTACACCCCATCCCGGTCAAGCAGACTGCTTCAC 354
Db 241 GCAGCGCGCGGACCAATGGGCTGTACACCCCATCCCGGTCAAGCAGAACTGCTTCAC 300
Qy 355 CGTCAACCGCTCTGCTTCTGCTTTCAGCAGGACAAAGTCTCGTCCGCAAAATACGGAAGCG 414
Db 301 CGTCAACCGCTCTGCTTCTGCTTTCAGCAGGACAAAGTCTCGTCCGCAAAATACGGAAGCG 360
Qy 415 CATCACCGAGTGGCTTCATTCGAGTATATGATCTGCGCCACCATCATTCGCAACTGCAT 474
Db 361 CATCACCGAGTGGCTTCATTCGAGTATATGATCTGCGCCACCATCATTCGCAACTGCAT 420
Qy 475 CGTCTGGCCCTTGAGCAGCACTCCCTGATGGGACAAACGCCCATGTCCGAGCGGCT 534
Db 421 CGTCTGGCCCTTGAGCAGCACTCCCTGATGGGACAAACGCCCATGTCCGAGCGGCT 480
Qy 535 GGACGACACGAGCGCTTATTCATCGGGATCTTTTGTCTTCAGGACGAGATCAAAATCAT 594
Db 481 GGACGACACGAGCGCTTATTCATCGGGATCTTTTGTCTTCAGGACGAGATCAAAATCAT 540
Qy 595 CGCTCTGGGCTTGTCTTCCAAAGGGCTCTTACCTCGGAAACGGCTGGAAACGTCATGGA 654

541 CGCTCTGGGCTTGTCTTCCAAAGGGCTCTTACCTGCGGAACGGCTGGAACGTCATGGA 600
655 CTTCTGTTGCTGCTCTCTCACAGGGATCCTTGCCACGGGTGGAATCTGACCTTCGACCTGCGAAC 714
601 CTTCTGTTGCTGCTCTCTCACAGGGATCCTTGCCACGGGTGGAATCTGACCTTCGACCTGCGAAC 660
715 ACTGAGGGCTGCTGCTGCTGCTGAGGGCCCTTGAAAGCTGCTGCTGAGGATTCAGATTTGCA 774
661 ACTGAGGGCTGCTGCTGCTGCTGAGGGCCCTTGAAAGCTGCTGCTGAGGATTCAGATTTGCA 720
775 GGTGTTGCTCAAGTCCATCATGAAAGCCATGTTCCACTCTCTCAGATTTGGGCTGCTTCT 834
721 GGTGTTGCTCAAGTCCATCATGAAAGCCATGTTTCCACTCTCTCAGATTTGGGCTGCTTCT 780
835 CTTCTTTTGGCATCCTCATGTTTCCCATCATTTGCGCTGGAGTTCTACATGCGGCAAGTTCCA 894
781 CTTCTTTTGGCATCCTCATGTTTCCCATCATTTGCGCTGGAGTTCTACATGCGGCAAGTTCCA 840
895 CAAGGCTGTTTCCCAACAGACACAGATGCGGAGCCGCTGGGTGACTTCCCTCTGTGGCAA 954
841 CAAGGCTGTTTCCCAACAGACACAGATGCGGAGCCGCTGGGTGACTTCCCTCTGTGGCAA 900
955 GAGGCCCCAGCCGCTGTCGAGGCGGACACTGAGTGCAGGAGTACTGGCCAGGACC 1014
901 GAGGCCCCAGCCGCTGTCGAGGCGGACACTGAGTGCAGGAGTACTGGCCAGGACC 960
1015 CAATTTTGGCATCACAACCTTTTGCACAAATATCTGTTTGCATCTTGACGCTGTTTCCAGTG 1074
961 CAATTTTGGCATCACAACCTTTTGCACAAATATCTGTTTGCATCTTGACGCTGTTTCCAGTG 1020
1075 CATCACCATGAGGGCTGGATCGACATCTCTATAATAACAGATGCGCCCGGCAACAC 1134
1021 CATCACCATGAGGGCTGGATCGACATCTCTATAATAACAGATGCGCCCGGCAACAC 1080
1135 CTGGAATGCTCTACTTCTCATCTCTCATCATCTGCGCTCTTCTTCACTGCTCAACCT 1194
1081 CTGGAATGCTCTACTTCTCATCTCTCATCATCTGCGCTCTTCTTCACTGCTCAACCT 1140
1195 GGTGCTGGGCGTCTCTCGGGGAGTTTGCAGGAGCGAGAGGGGTGAGAACCCCGG 1254
1141 GGTGCTGGGCGTCTCTCGGGGAGTTTGCAGGAGCGAGAGGGGTGAGAACCCCGG 1200
1255 CGCCTTCTGAACTCGCGCGGAGAGATCGAGCGAGAGCTCAACCGGTTACTGGA 1314
1201 CGCCTTCTGAACTCGCGCGGAGAGATCGAGCGAGAGCTCAACCGGTTACTGGA 1260
1315 GTGATCTTCAAGCGGAGGAACTCATGCTGCGCGGAGAGGACAGGATTCAGAGGAGAA 1374
1261 GTGATCTTCAAGCGGAGGAACTCATGCTGCGCGGAGGAGGACAGGATTCAGAGGAGAA 1320
1375 GTCCCTTTGGAGCTGCTGAAAGAGAGCGGCCCAAGAGAGCAGAAATGACCTGATCCA 1434
1321 GTCCCTTTGGAGCTGCTGAAAGAGAGCGGCCCAAGAGAGCAGAAATGACCTGATCCA 1380
1435 CGCAGAGGAGGAGAGGACCGGTTTCAGATCTCTGTGCTGTTGGATTCCTTCCCGCCG 1494
1381 CGCAGAGGAGGAGAGGACCGGTTTCAGATCTCTGTGCTGTTGGATTCCTTCCCGCCG 1440
1495 CGCCAGCTTCAAGAGCGGAGAGAGAGAGCTGCTCATCTTCCGAGGAGGAGAGAT 1554
1441 CGCCAGCTTCAAGAGCGGAGAGAGAGAGAGCTGCTCATCTTCCGAGGAGGAGAGAT 1500
1555 GTTCCGCTTTTATCCGCGCATGTTGAAAGGCTCAGAGCTTCTTACTGGGTGGTGTGTG 1614
1501 GTTCCGCTTTTATCCGCGCATGTTGAAAGGCTCAGAGCTTCTTACTGGGTGGTGTGTG 1560
1615 CGTGTGGCCCTGAACACACTGTGTGTGGCCATGTGTGCTCAATACAAACAGCCGCGGGCT 1674
1561 CGTGTGGCCCTGAACACACTGTGTGTGGCCATGTGTGCTCAATACAAACAGCCGCGGGCT 1620
1675 TACACGACCTGTATTTTGCAGAGTTGTTTTCCTGGGTCTTCTTCTCAGAGATGTC 1734

QY 3895 CATCAAGTCTCTGAGAGTCTCTTCTGTCTCTGCGGCCCTCAAGACCATCAAAACGGCTGCC 3954
DB CATCAAGTCTCTGAGAGTCTCTTCTGTCTCTGCGGCCCTCAAGACCATCAAAACGGCTGCC 3888
QY 3955 CAAGCTCAAGGCTGTGTTGACTGTGTGTGAATCTCCCTGAAGAAATGCTCTCAACATCTT 4014
DB CAAGCTCAAGGCTGTGTTGACTGTGTGTGAATCTCCCTGAAGAAATGCTCTCAACATCTT 3948
QY 4015 GATTGCTACATGCTCTTCACTGTTTCAATATTGTCGCTCAATTGCGGTGAGCTCTTCAAAGG 4074
DB GATTGCTACATGCTCTTCACTGTTTCAATATTGTCGCTCAATTGCGGTGAGCTCTTCAAAGG 4008
QY 4075 GAAGTTTTTCTACTGACAGATGAATCCAAGAGCTGAGAGGACATGCAAGGGTCACTA 4134
DB GAAGTTTTTCTACTGACAGATGAATCCAAGAGCTGAGAGGACATGCAAGGGTCACTA 4068
QY 4135 TTTTGGATTATTGAGAAAGGAGGATGGAAGCTACAGCCACAGGCAGTGGGAAGAAATACGACTT 4194
DB TTTTGGATTATTGAGAAAGGAGGATGGAAGCTACAGCCACAGGCAGTGGGAAGAAATACGACTT 4128
QY 4195 TCACTACGACAAATGTCTCTGGGCTCTGTGACGCTGTTCACAGTGTCCACGGGAGAAGG 4254
DB TCACTACGACAAATGTCTCTGGGCTCTGTGACGCTGTTCACAGTGTCCACGGGAGAAGG 4188
QY 4255 CTGGCCCATGGTGTGAAAACATCTCCGTGATGCCACCTATGAGAGCAGGGTCCAAAGCCC 4314
DB CTGGCCCATGGTGTGAAAACATCTCCGTGATGCCACCTATGAGAGCAGGGTCCAAAGCCC 4248
QY 4315 TGGGTACCGATGAGCTGTCCATCTTCTAGTGGTCTACTTTGTGCTCTTCCCTCTCTT 4374
DB TGGGTACCGATGAGCTGTCCATCTTCTAGTGGTCTACTTTGTGCTCTTCCCTCTCTT 4308
QY 4375 CTTGCTCAACATCTTTTGGCTTTTGATCATCATCACCTTCCAGGAGCAGGGGAGCAAGGT 4434
DB CTTGCTCAACATCTTTTGGCTTTTGATCATCATCACCTTCCAGGAGCAGGGGAGCAAGGT 4368
QY 4435 GATGCTGAATGAGCTTGAGAAAGACGAGAGGGCTTGATGACTTGGCCATCAGCGC 4494
DB GATGCTGAATGAGCTTGAGAAAGACGAGAGGGCTTGATGACTTGGCCATCAGCGC 4428
QY 4495 CAACCCCTGACACGGTACATGCCCCAAAACCGGACGTCTCCAGTATAGAGCTGGAC 4554
DB CAACCCCTGACACGGTACATGCCCCAAAACCGGACGTCTCCAGTATAGAGCTGGAC 4488
QY 4555 ATTTGTGGTCTCCCCGCCCTTTGAATACTTCATCATGGCCATGATAGCCCTCAACACTGT 4614
DB ATTTGTGGTCTCCCCGCCCTTTGAATACTTCATCATGGCCATGATAGCCCTCAACACTGT 4548
QY 4615 GGTGCTGATGATGAAGTTCTATGATGACCCCTATGAGTACGAGCTGATGTAATGCTT 4674
DB GGTGCTGATGATGAAGTTCTATGATGACCCCTATGAGTACGAGCTGATGTAATGCTT 4608
QY 4675 GAAATCGTGTTCATCCATGTTCTCCATGGAAATGCGTGAAGATCATCGCTTTGG 4734
DB GAAATCGTGTTCATCCATGTTCTCCATGGAAATGCGTGAAGATCATCGCTTTGG 4668
QY 4735 GGTGCTGAACTATTTCAGAGATGCTTGAATGTCTTTGACTTTTGCTACTGTGTGGGAAG 4794
DB GGTGCTGAACTATTTCAGAGATGCTTGAATGTCTTTGACTTTTGCTACTGTGTGGGAAG 4728
QY 4795 TATTACTGATATTTTATGATACAGAGATTGGGAAACGAACTTTTCATCAACCTCAGCTT 4854
DB TATTACTGATATTTTATGATACAGAGATTG-----CGAACTTTTCATCAACCTCAGCTT 4782
QY 4855 CCTCCGCTCTTTTCAGCTCGCGGCTGATCAAGCTGCTCGCCAGGGCTACACCATCCG 4914
DB CCTCCGCTCTTTTCAGCTCGCGGCTGATCAAGCTGCTCGCCAGGGCTACACCATCCG 4842
QY 4915 CATCCTGCTGGAACCTTTTGTCCAGTCTTCAAGGCCCTCGCCCTACGCTGTGTGCTCAT 4974
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QY 4975 TGCCATGCTGTTCTTCACTACGCCATCATCGGCATGCAAGGTGTTGGGAATATTGCCCCT 5034

DB 4903 TGCATGCTGTTCTTTCATCTACGCCATCATCGGCATGCAAGGTGTTTGGGAATATTGCCCCT 4962
QY 5035 GGATGATGACACAGCATCAAAACGCCCAACAACATTTCCGACCGTTTTTCGAAGCCCTGAT 5094
DB GGATGATGACACAGCATCAAAACGCCCAACAACATTTCCGACCGTTTTTCGAAGCCCTGAT 5022
QY 5095 GCTGCTGTTTCAGAGCGCCACCGGGGAGGCTGGCAGAGATCATGCTGCTGCTGCTGAG 5154
DB GCTGCTGTTTCAGAGCGCCACCGGGGAGGCTGGCAGAGATCATGCTGCTGCTGCTGAG 5082
QY 5155 CAACACGGCTGTGATGAGCAGAGCAATGCCCACCGAGTGTGGAAGTGAATTTCCCTACTT 5214
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DB GGATGATTCATCCGGTCTGGGCTGAATACGACCCGGCTGCGTGTGGGGCGATCAGTTA 5322
QY 5395 CAATGACATGTTTGAAGTGTGAAACACATGTCCCAGCTCTCTGGGGCTGGGGGAAGAAATG 5454
DB CAATGACATGTTTGAAGTGTGAAACACATGTCCCAGCTCTCTGGGGCTGGGGGAAGAAATG 5382
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DB CCTGCTCGAGTTGCTTTCAAGCGCTGTTCGATGAAACATGCCATCTCCAAACGAGGA 5442
QY 5515 CATGACTGTTCACTTCACGTCACAGTGTGGCCCTCATCCGACGCACTGGAGATCAA 5574
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QY 5995 TGCAACCCATGAGGGCAGGCCACCCCTGGAGCGTGCCACTCCACAGAGATCCTGTGGG 6054
DB TGCAACCCATGAGGGCAGGCCACCCCTGGAGCGTGCCACTCCACAGAGATCCTGTGGG 5982
QY 6055 GCGGTACGAGGCACTGGCTGTGACGTTGATGACAGGATTAACCCGAGGGGCGCTGA 6114

Db 5983 GCGGTGAGGAGCACTGGCTGTGGACGTTTCAGATGCAGAGCATAAACCGGAGGGGCCCTGA 6042
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Db 6043 TGGGGAGCCCCAGCCCTGGGCTGGAGAGCCAGGGTCGAGGGCTTCATGCCCGGCTTGC 6102
QY 6175 GCGGAGAGCTCAGCCCGTTCACAGATGCCAGCCCCATGAAGCGCTCATCTCCACGCTGCG 6234
Db 6103 GCGGAGAGCTCAGCCCGTTCACAGATGCCAGCCCCATGAAGCGCTCATCTCCACGCTGCG 6162
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QY 6775 CAACTCCTCACCCTACCTTCGCGGGGCTCAGACAGCCTCCTGCTCTCCCGCAGG 6834
Db 6703 CAACTCCTCACCCTACCTTCGCGGGGCTCAGACAGCCTCCTGCTCTCCCGCAGG 6762
QY 6835 CCGGCTCAGCCGTGGGCTTTCCGAACACACGCGCTGCTGCAGAGAGACCCCTCAGCCA 6894
Db 6763 CCGGCTCAGCCGTGGGCTTTCCGAACACACGCGCTGCTGCAGAGAGACCCCTCAGCCA 6822
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Db 6823 GCCCTGGCCCCGTGCTCTGAAATTGGCTCTGACCCCTTACCTGGGGGAGGCTGTGGACAG 6882
QY 6955 TGAGGCTCTGTCACGCGCTGCTGAGGACAGCTCACTTTTCAGAGGAGGCTGTGGCCAC 7014
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QY 7315 CTTCTCCCTCTTTTACTCTAGA 7338
Db 7243 CTTCTCCCTCTTTTACTCTAGA 7266
RESULT 10
ABZ58367
ID ABZ58367 standard; cDNA; 7177 BP.
XX
AC ABZ58367;
XX
DT 28-APR-2003 (first entry)
XX
DE Human N-type calcium channel alpha-1B subunit coding sequence.
XX
KW Human; calcium channel; voltage-gated ion channel; splice variant; gene;
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 146..6859
FT /*tag= a
FT /product= "Human calcium channel, alpha-1B subunit"
XX
DN WO2003006103-A2.
XX
PD 23-JAN-2003.
XX
PF 12-JUL-2002; 2002WO-US022161.
XX
PR 12-JUL-2001; 2001US-0304955P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Augustine PR, Bennett PB, Bugianesi RM, Garyantes TA, Imredy JP;
PI Kath GS, Mcmanus OB;
XX
DR WPI; 2003-221676/21.
DR P-PSDB; ABP72256.
XX
PT Identifying modulators of the activity of a voltage-gated ion channel,
PT comprises altering the transmembrane potential of a portion of the cell
PT membrane expressing the voltage-gated ion channel by electric field
PT stimulation.
XX
PS Disclosure; Fig 21A-C; 188pp; English.
XX
CC The present sequence is the coding sequence for a splice variant of the
CC alpha-1B subunit of the human T-type calcium channel. The invention
CC provides methods of identifying activators and inhibitors of voltage-
CC gated ion channels (VC). The methods use electrical field stimulation of
CC cells via extracellular electrodes to manipulate the open/close state
CC transitions of the VCs. This allows for more convenient, more precise
CC manipulation of these transitions and, coupled with efficient methods of
CC detecting ion flux or membrane potential, results in methods that are
CC especially suitable for high-throughput screening of compounds as
CC potential activators and inhibitors of VCs. The VC may be a sodium,
CC potassium calcium channel. The cells are e.g. HEK293 (ATCC 1573) cells
CC transfected with DNA encoding the VC, and may contain a fluorescent
CC indicator compound. Defective sodium, calcium and potassium VCs have been
CC implicated in a variety of disorders including long QT syndrome, ataxia,
CC migraine, muscle paralysis, deafness, and cardiac conduction
CC diseases

XX	SQ	Sequence	7177 BP; 1414 A; 2198 C; 2169 G; 1396 T; 0 U; 0 Other;
		Query Match	94.3%; Score 6958; DB 7; Length 7177;
		Best Local Similarity	97.3%; Pred. No. 0;
		Matches 7177; Conservative	0; Mismatches 0; Indels 199; Gaps 2;
Qy	1	GCGCGCGGCTGCGGCGTGGGCGCGGCGAGGTCGCGTGCCTGCGGCGGCTCCGCGT	60
Db	1	GCGCGCGGCGTGGCGGCGTGGGCGCGGCGAGGTCGCGTGCCTGCGGCGGCTCCGCGT	60
Qy	61	GCTGCTCCGCTCTCAGCGGCTGCGGCGCGCGCGCGCTCCCTGCGGCGGCGCTGGGCGG	120
Db	61	GCTGCTCCGCTCTCAGCGGCTGCGGCGCGCGCGCGCTCCCTGCGGCGGCGCTGGGCGG	120
Qy	121	GGGATGCACGCGGCGCGCGGAGCCATGGTCCGCTTCGGGAGCAGAGTCGGCGCGCGCTA	180
Db	121	GGGATGCACGCGGCGCGCGGAGCCATGGTCCGCTTCGGGAGCAGAGTCGGCGCGCGCTA	180
Qy	181	TGGAGGCCCGCGCGCGAGAGCGGCGCGGCGGCGGCGCGCGCGCGCGCGCGCGCGCC	240
Db	181	TGGAGGCCCGCGCGCGAGAGCGGCGCGGCGGCGGCGCGCGCGCGCGCGCGCGCGCC	240
Qy	241	GGGTCCCGGGGCTGCAGCCCGCGCGAGCGGCTCTCTACAGCAATCGATCGCGCGAGCG	300
Db	241	GGGTCCCGGGGCTGCAGCCCGCGCGAGCGGCTCTCTACAGCAATCGATCGCGCGAGCG	300
Qy	301	CGCGCGACCATGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	360
Db	301	CGCGCGACCATGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	360
Qy	361	CCGCTCGCTCTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	420
Db	361	CCGCTCGCTCTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	420
Qy	421	CGAGTGGCTCCATTCGAGTATATGATCTGGCCACCATCATCGCCAACTGCATCGTCT	480
Db	421	CGAGTGGCTCCATTCGAGTATATGATCTGGCCACCATCATCGCCAACTGCATCGTCT	480
Qy	481	GGCCCTTGAGCAGCACTCCCTGATGGGACAAAACGCCCATGTCGAGCGGCTGGACGA	540
Db	481	GGCCCTTGAGCAGCACTCCCTGATGGGACAAAACGCCCATGTCGAGCGGCTGGACGA	540
Qy	541	CACGAGCCCTATTTCATCGGGATCTTTTGTCTCAGGCGAGGATCAAAATCATCGCTCT	600
Db	541	CACGAGCCCTATTTCATCGGGATCTTTTGTCTCAGGCGAGGATCAAAATCATCGCTCT	600
Qy	601	GGGCTTTGTCTTCCACAGGCTCTTACCTCGGGAACGGCTGGAACGTCATGCACTTCGT	660
Db	601	GGGCTTTGTCTTCCACAGGCTCTTACCTCGGGAACGGCTGGAACGTCATGCACTTCGT	660
Qy	661	GGTCTCTCAGGGATCTTTCACGGCTGGAACCTGACTTCACCTGGACACTGAG	720
Db	661	GGTCTCTCAGGGATCTTTCACGGCTGGAACCTGACTTCACCTGGACACTGAG	720
Qy	721	GGCTGTGCTGTGTCGAGGCCCCGTAAGCTGGTGTCTGGGATTCGAAGTTTGAGGTGGT	780
Db	721	GGCTGTGCTGTGTCGAGGCCCCGTAAGCTGGTGTCTGGGATTCGAAGTTTGAGGTGGT	780
Qy	781	GCTCAAGTCCATCATGAAGGCCATGGTTCACCTCTCGAGATGGGCTGCTTCTTCTT	840
Db	781	GCTCAAGTCCATCATGAAGGCCATGGTTCACCTCTCGAGATGGGCTGCTTCTTCTT	840
Qy	841	TGCCATCTCATGTTTGCATATGGCTGGAGTTCTACATGGGCAAGTTTCACAAGGC	900
Db	841	TGCCATCTCATGTTTGCATATGGCTGGAGTTCTACATGGGCAAGTTTCACAAGGC	900
Qy	901	CTGTTTCCCAACACACAGATGCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	960
Db	901	CTGTTTCCCAACACACAGATGCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	960
Qy	961	CCAGCCCGGCTGTGCGAGGCGGACATGAGTGCAGGAGTACCTGGCGCAGGACCCAACTT	1020
Db	961	CCAGCCCGGCTGTGCGAGGCGGACATGAGTGCAGGAGTACCTGGCGCAGGACCCAACTT	1020

Db	961	CCAGCCCGGCTGTGCGAGGCGGACACTGAGTGCCGGAGTACTGGCCAGGACCCAACTT	1020
Qy	1021	TGGCATCACCAACTTTTGACAATATCTGTGTTGCCATCTTGACGGTGTTCAGTGCATCAC	1080
Db	1021	TGGCATCACCAACTTTTGACAATATCTGTGTTGCCATCTTGACGGTGTTCAGTGCATCAC	1080
Qy	1081	CATGGAGGCTGGAATGACATCTCTATATATCAAAAGATGCGGCGGCAACACCTGGAA	1140
Db	1081	CATGGAGGCTGGAATGACATCTCTATATATCAAAAGATGCGGCGGCAACACCTGGAA	1140
Qy	1141	CTGCTCTACTTCTCATCCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGCT	1200
Db	1141	CTGCTCTACTTCTCATCCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGCT	1200
Qy	1201	GGGCGTGTCTCTCGGGGAGTTTCCAAAGAGCGAGAGGTTGGAGAACCGCGCGCTT	1260
Db	1201	GGGCGTGTCTCTCGGGGAGTTTCCAAAGAGCGAGAGGTTGGAGAACCGCGCGCTT	1260
Qy	1261	CCTGAAGCTCGCGCGGAGCAGATCGAGCGAGAGCTCAAAGGTACCTGGTGAGTGAT	1320
Db	1261	CCTGAAGCTCGCGCGGAGCAGATCGAGCGAGAGCTCAAAGGTACCTGGTGAGTGAT	1320
Qy	1321	CTTCAAGCGGAGGAAAGTCTATGCTGGCCGAGGAGGACAGGAATGCGAGGAGTCCCC	1380
Db	1321	CTTCAAGCGGAGGAAAGTCTATGCTGGCCGAGGAGGACAGGAATGCGAGGAGTCCCC	1380
Qy	1381	TTTGGAGCTGCTCAAGAGAGCGGCCAACAAAGAGCAGAAATGACCTGATCCACGAGA	1440
Db	1381	TTTGGAGCTGCTCAAGAGAGCGGCCAACAAAGAGCAGAAATGACCTGATCCACGAGA	1440
Qy	1441	GGAGGAGAGGACCGGTTTCAGATCTCTGTCTGTTGGATTCCTTCCGCGCGGCGCAG	1500
Db	1441	GGAGGAGAGGACCGGTTTCAGATCTCTGTCTGTTGGATTCCTTCCGCGCGGCGCAG	1500
Qy	1501	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATCTTCCGAGGAAGAGAGATGTTCCG	1560
Db	1501	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATCTTCCGAGGAAGAGAGATGTTCCG	1560
Qy	1561	GTTTTTTATCCGGCGCATGTTGAAGCTCTACTGGGTGGTGTGCTGCGTGGT	1620
Db	1561	GTTTTTTATCCGGCGCATGTTGAAGCTCTACTGGGTGGTGTGCTGCGTGGT	1620
Qy	1621	GGCCCTGAAACACTGTGTGTGCGCATGTTGTCATTAACAACGCGCGGCGGCTTACAC	1680
Db	1621	GGCCCTGAAACACTGTGTGTGCGCATGTTGTCATTAACAACGCGCGGCGGCTTACAC	1680
Qy	1681	GACCTGTATTTTGCAGAGTTTCTTCTGGGTCTCTTCTCACAGAGATGCCCTGAA	1740
Db	1681	GACCTGTATTTTGCAGAGTTTCTTCTGGGTCTCTTCTCACAGAGATGCCCTGAA	1740
Qy	1741	GATGTATGGCTCGGGCCACAGAACTACTTCCGCTCTCTTCAACTGCTTCGACTTTGG	1800
Db	1741	GATGTATGGCTCGGGCCACAGAACTACTTCCGCTCTCTTCAACTGCTTCGACTTTGG	1800
Qy	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCCGGGAAAGCTCCTT	1860
Db	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCCGGGAAAGCTCCTT	1860
Qy	1861	TGGGATCAGTGTCTCGGGCCCTCGGCTGCTGAGGATCTTCAAAAGTCAAGTACTG	1920
Db	1861	TGGGATCAGTGTCTCGGGCCCTCGGCTGCTGAGGATCTTCAAAAGTCAAGTACTG	1920
Qy	1921	GAGCTCCCTCGGAAACCTGGTGTGTCTCTGCTGAACTCCATGAAGTCCATCATAGCCT	1980
Db	1921	GAGCTCCCTCGGAAACCTGGTGTGTCTCTGCTGAACTCCATGAAGTCCATCATAGCCT	1980
Qy	1981	GCTCTTCTGCTCTTCTGTTCATGTTGCTTTCGCCCTGCTGGGAGTGCAGCTGTTGG	2040
Db	1981	GCTCTTCTGCTCTTCTGTTCATGTTGCTTTCGCCCTGCTGGGAGTGCAGCTGTTGG	2040
Qy	2041	GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTTCGACCTTCCCTGCGCG	2100
Db	2041	GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTTCGACCTTCCCTGCGCG	2100

Db 4249 CATGGTCTGAAACACTCCGTGGATGCCACTATAGGAGCAGGGTCAAAGCCCTGGGTA 4308
Qy |||||
Db 4321 CCGCATGGAGCTGTCACATCTTCTACGTGGTCTACTTTTGTGTCTTTCCCTTCTTCTCGT 4380
Qy |||||
Db 4309 CCGCATGGAGCTGTCACATCTTCTACGTGGTCTACTTTTGTGTCTTTCCCTTCTTCTCGT 4368
Qy |||||
Db 4381 CAACATCTTTTGTGGCTTTGTATCATCATCATCTCCAGGAGCAGGGGACAAGGTGATGTC 4440
Qy |||||
Db 4369 CAACATCTTTTGTGGCTTTGTATCATCATCATCTCCAGGAGCAGGGGACAAGGTGATGTC 4428
Qy |||||
Db 4441 TGAATGAGCTTGGAGAACGAGAGGGCTTGCATTGACTTGCCTATGAGCGCCAAACC 4500
Qy |||||
Db 4429 TGAATGAGCTTGGAGAACGAGAGGGCTTGCATTGACTTGCCTATGAGCGCCAAACC 4488
Qy |||||
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Qy |||||
Db 4489 CCTGACACGGTACATGCCCCCAAAACCGGCAGTCTGTTCCAGTATAAGACGTGGACATTGT 4548
Qy |||||
Db 4561 GGTCTCCCCGCCCTTTGAATCACTTTCATCATGCGCATGATAGCCCTCAACACTGTGGTGTCT 4620
Qy |||||
Db 4549 GGTCTCCCCGCCCTTTGAATCACTTTCATCATGCGCATGATAGCCCTCAACACTGTGGTGTCT 4608
Qy |||||
Db 4621 GATGATGAAGTTCTATGATGCACCTATGATGATGATGATGATGATGATGATGATGATGAT 4680
Qy |||||
Db 4609 GATGATGAAGTTCTATGATGCACCTATGATGATGATGATGATGATGATGATGATGATGAT 4668
Qy |||||
Db 4681 CGTGTTCACATCCATGTTCTCCATGGAATGGTCTGAAGATCATCGCCCTTTGGGGTGTCT 4740
Qy |||||
Db 4669 CGTGTTCACATCCATGTTCTCCATGGAATGGTCTGAAGATCATCGCCCTTTGGGGTGTCT 4728
Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
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Db 4981 GCTGTCTTCTCATCTACGCCATCATCGGCATGACGGTGTTTGGGAATATTGCCCTGGATGA 5040
Qy |||||
Db 4969 GCTGTCTTCTCATCTACGCCATCATCGGCATGACGGTGTTTGGGAATATTGCCCTGGATGA 5028
Qy |||||
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Qy |||||
Db 5029 TGACACAGCATCAACCGCCACAACAACCTTCGGAGCGTTTTTTCGACGCCCTGATGTGCT 5088
Qy |||||
Db 5101 GTTCAGAGCGCCACGCGGGAGGCTTGCGACGAGATCATGTGTCTGCTGCTGAGCAACCA 5160
Qy |||||
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Qy |||||
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Qy |||||
Db 5209 CGTCTCTCTCATCTTCTGTGCTCTCTTCTGTATGTGTAACCTCTTTGTGGCTGTGATCAT 5268
Qy |||||
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Qy |||||
Db 5269 GGACAAATTTTGTAGTACCTCAGCGGGGACTCTTTCATCTTAGTCTCCTCACCACTTGGATGA 5328
Qy |||||
Db 5341 GTTCATCCGGGTCTGGGCTGAATACGACCGCGGTGCGTGTGGGCGCATCAGTTACAATGA 5400
Qy |||||

Db 5329 GTTCATCCGGGTCTGGGCTGAATAAGACCGCGGTGCGTGTGGCGCATCAGTTACAAATGA 5388
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Qy |||||
Db 5389 CATGTTTGTAGATGCTGAAACACACATGTCCCGCCTCTGGGGCTGGGGAAGAAATGCCCTGTC 5448
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Qy |||||
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Qy |||||
Db 5581 CCAGCTGGGACAAAACGAGCATCAGTGTGACGCGAGTTGAGGAAGAGATTTCCGTTGT 5640
Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
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Db 6349 GAAAGGGCCAGCGCTGTCTGCCGATATGGATGGCGCAACAAAGCAGTGTGTGTGGGGCCGGG 6408
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Db 6409 GCTGCCCGCCGGAGAGGGGCTTACAGGCTCCCGCGGGAAACGAGAGCGCCGCGAGGAGCG 6468
Qy |||||

Qy 121 GGGATGACCGCGGGCCGGAGCCATGGTCCGCTTCGGGGAAGAGCTGGCGGCGCCCTA 180
Db 119 GGGATGACCGCGGGCCCGGAGCCATGGTCCGCTTCGGGGAAGAGCTGGCGGCGCCCTA 178
Qy 181 TGGAGGCCCGCGCGGAGAGCGGGCCCGGGGCGGCGGGCGGCGGGGGGCGCC 240
Db 179 TGGAGGCCCGCGCGGAGAGCGGGCCCGGGGCGGCGGGCGGCGGGGGGCGCC 238
Qy 241 GGGTCCGGGGGGGTGACGCCCGGCGAGCGGGTCTCTTACAAGCAATCGATCGCGCAGCG 300
Db 239 GGGTCCCGGGGGGTGACGCCCGGCGAGCGGGTCTCTTACAAGCAATCGATCGCGCAGCG 298
Qy 301 CGCGGAGACCATGGCGCTGTACAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 360
Db 299 CGCGGAGACCATGGCGCTGTACAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 358
Qy 361 CGGCTCGCTCTTCGCTTCACGAGGACAAAGTCGTCGGCAATACCGAGCGCATCAC 420
Db 359 CGGCTCGCTCTTCGCTTCACGAGGACAAAGTCGTCGGCAATACCGAGCGCATCAC 418
Qy 421 CGAGTGGCCTCCATTCGAGTATATGATCTTGGCCACCACCATATCGCCAACTGCAATCGTGCT 480
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Db 2879 CGAGGCG 2938
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Db 3179 CAAAGAAAGGAGCTCGGAAACCAAGCCCGGAGCGCACCTGTGACCTGGAGAGCCAG 3238
Qy 3241 TGGGACTGTGCTGGGTCCCATGACACACTCCGAGCAGCTGTCTCCAGAGGTGGA 3300
Db 3239 TGGGACTGTGCTGGGTCCCATGACACACTCCGAGCAGCTGTCTCCAGAGGTGGA 3298
Qy 3301 GGAAAGCAGGAGGATGAGCAAACTCAGCGGAAGTCACTCGCATGGGCGAGTCAAGCCCC 3360
Db 3299 GGAAAGCAGGAGGATGAGCAAACTCAGCGGAAGTCACTCGCATGGGCGAGTCAAGCCCC 3358
Qy 3361 AGACCCGAACACTATTGTATATATCCAGTATGCTGAGCGGCGCTCTTGGGGAAGCCAC 3420
Db 3359 AGACCCGAACACTATTGTATATATCCAGTATGCTGAGCGGCGCTCTTGGGGAAGCCAC 3418

Qy 3421 GGTCTTTCCAGTGTAACTGGGACCTGGAAAGCAAGCAGAGGGGAGAGGAGGTGGA 3480
Db 3419 GGTCTTTCCAGTGTAACTGGGACCTGGAAAGCAAGCAGAGGGGAGAGGAGGTGGA 3478
Qy 3481 AGCGGATGACGTGATGAGGAGCGGCGCGCGCGCTATCGTCCCATACAGCTCCATGTTCTG 3540
Db 3479 AGCGGATGACGTGATGAGGAGCGGCGCGCGCGCTATCGTCCCATACAGCTCCATGTTCTG 3538
Qy 3541 TTTAAGCCCAACCAACTGCTCCGCGCTTCTGCGACTTACATCGTACCATACAGCTTACTT 3600
Db 3539 TTTAAGCCCAACCAACTGCTCCGCGCTTCTGCGACTTACATCGTACCATACAGCTTACTT 3598
Qy 3601 CGAGTGTGTCTTCTGCTGCTGAGCAGCATCGCCCTGCTGCTGAGGAGCC 3660
Db 3599 CGAGTGTGTCTTCTGCTGCTGAGCAGCATCGCCCTGCTGCTGAGGAGCC 3658
Qy 3661 AGTCGCAAGACTCGCCAGGAAACGCTCTGAAATACCTGAAATTTACATTTTCACTGG 3720
Db 3659 AGTCGCAAGACTCGCCAGGAAACGCTCTGAAATACCTGAAATTTACATTTTCACTGG 3718
Qy 3721 TGTCTTTACCTTTGAGATGATGATAAAGATGATCGACTTGGGACTGCTGCTTCACTGG 3780
Db 3719 TGTCTTTACCTTTGAGATGATGATAAAGATGATCGACTTGGGACTGCTGCTTCACTGG 3778
Qy 3781 AGCTATTTCCGGGACTTGGGAAACATTTCTGAGCTTCAATGCTGCTGCTGCTGCTGCT 3840
Db 3779 AGCTATTTCCGGGACTTGGGAAACATTTCTGAGCTTCAATGCTGCTGCTGCTGCTGCT 3838
Qy 3841 GGGCTTTGCTTTCTCGAGCTTCTGCGGAGGATCCAAAGGGGAAAGACATCAATACCAATCAA 3900
Db 3839 GGGCTTTGCTTTCTC-----AGGATCCAAAGGGGAAAGACATCAATACCAATCAA 3886
Qy 3901 GTCTCTGAGAGTCTTCTGCTGCTGCTGCGGCGCTTCAAGACCATCAAAAGCGTGGCCAGCT 3960
Db 3887 GTCTCTGAGAGTCTTCTGCTGCTGCGGCGCTTCAAGACCATCAAAAGCGTGGCCAGCT 3946
Qy 3961 CAAAGCTGTCTTGTGACTGTGTGTAACCTCCCTGAAAGATGCTCTCAACATCTTGAATGT 4020
Db 3947 CAAAGCTGTCTTGTGACTGTGTGTAACCTCCCTGAAAGATGCTCTCAACATCTTGAATGT 4006
Qy 4021 CTACATGCTCTTCAATGTTTCAATTTTCCGCTCAATGCGGTGCTGCTCTTCAAGAGGAAGTT 4080
Db 4007 CTACATGCTCTTCAATGTTTCAATTTTCCGCTCAATGCGGTGCTGCTCTTCAAGAGGAAGTT 4066
Qy 4081 TTTCTACTCAGAGATGAATCCAAAGAGCTGGAGAGGAGTGGAGGGGTCTGATTTTGA 4140
Db 4067 TTTCTACTCAGAGATGAATCCAAAGAGCTGGAGAGGAGTGGAGGGGTCTGATTTTGA 4126
Qy 4141 TTATGAGAAGGAGGAAGTGGAAAGCTCAGCCAGGAGTGGAAAGAAATACGACTTTTCACTA 4200
Db 4127 TTATGAGAAGGAGGAAGTGGAAAGCTCAGCCAGGAGTGGAAAGAAATACGACTTTTCACTA 4186
Qy 4201 CGCAATGTCTTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4260
Db 4187 CGCAATGTCTTGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4246
Qy 4261 CATGTGTCTGAAACACTCCGCTGATGCCACTTATGAGGAGCAGGCTTCAAGCCCTGGGTA 4320
Db 4247 CATGTGTCTGAAACACTCCGCTGATGCCACTTATGAGGAGCAGGCTTCAAGCCCTGGGTA 4306
Qy 4321 CCGCATGGAGCTGTCTTCTTCACTGCTGCTTCTTCTGCTGCTTCTTCTGCTTCTTCTGCT 4380
Db 4307 CCGCATGGAGCTGTCTTCTTCACTGCTGCTTCTTCTGCTGCTTCTTCTGCTTCTTCTGCT 4366
Qy 4381 CAAACATCTTTTGGCTTTGATCATCATCTTCCAGGAGCAGGAGGAGGAGGATGATGTC 4440
Db 4367 CAAACATCTTTTGGCTTTGATCATCATCTTCCAGGAGCAGGAGGAGGAGGATGATGTC 4426
Qy 4441 TGAATGAGCCTGGAGAAAGACGAGAGGCTTGAATGACTTCCGCAATCAGCGCCAAACC 4500
Db 4427 TGAATGAGCCTGGAGAAAGACGAGAGGCTTGAATGACTTCCGCAATCAGCGCCAAACC 4486

Db	6630	-----	6629
Qy	6721	GCAGCTCCCCAGAGAGCCCTGACTCCCGGCCAGCATCACCTACAAGACGGCAACTC	6780
Db	6630	-----	6629
Qy	6781	CTCACCACATCCACTTCGCGGGGCTCAGACAGCCTCCCTGCTTCTCCCAAGCGCGCT	6840
Db	6630	-----	6639
Qy	6841	CAGCCGTGGGCTTTCCGACACAAACAGCCCTGCTGCAGAGAGACCCCTCAGCAGCCCT	6900
Db	6640	CAGCCGTGGGCTTTCCGACACAAACAGCCCTGCTGCAGAGAGACCCCTCAGCAGCCCT	6999
Qy	6901	GGCCCTTGGCTCTCGAATTGGCTCTGACCCCTTACCTGGGGCAGCGCTCTGGACAGTGAGGC	6960
Db	6700	GGCCCTTGGCTCTCGAATTGGCTCTGACCCCTTACCTGGGGCAGCGCTCTGGACAGTGAGGC	6759
Qy	6961	CTCTGTCCAGCCCTGCTGAGGACACGCTCACTTTTCGAGGAGGCTGTGGCCACCAATC	7020
Db	6760	CTCTGTCCAGCCCTGCTGAGGACACGCTCACTTTTCGAGGAGGCTGTGGCCACCAATC	6819
Qy	7021	GGCCCTTCTCTCAGGACTTCTTACGTGCTCTCCCTGACCTCCAGTCTCACTCCCTCTCG	7080
Db	6820	GGCCCTTCTCTCAGGACTTCTTACGTGCTCTCCCTGACCTCCAGTCTCACTCCCTCTCG	6879
Qy	7081	CGCGTGCCCAAGGTTACCACTGACACCTCGGACTCGGCTGGCCGAGCAGCGCA	7140
Db	6880	CGCGTGCCCAAGGTTACCACTGACACCTCGGACTCGGCTGGCCGAGCAGCGCA	6939
Qy	7141	CAGCTACCAACCCCTGACCAAGACACATGCTGCTAGCTGCAACCGTACCGCTCAGAGC	7200
Db	6940	CAGCTACCAACCCCTGACCAAGACACATGCTGCTAGCTGCAACCGTACCGCTCAGAGC	6999
Qy	7201	CTGCATGACAGAGGCTGTGTTCCAGTGATCAGTATTTATCATCCACAGGGGAGTGG	7260
Db	7000	CTGCATGACAGAGGCTGTGTTCCAGTGATCAGTATTTATCATCCACAGGGGAGTGG	7059
Qy	7261	CCCTGGGGAGGCTTGGCCACCTTGTGTGAGGCTCTGTGGCCCTCCCTCCCTCTCT	7320
Db	7060	CCCTGGGGAGGCTTGGCCACCTTGTGTGAGGCTCTGTGGCCCTCCCTCCCTCTCT	7119
Qy	7321	CCCTCTTTTACTCTAGACGAGCAATAAGCCCTCTGCTTGAGTGATCGTACGCG	7376
Db	7120	CCCTCTTTTACTCTAGACGAGCAATAAGCCCTCTGCTTGAGTGATCGTACGCG	7175
RESULT 12			
ID	AAV42686		
XX	AAV42686 standard; DNA; 7175 BP.		
AC	AAV42686;		
XX			
DT	25-MAR-2003 (revised)		
DT	12-OCT-1998 (first entry)		
XX			
DE	DNA encoding human calcium channel alpha-1B-1 subunit.		
XX			
KW	Alpha-1B subunit; human; calcium channel; assay; detection;		
XX	characterisation; Lambert Eaton Syndrome; LES; diagnosis; ds.		
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	5'UTR	1..143	
FT	FT	/*tag= a	
FT	CDS	144..6857	
FT	FT	/*tag= b	
FT	FT	6855..7175	
FT	FT	/*tag= c	
XX			
PN	US5792846-A.		
XX			

PD	11-AUG-1998.		
XX			
PF	31-MAY-1995;	95US-00455543.	
XX			
PR	04-APR-1988;	88US-00176899.	
PR	04-APR-1989;	89WO-US001408.	
PR	20-FEB-1990;	90US-00482384.	
PR	08-NOV-1990;	90US-00603751.	
PR	30-NOV-1990;	90US-00620250.	
PR	15-AUG-1991;	91US-00745206.	
PR	04-APR-1994;	94US-00223305.	
XX	(SIBI-) SIBIA NEUROSCIENCES INC.		
XX	Brenner R, Ellis SB, Williams ME, Feldman DH, Mecue AP;		
PI	Harbold WM;		
XX			
DR	WPI; 1998-456192/39.		
DR	P-PSDB; AAW63142.		
XX			
PT	DNA encoding human calcium channel alpha 1B subunit protein - useful for		
PT	recombinant production of the channel for screening of its modulators,		
XX	and diagnosis of Lambert Eaton Syndrome.		
PS	Claim 1; Col 91-106; 166pp; English.		
XX			
CC	The present sequence encodes the alpha-1B subunit of a human calcium		
CC	channel. The present sequence is derived from alternative splicing of		
CC	AAV42685. Calcium channels are membrane-spanning, multi-subunit proteins		
CC	that allow controlled entry of calcium ions into cells. This leads to		
CC	depolarisation events required for muscle contraction. The recombinant		
CC	subunit, when expressed with nucleic acids encoding the complete calcium		
CC	channel, can be used in assays for the detection and characterisation of		
CC	compounds that modulate the channel. The DNA encoding the subunit can be		
CC	alternatively spliced when transcribed, giving more than one form of the		
CC	protein from the same transcript, each having slightly different		
CC	properties. In addition, the reactivity of the alpha 1 subunit with IgG		
CC	molecules from the serum of an individual with Lambert Eaton Syndrome		
CC	(LES) can be used as a diagnostic for the disease. (Updated on 25-MAR-		
CC	2003 to correct PR field.)		
XX			
SQ	Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 U; 0 Other;		
Query Match 94.0%; Score 6932.4; DB 2; Length 7175;			
Best Local Similarity 97.3%; Pred. No. 0;			
Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;			
Qy	1	CGCGCGCGGCTCGCGCGGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	60
Db	1	CGCGCGCGGCTCGCGCGGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	59
Qy	61	GCTGCTCCGCTCTGAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	120
Db	60	GCTGCTCCGCTCTGAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	118
Qy	121	GGGATCACCGTA	180
Db	119	GGGATCACCGTA	178
Qy	181	TGGAGCG	240
Db	179	TGGAGCG	238
Qy	241	GGGTCCCG	300
Db	239	GGGTCCCG	298
Qy	301	CGCGCGGACCATGGCGCTGTACAACCCCATCCCGGTCAAGCAGAGAACTGCTTACCGTCAA	360
Db	299	CGCGCGGACCATGGCGCTGTACAACCCCATCCCGGTCAAGCAGAGAACTGCTTACCGTCAA	358
Qy	361	CGGCTCGCTTTCGTTTTCAGGCGAGCAAACTGCTCGCAAAATACGCGAGCGATCAC	420

Db 359 CCGCTCGCTCTTCTGCTTTACGGAGGACAACGTCGTCTCGGCAATATACGGGAAGCGCATCAC 418
Qy 421 CGAGTGGCTCCATTCGAGATATATGATCTTGGCCACCACCATCATGCCAACTGCACTGCTGCT 480
Db 419 CGAGTGGCTCCATTCGAGATATATGATCTTGGCCACCACCATCATGCCAACTGCACTGCTGCT 478
Qy 481 GGCCTCGAGCAGACCTCCCTGATGGGACAAAACGCCCATGTCGAGCGGCTGGACGA 540
Db 479 GGCCTCGAGCAGACCTCCCTGATGGGACAAAACGCCCATGTCGAGCGGCTGGACGA 538
Qy 541 CACGAGCCCTATTTCTCGGGATCTTTTGTCTCGAGCAGGGATCAAAATCATCGCTCT 600
Db 539 CACGAGCCCTATTTCTCGGGATCTTTTGTCTCGAGCAGGGATCAAAATCATCGCTCT 598
Qy 601 GGGCTTTGCTTCCACAAGGCTCTTACCTGCGGAACGGCTGGAACTGATGGAATTCGT 660
Db 599 GGGCTTTGCTTCCACAAGGCTCTTACCTGCGGAACGGCTGGAACTGATGGAATTCGT 658
Qy 661 GGTGCTCTCACAGGATCTTGGCCACGGCTGGAACTGATGGAATTCGAACTGAG 720
Db 659 GGTGCTCTCACAGGATCTTGGCCACGGCTGGAACTGATGGAATTCGAACTGAG 718
Qy 721 GGTGCTGCTGTGCTGAGGCCCTTGAAGCTGCTGCTGGATTCGAAGTTTGCAGGNGGT 780
Db 719 GGTGCTGCTGTGCTGAGGCCCTTGAAGCTGCTGCTGGATTCGAAGTTTGCAGGNGGT 778
Qy 781 GCTCAAGTCCATCATGAAGGCTATGTTCCACTCTCTGAGATTTGGGCTGCTCTTCTT 840
Db 779 GCTCAAGTCCATCATGAAGGCTATGTTCCACTCTCTGAGATTTGGGCTGCTCTTCTT 838
Qy 841 TGGCATCTCATGTTTGGCATCATTTGGCTTGGAGTTCTATATGGGGAAGTTCCAAAGGC 900
Db 839 TGGCATCTCATGTTTGGCATCATTTGGCTTGGAGTTCTATATGGGGAAGTTCCAAAGGC 898
Qy 901 CTGTTTCCCAACAGCAGATGCGAGCCGCTGGGTGACTTCCCTGTGCGAAGGAGGC 960
Db 899 CTGTTTCCCAACAGCAGATGCGAGCCGCTGGGTGACTTCCCTGTGCGAAGGAGGC 958
Qy 961 CCCAGCCGGCTGTGCGAGGCGGACACTGAGTGCAGGAGTACTGCGCAGGACCCAACTT 1020
Db 959 CCCAGCCGGCTGTGCGAGGCGGACACTGAGTGCAGGAGTACTGCGCAGGACCCAACTT 1018
Qy 1021 TGGCATCACCACTTTGACAAATATCTGTTTGGCCATCTTGAAGGTTTCAAGTGCATCAC 1080
Db 1019 TGGCATCACCACTTTGACAAATATCTGTTTGGCCATCTTGAAGGTTTCAAGTGCATCAC 1078
Qy 1081 CATGAGGCTGGAATGACATCTCTATATACAAACGATGCGGCGCGCAACCTCGAA 1140
Db 1079 CATGAGGCTGGAATGACATCTCTATATACAAACGATGCGGCGCGCAACCTCGAA 1138
Qy 1141 CTGGCTCTACTTCTATCCCTCTCATCATCATCGGCTCTTCTTCAATGCTCAACCTGGTCT 1200
Db 1139 CTGGCTCTACTTCTATCCCTCTCATCATCATCGGCTCTTCTTCAATGCTCAACCTGGTCT 1198
Qy 1201 GGGCGTGTCTCTGGGGAGTTTGGCAAGGACGAGAGGTTGAGAAACCGCCGCGCTT 1260
Db 1199 GGGCGTGTCTCTGGGGAGTTTGGCAAGGACGAGAGGTTGAGAAACCGCCGCGCTT 1258
Qy 1261 CCTGAAGTGGCGGAGCAGATGCTGAGCAGAGCTCAACGGGTACCTGGAGTGGAT 1320
Db 1259 CCTGAAGTGGCGGAGCAGATGCTGAGCAGAGCTCAACGGGTACCTGGAGTGGAT 1318
Qy 1321 CTTCAAGCGGAGGAAGTCTATGCTGGCGGAGGAGCAGGAATGCAGAGAGAGTCCCC 1380
Db 1319 CTTCAAGCGGAGGAAGTCTATGCTGGCGGAGGAGCAGGAATGCAGAGGAGATCCCC 1378
Qy 1381 TTTGGAAGTGTGAAGAGAGGGCCACCAAGAGAGCAGAAATGACTGATTCACGAGA 1440
Db 1379 TTTGGAAGTGTGAAGAGAGGGCCACCAAGAGAGCAGAAATGACTGATTCACGAGA 1438
Qy 1441 GGAGGAGAGACCGGTTTGCAGATCTCTGTGCTGTTGGATCCCTTCCGCGCGCAG 1500
Db 1439 GGAGGAGAGACCGGTTTGCAGATCTCTGTGCTGTTGGATCCCTTCCGCGCGCAG 1498

Qy 1501 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCTATATCTTCCGGAAGGAAGAGATGTTCCG 1560
Db 1499 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCTATATCTTCCGGAAGGAAGAGATGTTCCG 1558
Qy 1561 GTTTTTTATCCGGCGCATGCTGAAGGCTCAGAGCTTCTACTTGGGTGCTGCTGCGTGGT 1620
Db 1559 GTTTTTTATCCGGCGCATGCTGAAGGCTCAGAGCTTCTACTTGGGTGCTGCTGCGTGGT 1618
Qy 1621 GGCCTCGAAACACTGTGTGGCCATGTGTGCAATTAACAACAGCCGCGCGGCTTACCA 1680
Db 1619 GGCCTCGAAACACTGTGTGGCCATGTGTGCAATTAACAACAGCCGCGCGGCTTACCA 1678
Qy 1681 GACCTGTATTTTGCAGAGTTGTTTCTTGGGTCTTCTCTCACAGAGATGCTCCTGAA 1740
Db 1679 GACCTGTATTTTGCAGAGTTGTTTCTTGGGTCTTCTCTCACAGAGATGCTCCTGAA 1738
Qy 1741 GATGTATGGCTCGGGCCCAAGAGCTTCTCCGGTCTCTCTCAACTGCTTCCAGTCTTGG 1800
Db 1739 GATGTATGGCTCGGGCCCAAGAGCTTCTCCGGTCTCTCTCAACTGCTTCCAGTCTTGG 1798
Qy 1801 GGTCACTCGTGGGAGCGTCTTTGAAAGTGTCTCGGGGCGCATCAAGCCGGAAGCTCTT 1860
Db 1799 GGTCACTCGTGGGAGCGTCTTTGAAAGTGTCTCGGGGCGCATCAAGCCGGAAGCTCTT 1858
Qy 1861 TGGGATCAGTGTCTGCGGCGCTTCCGCTGTCTGAGGATCTTCAAAGTCAAGAGTACTG 1920
Db 1859 TGGGATCAGTGTCTGCGGCGCTTCCGCTGTCTGAGGATCTTCAAAGTCAAGAGTACTG 1918
Qy 1921 GAGCTCCCTCGGAACTGCTGTGGTGTCCCTGCTGAACTCCATGAGTCCATCATCAGCCT 1980
Db 1919 GAGCTCCCTCGGAACTGCTGTGGTGTCCCTGCTGAACTCCATGAGTCCATCATCAGCCT 1978
Qy 1981 GCTCTTCTGCTCTCTCTGTTCAATGTGTGTTCTCGCCCTGCTGGGATGAGCTGTTGG 2040
Db 1979 GCTCTTCTGCTCTCTCTGTTCAATGTGTGTTCTCGCCCTGCTGGGATGAGCTGTTGG 2038
Qy 2041 GGAACAGTTCAAATTCAGGATGAGATCCCAACAACAACTTCGACACCTTCCCTGCGCG 2100
Db 2039 GGAACAGTTCAAATTCAGGATGAGATCCCAACAACAACTTCGACACCTTCCCTGCGCG 2098
Qy 2101 CATCTCTACCTGTTTCCAGATCTCTGAGGAGGAGTGGAAATGCAATGATGATCAGCG 2160
Db 2099 CATCTCTACCTGTTTCCAGATCTCTGAGGAGGAGTGGAAATGCAATGATGATCAGCG 2158
Qy 2161 GATCGAATCGAAGGCGGCTCAGCAAGGATGTTCTCGTCTCTTTTACTTCTATGTCCT 2220
Db 2159 GATCGAATCGAAGGCGGCTCAGCAAGGATGTTCTCGTCTCTTTTACTTCTATGTCCT 2218
Qy 2221 GACACTGTTTGGAAAATACACTCTGCTGAATGTTTCTGGCCATCGCTGTGACAACT 2280
Db 2219 GACACTGTTTGGAAAATACACTCTGCTGAATGTTTCTGGCCATCGCTGTGACAACT 2278
Qy 2281 GGCACAGCCCAAGCTGACCAAGATGAGAGGAGATGGAAGAGCAGCCCAATCAGAA 2340
Db 2279 GGCACAGCCCAAGCTGACCAAGATGAGAGGAGATGGAAGAGCAGCCCAATCAGAA 2338
Qy 2341 GCTTGTCTTGAAGGCAAGAGTGGCTGAAGTCAAGGCTCAGCCCATGCTTCCCGCGAAT 2400
Db 2339 GCTTGTCTTGAAGGCAAGAGTGGCTGAAGTCAAGGCTCAGCCCATGCTTCCCGCGAAT 2398
Qy 2401 CTCATCTGCGCGCAGGACAGAACTCGGCCAAAGGCGCTCGGTGTGGAGCAGCGGGC 2460
Db 2399 CTCATCTGCGCGCAGGACAGAACTCGGCCAAAGGCGCTCGGTGTGGAGCAGCGGGC 2458
Qy 2461 CAGCAGCTACGCTCGAGAACTTGGCGGCGAGCTGCGAGGCGCTGTACAGCGAGTGA 2520
Db 2459 CAGCAGCTACGCTCGAGAACTTGGCGGCGAGCTGCGAGGCGCTGTACAGCGAGTGA 2518
Qy 2521 CCCGAGGAGCGCTGCGCTTTCGCCACTACGCCCACTTCCGCCCGCGACATGAAGAGCA 2580
Db 2519 CCCGAGGAGCGCTGCGCTTTCGCCACTACGCCCACTTCCGCCCGCGACATGAAGAGCA 2578

Db 4727 GAACCTATTTGAGAGATGCGCTGGAAATGCTTTTGACTTTTGTCATCTGTGTGGAAAGTATTAC 4786
Qy 4801 TGATAATTTTAGTAAACAGAGATTTGGGAAACGAAACAAATTTTCATCAACCTCAGCTTCTCTCCG 4860
Db 4787 TGATAATTTTAGTAAACAGAGATTTGGGAAACGAAACAAATTTTCATCAACCTCAGCTTCTCTCCG 4846
Qy 4861 CCTCTTTGAGAGTGGCGGCTGTATCAAGCTGTCTCCGCCAGGGCTACACCATCCGATCCCT 4920
Db 4847 CCTCTTTGAGAGTGGCGGCTGTATCAAGCTGTCTCCGCCAGGGCTACACCATCCGATCCCT 4906
Qy 4921 GCTGTGACCTTTGTCCAGTCCCTTCAAGSCCCTGCCCTAGCTGTGTCTCATTTGCCAT 4980
Db 4907 GCTGTGACCTTTGTCCAGTCCCTTCAAGSCCCTGCCCTAGCTGTGTCTCATTTGCCAT 4966
Qy 4981 GCTCTTTCTTCATCTACGCCCATCATCGGCATGCAAGTGTTTGGGAATATTTGCCCTGATGA 5040
Db 4967 GCTGTCTTCATCTACGCCCATCATCGGCATGCAAGTGTTTGGGAATATTTGCCCTGATGA 5026
Qy 5041 TGACACAGCATCAACCGCCACAAACAACTTCCGGACGTTTTTGGAAAGCCTGTATGCTGCT 5100
Db 5027 TGACACAGCATCAACCGCCACAAACAACTTCCGGACGTTTTTGGAAAGCCTGTATGCTGCT 5086
Qy 5101 GTTCAGAGCGCCACGGGGAGGCGCTGGCAGGATCATGCTGTCTGCCCTGAGCAACCA 5160
Db 5087 GTTCAGAGCGCCACGGGGAGGCGCTGGCAGGATCATGCTGTCTGCCCTGAGCAACCA 5146
Qy 5161 GGCCTGTGATGAGCAGCGCAATGCCACCGAGTGTGGAAGTGAATTTGCGCTACTTCTACTT 5220
Db 5147 GGCCTGTGATGAGCAGCGCAATGCCACCGAGTGTGGAAGTGAATTTGCGCTACTTCTACTT 5206
Qy 5221 CGTCTCTCTCATCTTCTGTGCTCTCTTCTGTATGTTGAACTCTTTGTGGCTGTGATCAT 5280
Db 5207 CGTCTCTCTCATCTTCTGTGCTCTCTTCTGTATGTTGAACTCTTTGTGGCTGTGATCAT 5266
Qy 5281 GGAACAATTTTGAATACCTCAGCGGGACTCTTCCATCCTAGGTCCTCACACATTTGGATGA 5340
Db 5267 GGAACAATTTTGAATACCTCAGCGGGACTCTTCCATCCTAGGTCCTCACACATTTGGATGA 5326
Qy 5341 GTTCATCCGGCTCTGGGCTGAATACGACCGGGCTGCGTGTGGGCGCATCAGTTACATGA 5400
Db 5327 GTTCATCCGGCTCTGGGCTGAATACGACCGGGCTGCGTGTGGGCGCATCAGTTACATGA 5386
Qy 5401 CATGTTTGAATGTGAAACATGTCCTCCGCTCTCTGGGCTGGGGAAGAAATGCCCTGC 5460
Db 5387 CATGTTTGAATGTGAAACATGTCCTCCGCTCTCTGGGCTGGGGAAGAAATGCCCTGC 5446
Qy 5461 TCGAGTTGCTTACAGCGCTGGTTCCATGAACATGCCCATCTCCAAACGAGACATGAC 5520
Db 5447 TCGAGTTGCTTACAGCGCTGGTTCCGATGAACATGCCCATCTCCAAACGAGACATGAC 5506
Qy 5521 TGTTCACTTTCACGCTCAGCTGATGGCCCTCATCCGACGGCATCTGGAGATCAAGCTGGC 5580
Db 5507 TGTTCACTTTCACGCTCAGCTGATGGCCCTCATCCGACGGCATCTGGAGATCAAGCTGGC 5566
Qy 5581 CCCAGCTGGGAACAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGAGATTTCCGTTGT 5640
Db 5567 CCCAGCTGGGAACAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGAGATTTCCGTTGT 5626
Qy 5641 GTGGGCCAATCTGCCCAGAGACTTTGGACTTCTGTTACCAACCCCATTAAGCTGTATGA 5700
Db 5627 GTGGGCCAATCTGCCCAGAGACTTTGGACTTCTGTTACCAACCCCATTAAGCTGTATGA 5686
Qy 5701 GATGACAGTGGGAAGGTTTATGAGCTCTGATGATATTTGACTTCTACAGAGCAACAA 5760
Db 5687 GATGACAGTGGGAAGGTTTATGAGCTCTGATGATATTTGACTTCTACAGAGCAACAA 5746
Qy 5761 AACCAACAGAGACAGATGACAGAGGCTCTCGAGGCGCTCTCCAGATGGGTCTCTGTGC 5820
Db 5747 AACCAACAGAGACAGATGACAGAGGCTCTCGAGGCGCTCTCCAGATGGGTCTCTGTGC 5806
Qy 5821 CCTGTTCCACCTCTGAAGGCCACCTGGAGCAGACACAGCCGCTGTCTCCGAGGAGC 5880
Db 5807 CCTGTTCCACCTCTGAAGGCCACCTGGAGCAGACACAGCCGCTGTCTCCGAGGAGC 5866

Qy 5881 CCGGGTTTTCTTTCGACAGAGAGTTTCCACCTCCCTCAGCAATGGCGGGGCCATACAAAA 5940
Db 5867 CCGGGTTTTCTTTCGACAGAGAGTTTCCACCTCCCTCAGCAATGGCGGGGCCATACAAAA 5926
Qy 5941 CCAAGAGATGGGATCAAGAGTCTGTCTCTGGGGCACTCAAGGACCCAGATGCACC 6000
Db 5927 CCAAGAGATGGGATCAAGAGTCTGTCTCTGGGGCACTCAAGGACCCAGATGCACC 5986
Qy 6001 CCATGAGGCGAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGGGGTC 6060
Db 5987 CCATGAGGCGAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGGGGTC 6046
Qy 6061 AGGAGCACTGGCTGTGGACGTTTCAGATGACAGATAAACCCGAGGGGCGCTCATGAGGGA 6120
Db 6047 AGGAGCACTGGCTGTGGACGTTTCAGATGACAGATAAACCCGAGGGGCGCTCATGAGGGA 6106
Qy 6121 GCCCAGCCTGGGCTGGAGAGCCAGGTCGAGGGGCTCCATGCCCGCTTGGGGCCGA 6180
Db 6107 GCCCAGCCTGGGCTGGAGAGCCAGGTCGAGGGGCTCCATGCCCGCTTGGGGCCGA 6166
Qy 6181 GACTCAGCCCGTCAAGATGCCAGCCCATGAAGCGTCTCATCTCAACGCTGGCCAGCG 6240
Db 6167 GACTCAGCCCGTCAAGATGCCAGCCCATGAAGCGTCTCATCTCAACGCTGGCCAGCG 6226
Qy 6241 GCCCGTGGGACTCATCTTTTGACGACCAACCCCGGACCGGCCACCCCTTAGCGGCTC 6300
Db 6227 GCCCGTGGGACTCATCTTTTGACGACCAACCCCGGACCGGCCACCCCTTAGCGGCTC 6286
Qy 6301 GTCCGACCAACCAACCAACCGCTGCCACCGCCGAGGGACAGGAAGCAGAGTCCCTTGA 6360
Db 6287 GTCCGACCAACCAACCAACCGCTGCCACCGCCGAGGGACAGGAAGCAGAGTCCCTTGA 6346
Qy 6361 GAAGGGGCCCAGCGCTGTCTGCCGATATGATGCGCACCAAGCAGTCTCTGTGGGGCGGG 6420
Db 6347 GAAGGGGCCCAGCGCTGTCTGCCGATATGATGCGCACCAAGCAGTCTCTGTGGGGCGGG 6406
Qy 6421 GCTGCCCGCGGAGAGGGGCTTACAGGCTGCCCGCGGGAACGAGAGCGCCGGCAGGAGCG 6480
Db 6407 GCTGCCCGCGGAGAGGGGCTTACAGGCTGCCCGCGGGAACGAGAGCGCCGGCAGGAGCG 6466
Qy 6481 GGCGCCGCTCCAGGAGGGAGCGGCGCTCATCTCTCTCGGAGAGAGCGCTTCTA 6540
Db 6467 GGCGCCGCTCCAGGAGGGAGCGGCGCTCATCTCTCTCGGAGAGAGCGCTTCTA 6526
Qy 6541 CTCTCGACCGCTTTGGGGCGGTGAGCCCCCGAAGCCCAAGCCCTCCTCCTCAGCAGCCA 6600
Db 6527 CTCTCGACCGCTTTGGGGCGGTGAGCCCCCGAAGCCCAAGCCCTCCTCCTCAGCAGCCA 6586
Qy 6601 CCCAACGTCGCCAACAGCTGGCCAGGAGCGGGAACCCCAACCCCAAGGGCAGTGGTTCCGT 6660
Db 6587 CCCAACGTCGCCAACAGCTGGCCAGGAGCGGGAACCCCAACCCCAAGGGCAGTGGTTCCGT 6629
Qy 6661 GAATGGGAGGCCCTTGTCTGTCAACATCTGGTGTAGCACCCCGCGCGGCTGGGGGAG 6720
Db 6630 ----- 6629
Qy 6721 GCAGCTCCCCAGACGCCCCCTGACTCCCCCGCCCCAGCATCACCTACAGACGGCCAACTC 6780
Db 6630 ----- 6629
Qy 6781 CTCACCCATCCACTTCGCGGGGCTCAGACGCTCCTTCCTTCCTCCAGCCGGCT 6840
Db 6630 ----- 6639
Qy 6841 CAGCGTGGGCTTTCCGAACACACCGCCCTGTGTCAGAGAGACCCCTCAGCCAGCCCT 6900
Db 6640 CAGCGTGGGCTTTCCGAACACACCGCCCTGTGTCAGAGAGACCCCTCAGCCAGCCCT 6899
Qy 6901 GGCCCCCTGGCTCTCGAAATTTGGCTCTGACCTTACCTTGGGGGAGCGCTCTGACAGTGGGC 6960
Db 6700 GGCCCCCTGGCTCTCGAAATTTGGCTCTGACCTTACCTTGGGGGAGCGCTCTGACAGTGGGC 6759

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QY 6961 CTCTGTCCACGCCCTGCTGAGGACACGCTCACTTTCGAGGAGGCTGTGGCCACCAACTC 7020
Db CTCTGTCCACGCCCTGCTGAGGACACGCTCACTTTCGAGGAGGCTGTGGCCACCAACTC 6819
QY 7021 GGCGCGCTCTCCAGAGCTTCCTACGTGCTCCTCCCTGACCTCCAGTCTCACTCCCTCCG 7080
Db GGCGCGCTCTCCAGAGCTTCCTACGTGCTCCTCCCTGACCTCCAGTCTCACTCCCTCCG 6879
QY 7081 CCCTGTGCCCCAAGCTTACCACTGCACCTGGGACTCAGCTGGGTGGCGGAGCAGCA 7140
Db CCCTGTGCCCCAAGCTTACCACTGCACCTGGGACTCAGCTGGGTGGCGGAGCAGCA 6939
QY 7141 CAGCTACCAACCCCTGACCAAGACACACTGGTGTAGCTGCACCTGACCGCTCAGAGCG 7200
Db CAGCTACCAACCCCTGACCAAGACACACTGGTGTAGCTGCACCTGACCGCTCAGAGCG 6999
QY 7201 CTGCATGCAGCAGCGCTGTGTTCCAGTGCATGATGATTTTATCATCCACAGGGGCGAGTCGG 7260
Db CTGCATGCAGCAGCGCTGTGTTCCAGTGCATGATGATTTTATCATCCACAGGGGCGAGTCGG 7059
QY 7261 CCCTCGGGGAGGCTTGGCCACCTTGGTGGGCTCCTGTGGCCCTCCCTCCCTCCCT 7320
Db CCCTCGGGGAGGCTTGGCCACCTTGGTGGGCTCCTGTGGCCCTCCCTCCCTCCCT 7119
QY 7321 CCCTCTTTTACTCTAGACGAGCAATAAAGCCCTGTGCTTGAGTGTAGTACCGC 7376
Db CCCTCTTTTACTCTAGACGAGCAATAAAGCCCTGTGCTTGAGTGTAGTACCGC 7175

RESULT 13
AA71704
ID AAA71704 standard; DNA; 7175 BP.
AC AAA71704;
DT 22-DEC-2000 (first entry)
DE Human calcium channel alpha1B-2 subunit encoding DNA.
EX Human; calcium channel; calcium channel subunit; diagnosis;
KW Lambert Eaton Syndrome; calcium channel subunit alpha1B-2; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 144..6857
FT CDS /*tag= a
FT /*product= "calcium channel alpha1B-2 subunit"
XX
PN US096514-A.
XX 01-AUG-2000.
XX 25-MAY-1995; 95US-00450562.
XX 04-APR-1988; 88US-00176899.
XX 02-FEB-1990; 90US-00482384.
XX 08-NOV-1990; 90US-00603751.
XX 30-NOV-1990; 90US-00620250.
XX 15-AUG-1991; 91US-00745206.
XX 10-APR-1992; 92US-00868354.
XX 13-JUL-1992; 92US-00914231.
XX 11-AUG-1993; 93US-00105536.
XX 05-NOV-1993; 93US-00149097.
XX 07-FEB-1994; 94US-00193078.
XX 04-APR-1994; 94US-00223305.
XX 15-AUG-1994; 94US-00290012.
XX 23-SEP-1994; 94US-00311363.
XX 28-SEP-1994; 94US-00314083.
XX 07-NOV-1994; 94US-00336257.
XX 13-MAR-1995; 95US-00404950.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
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XX Ellis SB, Williams ME, Mccue AP, Harpold MM;
PI WPI; 2000-548230/50.
XX P-PSDB; AAB10573.
XX Human calcium channel beta subunit polynucleotides, useful for producing
XX recombinant eukaryotic cells and for diagnosing Lambert Eaton Syndrome.
XX Example II; Col 113-128; 153pp; English.
XX This invention describes a novel isolated DNA molecule (I) comprising a
XX sequence encoding a beta3-1 subunit of a human calcium channel. Nucleic
XX acid probes comprising 14-30 contiguous nucleotides of beta 3 subunit
XX encoding DNA are useful for isolation and cloning of calcium channel
XX subunit-encoding DNA. Recombinant eukaryotic cells that express
XX heterologous calcium channel are useful for identifying compounds that
XX modulate calcium channel activity and in assays for identifying agonists
XX and antagonists of calcium channel activity in humans. Human calcium
XX channel subunit or eukaryotic cells expressing the channel are useful for
XX diagnosing Lambert Eaton Syndrome (LES) in a human. This sequence encodes
XX the human calcium channel alpha1B-2 subunit which is described in the
XX method of the invention
XX Sequence 7175 BP; 1415 A; 2197 C; 2168 G; 1395 T; 0 U; 0 Other;
XX Query Match 94.0%; Score 6932.4; DB 3; Length 7175;
XX Best Local Similarity 97.3%; Pred. No. 0;
XX Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;
QY 1 GCGGCGCGGCTGCGGCGGTGGGCGGAGGTCCGCTGCGGTCCCGGCGGCTCGGTG 60
Db 1 GCGGCGGCGGCTGCGGCGGTGGGCGGAGGTCCG-TGCGGTCCCGGCGGCTCGGTG 59
QY 61 GCTGCTCCGCTCTGAGCGCTTGGCGGCCCGCGCCCTCCCTCCCGGGGCGTGGGCGG 120
Db 60 GCTGCTCCGCTCTGAGCGCTT-GCGGCGGCCCGCGCCCTCCCTCCCGGGGCGTGGGCGG 118
QY 121 GGGATGCACGCGGGGCGCGGAGCCATGTCGCTTCCGGGAGAGTGGTGGCGCGCTA 180
Db 119 GGGATGCACGCGGGGCGCGGAGCCATGTCGCTTCCGGGAGAGTGGTGGCGCGCTA 178
QY 181 TGGAGGCGCGCGGCGGAGAGCGGCGCGCGGCGCGGCGCGGCGGCGGCGGCGGCGG 240
Db 179 TGGAGGCGCGCGGCGGAGAGCGGCGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGG 238
QY 241 GGGTCCCGGGGCGCTGAGCGCCCGCGCGAGCGGTCTCTCAAGCAATCGATCCGCGAGCG 300
Db 239 GGGTCCCGGGGCGCTGAGCGCCCGCGCGAGCGGTCTCTCAAGCAATCGATCCGCGAGCG 298
QY 301 CGCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTACCGCTCA 360
Db 299 CGCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTACCGCTCA 358
QY 361 CGCTCGCTTTCGTTTTCAGCGAGGACAAACGCTCGTCCGCAATACGCGANGCGCATCAC 420
Db 359 CGCTCGCTTTCGTTTTCAGCGAGGACAAACGCTCGTCCGCAATACGCGANGCGCATCAC 418
QY 421 CGAGTGGCTTCCATTCGAGTATATGATCTCTGGCCACCATCTGCCAACTGATCTGTGT 480
Db 419 CGAGTGGCTTCCATTCGAGTATATGATCTCTGGCCACCATCTGCCAACTGATCTGTGT 478
QY 481 GGCCCTGGAGCAGCAGCTCCCTGATGGGGAACAAACGCGCCATGTCGAGCGCTGGAGCGA 540
Db 479 GGCCCTGGAGCAGCAGCTCCCTGATGGGGAACAAACGCGCCATGTCGAGCGCTGGAGCGA 538
QY 541 CACGAGGCCCTATTTCATCGGATCTTTTGTCTTCGAGGCGAGGATCAAAATCATCGCTCT 600
Db 539 CACGAGGCCCTATTTCATCGGATCTTTTGTCTTCGAGGCGAGGATCAAAATCATCGCTCT 598
QY 601 GGGCTTTGTCTTCCAAAGGGGCTTACCTCGGGAACGCGCTGGAACGTCAAGACTTCGT 660
Db 599 GGGCTTTGTCTTCCAAAGGGGCTTACCTCGGGAACGCGCTGGAACGTCAAGACTTCGT 658
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Qy 661 GGTGTCCTCACAAGGATCCTTGGCCACGCGCTGGAACTGACTTCCAACTTGCAGCACTTGAG 720
Db 659 GGTGTCCTCACAAGGATCCTTGGCCACGCGCTGGAACTGACTTCCAACTTGCAGCACTTGAG 718
Qy 721 GGTGTCGCTGCTGAGGCGCCCTGAAGCTGGTCTCTGGGATTCGAAGTTTGCAGGTGGT 780
Db 719 GGTGTCGCTGCTGAGGCGCCCTGAAGCTGGTCTCTGGGATTCGAAGTTTGCAGGTGGT 778
Qy 781 GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCCTGCAGATTTGGGCTCTCTTCTTCTT 840
Db 779 GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCCTGCAGATTTGGGCTCTCTTCTTCTT 838
Qy 841 TGCATCCTCATGTTTGCATCATTTGGCTGTGAGTCTTACATGGGCAAGTTTCCAAAGGC 900
Db 839 TGCATCCTCATGTTTGCATCATTTGGCTGTGAGTCTTACATGGGCAAGTTTCCAAAGGC 898
Qy 901 CTGTTTTCCCAACAGCAGATGCGGAGCCCGTGGGTGACTTCCCTGTGCGAAGGAGGC 960
Db 899 CTGTTTTCCCAACAGCAGATGCGGAGCCCGTGGGTGACTTCCCTGTGCGAAGGAGGC 958
Qy 961 CCCAGCCGGCTGTGCGAGGCGCACACTGAGTGCGGGAGTACTGGCCAGGACCCAACTT 1020
Db 959 CCCAGCCGGCTGTGCGAGGCGCACACTGAGTGCGGGAGTACTGGCCAGGACCCAACTT 1018
Qy 1021 TGGCATCAACCAACTTTGACAAATATCCTGTTTGGCCATCTTGACGGTGTTCAGTGCATCAC 1080
Db 1019 TGGCATCAACCAACTTTGACAAATATCCTGTTTGGCCATCTTGACGGTGTTCAGTGCATCAC 1078
Qy 1081 CANTGGGCTGGACTGCATCCTCTATATACAAACGATGCGGCGGCAACCTTGAA 1140
Db 1079 CATGGAGGCTGGACTGACATCCTCTATAATACAAACGATGCGGCGGCAACCTTGAA 1138
Qy 1141 CTGGCTCTACTTCTATCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGCT 1200
Db 1139 CTGGCTCTACTTCTATCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTGCT 1198
Qy 1201 GGGCGTCTCTCGGGGAGTTTGCAGAGCGAGAGAGGTTGAGAAACCGCCGCGCTT 1260
Db 1199 GGGCGTCTCTCGGGGAGTTTGCAGAGCGAGAGAGGTTGAGAAACCGCCGCGCTT 1258
Qy 1261 CCTGAAGCTGCGCGGAGAGAGAGATCGAGGAGAGCTCAACGGGTACCTGGAGTGGAT 1320
Db 1259 CCTGAAGCTGCGCGGAGAGAGAGATCGAGGAGAGCTCAACGGGTACCTGGAGTGGAT 1318
Qy 1321 CTTCAAGCGGAGGAAGTCACTGTGCGCGAGAGGACAGGAATGCAGAGAGAGTCCCC 1380
Db 1319 CTTCAAGCGGAGGAAGTCACTGTGCGCGAGAGGACAGGAATGCAGAGAGAGTCCCC 1378
Qy 1381 TTTGGACGTGTGAAGAGAGCGGCCACCAAGAGAGAGAAATGACCTGATCCACGCAGA 1440
Db 1379 TTTGGACGTGTGAAGAGAGCGGCCACCAAGAGAGAGAAATGACCTGATCCACGCAGA 1438
Qy 1441 GGAGGAGAGAGACGGTTTCAGATCTCTGTGCTGTGGATCCCTTCCCGCGCGCAG 1500
Db 1439 GGAGGAGAGAGACGGTTTCAGATCTCTGTGCTGTGGATCCCTTCCCGCGCGCAG 1498
Qy 1501 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCTATCTTCCGAGGAAGAGAGATGTTCCG 1560
Db 1499 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCTATCTTCCGAGGAAGAGAGATGTTCCG 1558
Qy 1561 GTTTTTTATCCGGCGCATGTGTAAGGCTCAGAGCTTCTACTGGGTGTGCTGTGCGTGGT 1620
Db 1559 GTTTTTTATCCGGCGCATGTGTAAGGCTCAGAGCTTCTACTGGGTGTGCTGTGCGTGGT 1618
Qy 1621 GGCCCTGAACACACTGTGTGTGGCCATGTGTCATTACAAACAGCCGCGGCTTACCAC 1680
Db 1619 GGCCCTGAACACACTGTGTGTGGCCATGTGTCATTACAAACAGCCGCGGCTTACCAC 1678
Qy 1681 GACCCTGTATTTCAGAGTTTGTGTTTCCCTGGGTCTCTTCTCACAGAGATGTCCTGAA 1740
Db 1679 GACCCTGTATTTCAGAGTTTGTGTTTCCCTGGGTCTCTTCTCACAGAGATGTCCTGAA 1738

Qy 1741 GATGTATGGCTGGGCGCCAGAAAGCTACTTCCGGTCTCTCTTCAAATGCTTGCATTTGG 1800
Db 1739 GATGTATGGCTGGGCGCCAGAAAGCTACTTCCGGTCTCTCTTCAAATGCTTGCATTTGG 1798
Qy 1801 GGTCAATCGTGGGAGAGGTCTTTGAAGTGGTCTGGGCGCCATCAAGCCGGGAAGCTCCTT 1860
Db 1799 GGTCAATCGTGGGAGAGGTCTTTGAAGTGGTCTGGGCGCCATCAAGCCGGGAAGCTCCTT 1858
Qy 1861 TGGGATCAAGTGTCTGGGCGCCCTCCGCTGTCTGAGGATCTTCAAAGTCAAGATGACTG 1920
Db 1859 TGGGATCAAGTGTCTGGGCGCCCTCCGCTGTCTGAGGATCTTCAAAGTCAAGATGACTG 1918
Qy 1921 GAGTCCCTCGCGAAACCTGCTGTGCTCCCTGCTGAACCTCATGAATCCATCATCAGCCT 1980
Db 1919 GAGTCCCTCGCGAAACCTGCTGTGCTCCCTGCTGAACCTCATGAATCCATCATCAGCCT 1978
Qy 1981 GCTCTTCTGCTCTTCTCTGTTCAATTTGGTCTTTCGCCCTGCTGGGGATGAGCTGTTGG 2040
Db 1979 GCTCTTCTGCTCTTCTCTGTTCAATTTGGTCTTTCGCCCTGCTGGGGATGAGCTGTTGG 2038
Qy 2041 GGGACAGTTCAACTTCCAGGATGAGATCCCAACAACAACTTCGACACCTTCCCTGCGCG 2100
Db 2039 GGGACAGTTCAACTTCCAGGATGAGATCCCAACAACAACTTCGACACCTTCCCTGCGCG 2098
Qy 2101 CATCTCTCATGTCTTCCAGATCCTGACGGGAGAGGACTGGAATGCAGTGTATCAGG 2160
Db 2099 CATCTCTCATGTCTTCCAGATCCTGACGGGAGAGGACTGGAATGCAGTGTATCAGG 2158
Qy 2161 GATCGAATCCAAAGCGGCTCAGCAAGAGCATGTTCTCGTCTCTTTTACTTTCATTTGCT 2220
Db 2159 GATCGAATCCAAAGCGGCTCAGCAAGAGCATGTTCTCGTCTCTTTTACTTTCATTTGCT 2218
Qy 2221 GACACTGTTTCGGAAACTTACACTCTGCTGTAATGTTCTTTCTGGCCATCGCTGTGACAACT 2280
Db 2219 GACACTGTTTCGGAAACTTACACTCTGCTGTAATGTTCTTTCTGGCCATCGCTGTGACAACT 2278
Qy 2281 GGCACACGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGACGACGCCAATCAGAA 2340
Db 2279 GGCACACGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGACGACGCCAATCAGAA 2338
Qy 2341 GTTTGCTCTCAAAAAGCCAAAGAGTGGCTGAAGTCAGCCCATGCTCTCCCGCAACAT 2400
Db 2339 GCTTGTCTCTCAAAAAGCCCAAGAGTGGCTGAAGTCAGCCCATGCTCTCCCGCAACAT 2398
Qy 2401 CTCATCTCGCCGCGCAGCAGCAGAACTCGGCCAAGGCGCTCGGTGTGGAGCAGCGGGC 2460
Db 2399 CTCATCTCGCCGCGCAGCAGCAGAACTCGGCCAAGGCGCTCGGTGTGGAGCAGCGGGC 2458
Qy 2461 CAGCGAGCTACGGCTGAGAAACCTGCGGGCCAGCTGGAGGCGCTGTACAGCAGATGGA 2520
Db 2459 CAGCGAGCTACGGCTGAGAAACCTGCGGGCCAGCTGGAGGCGCTGTACAGCAGATGGA 2518
Qy 2521 CCCGAGGAGCGGCTCGGCTTCCCACTACGCCCACTTCCGCCCGCACATGAAGAGCA 2580
Db 2519 CCCGAGGAGCGGCTCGGCTTCCCACTACGCCCACTTCCGCCCGCACATGAAGAGCA 2578
Qy 2581 CTTGGACCGGCCCTGTTGGTGGAGCTGGGCCCGCAGCGCGCGGGGGCCCGTGGGAGG 2640
Db 2579 CTTGGACCGGCCCTGTTGGTGGAGCTGGGCCCGCAGCGCGCGGGGGCCCGTGGGAGG 2638
Qy 2641 CAAAGCCGACCTTGAAGCTGCGGAGCGCCCGAGGGGCTGACCCCTCGCGCAGGACCA 2700
Db 2639 CAAAGCCGACCTTGAAGCTGCGGAGCGCCCGAGGGGCTGACCCCTCGCGCAGGACCA 2698
Qy 2701 CCGGCACCGCGACAAGGACAAAGACCCCGCGGGGGACCCAGGACCGGAGGCGCC 2760
Db 2699 CCGGCACCGCGACAAGGACAAAGACCCCGCGGGGGACCCAGGACCGGAGGCGCC 2758
Qy 2761 GAAAGCGGAGAGCGGGAGCCCGTGTCCGGGAGGAGCGGCGCGCGCACCGCACGCA 2820
Db 2759 GAAGGCGGAGAGCGGGAGCCCGTGTCCCGGAGGAGCGGCGCGCGCACCGCACGCA 2818
Qy 2821 CAGCAAGGAGGCGCGGGGCGCCCGGAGGCGCGGAGCGGCGGCGGCGGCGGCGCC 2880

Db ||||| CAGCAAGAGGCGCGGGCCCCCGAGAGCGCGGCGAGGCCAGGCC 2878
QY CGAGGGCGCGCGGCGCACACCGCGCGGCTCCCGAGAGAGCGCGCGAGCGCC 2940
Db CGAGGGCGCGCGGCGCACACCGCGCGGCTCCCGAGAGAGCGCGCGAGCGCC 2938
QY CCGACGCGCACCGGCGCACCGGCGCACAGGATCCAGCAAGGAGTGGCGCGGCGCAAGGG 3000
Db CCGACGCGCACCGGCGCACCGGCGCACAGATCCAGCAAGGAGTGGCGCGGCGCAAGGG 2998
QY CGAGCGCGCGCGGCGCACCGGCGCGCCCCCGAGCGGGCCCCCGAGCGAGCGG 3060
Db CGAGCGCGCGCGGCGCACCGGCGCGCCCCCGAGCGGGCCCCCGAGCGAGCGG 3058
QY GGAGGAGCGCGCGGCGCACCGGCGCGCCCCCGAGCGGGCCCCCGAGCGAGCGG 3120
Db GGAGGAGCGCGCGGCGCACCGGCGCGCCCCCGAGCGGGCCCCCGAGCGAGCGGCTGT 3118
QY GGAGAGGAGACACACGAGAGAGAGGCCACGGAGAGAGGCTGAGATAGTGGAGCGGA 3180
Db GGAGAGGAGACACACGAGAGAGAGGCCACGGAGAGAGGCTGAGATAGTGGAGCGGA 3178
QY CAAGGAAAGGAGCTCGGAAACACAGCGCGCGGAGCCACACTGTGACCTGGAGACCAG 3240
Db CAAGGAAAGGAGCTCGGAAACACAGCGCGCGGAGCCACACTGTGACCTGGAGACCAG 3238
QY TGGGACTGTGACTGTGGGTCCCATGCACACACTGCCAGCACTGTCTCCAGAAAGGTGA 3300
Db TGGGACTGTGACTGTGGGTCCCATGCACACACTGCCAGCACTGTCTCCAGAAAGGTGA 3298
QY GGAAAGCGAGAGGATGCAGAACTCAGCGGAAACGTCACTCGCATGGGCGAGTCAGCCCC 3360
Db GGAAAGCGAGAGGATGCAGAACTCAGCGGAAACGTCACTCGCATGGGCGAGTCAGCCCC 3358
QY AGACCCGAACACTATGTGACATATCCAGTATGCTGAGCGGCCCTCTTGGGAAAGCCAC 3420
Db AGACCCGAACACTATGTGACATATCCAGTATGCTGAGCGGCCCTCTTGGGAAAGCCAC 3418
QY GGTCTGTCCTCAGTGTGTAACGTGGACTGGAAAGCCAAAGCAGAGGGGAAAGAGGTTGA 3480
Db GGTCTGTCCTCAGTGTGTAACGTGGACTGGAAAGCCAAAGCAGAGGGGAAAGAGGTTGA 3478
QY ACGGATGAGCTGATGAGAGGCGGCGCGGCTATCGTCCATACAGCTCCATGTTCTG 3540
Db ACGGATGAGCTGATGAGAGGCGGCGCGGCTATCGTCCATACAGCTCCATGTTCTG 3538
QY TTTAAGCCCGACCAACCTGCTCCGCGCTTTCGCCACTACATCGTACCATGAGGTACTT 3600
Db TTTAAGCCCGACCAACCTGCTCCGCGCTTTCGCCACTACATCGTACCATGAGGTACTT 3598
QY CGAGTGTGTCATTCTGTTGTCATCGCTTGAGCAGCATCGCCCTGCTGAGGACCC 3660
Db CGAGTGTGTCATTCTGTTGTCATCGCTTGAGCAGCATCGCCCTGCTGAGGACCC 3658
QY AGTGGCGCAGACTCGCCAGGAAACACGCTCTGAAATACCTGATATCACTTTCACTGG 3720
Db AGTGGCGCAGACTCGCCAGGAAACACGCTCTGAAATACCTGATATCACTTTCACTGG 3718
QY TGTCTTTTACCTTTGAGATGGTGATAAAGATGATCGACTTGGGACTGTGCTTCAACCTGG 3780
Db TGTCTTTTACCTTTGAGATGGTGATAAAGATGATCGACTTGGGACTGTGCTTCAACCTGG 3778
QY AGCTATTTCCGGGACTTGTGGAAACATTTCTGGAATTTGATGTGAGTGGCGCCCTGGT 3840
Db AGCTATTTCCGGGACTTGTGGAAACATTTCTGGAATTTGATGTGAGTGGCGCCCTGGT 3838
QY GCGCTTTCTTCGAGCTTCGTGGGAGATCCAAAGGGAAGACATCAATACATCAA 3900
Db GCGCTTTCTTCGAGCTTCGTGGGAGATCCAAAGGGAAGACATCAATACATCAA 3886
QY GTCTCTGAGAGTCCTTCGTGCTCGCGGCCCTCAAGACCATCAACCGGCTGCCCAAGCT 3960

Db 3887 GTCTCTGAGAGTCCTTCGTGCTCGCGGCCCTCAAGACCATCAAAACGGCTGCCCCAAGCT 3946
QY CAAGCTCTGTTTGACTGTGTGGTGAACTCCCTGAAGAAATGTCTCTCAACATCTTTGATGT 4020
Db CAAGCTCTGTTTGACTGTGTGGTGAACTCCCTGAAGAAATGTCTCTCAACATCTTTGATGT 4006
QY CTACATGCTCTTCATGTTTCATATTTGGCGTCATTTGGCGTGAGCTCTTCAAGAGGAAGTT 4080
Db CTACATGCTCTTCATGTTTCATATTTGGCGTCATTTGGCGTGAGCTCTTCAAGAGGAAGTT 4066
QY TTTTCTACTGCACAGATCAATCCAAAGGAGCTGAGAGGAGCTGCAGGGTCAAGTATTTGGA 4140
Db TTTTCTACTGCACAGATCAATCCAAAGGAGCTGAGAGGAGCTGCAGGGGTCAAGTATTTGGA 4126
QY TTATGAGAGAGAGAGTGGAAAGCTCAGGCCAGGCACTGGAAGAAATAACACTTTTCACTA 4200
Db TTATGAGAGAGAGAGTGGAAAGCTCAGGCCAGGCACTGGAAGAAATAACACTTTTCACTA 4186
QY CGACAATGTCTCTGGGCTCTGTGACGCTGTTTCAAGTGTCCACGGAGAGAGCTGGCC 4260
Db CGACAATGTCTCTGGGCTCTGTGACGCTGTTTCAAGTGTCCACGGAGAGAGCTGGCC 4246
QY CATGGTCTGAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCTTGGGTA 4320
Db CATGGTCTGAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAAGCTTGGGTA 4306
QY CCGCATCGAGCTGTCCATCTTCTACGTGTCTACTTTGTGGTCTTTCCCTCTCTTCTCGT 4380
Db CCGCATCGAGCTGTCCATCTTCTACGTGTCTACTTTGTGGTCTTTCCCTCTCTTCTCGT 4366
QY CAACATCTTTGTGGCTTTGATCATCATCTTCCAGAGCAGGGGACAGGTGATGTC 4440
Db CAACATCTTTGTGGCTTTGATCATCATCTTCCAGAGCAGGGGACAGGTGATGTC 4426
QY TGAATGAGCCTCGAGAGAAACGAGAGGCTTGCACTTGCCCATCAAGCGCCAAAC 4500
Db TGAATGAGCCTCGAGAGAAACGAGAGGCTTGCACTTGCCCATCAAGCGCCAAAC 4486
QY CCTGACACGCTACATGCCCCAAACCGGCACTGTTCCAGTATAGACGTGAGCATTTGT 4560
Db CCTGACACGCTACATGCCCCAAACCGGCACTGTTCCAGTATAGACGTGAGCATTTGT 4546
QY GGTCTCCCGCCCTTTGAATACCTTCATCATGGCCATGATAGCCCTCAACATCTGTGTGT 4620
Db GGTCTCCCGCCCTTTGAATACCTTCATCATGGCCATGATAGCCCTCAACATCTGTGTGT 4606
QY GATGATGAAGTCTTATGATGACCCCTATGAGTACGAGCTGATGCTGAAATGCTGAACAT 4680
Db GATGATGAAGTCTTATGATGACCCCTATGAGTACGAGCTGATGCTGAAATGCTGAACAT 4666
QY CGTGTTCACATCCATGTTCTTCATGGAATGCGTGTGAAGATCATCGCTTTGGGGTGT 4740
Db CGTGTTCACATCCATGTTCTTCATGGAATGCGTGTGAAGATCATCGCTTTGGGGTGT 4726
QY GAACTATTTCAAGAGTGCCTGGAAATCTTTGACTTTGTCACCTGTGGGAAAGTATTAC 4800
Db GAACTATTTCAAGAGTGCCTGGAAATCTTTGACTTTGTCACCTGTGGGAAAGTATTAC 4786
QY TGAATATTTTAGTAAACAGAGTTCGGGAAACGAACATTTTCATCACTTCCTCCCG 4860
Db TGAATATTTTAGTAAACAGAGTTCGGGAAACGAACATTTTCATCACTTCCTCCCG 4846
QY CCTCTTTCGAGCTGCGCGGCTGATCAAGCTGTCCGCGAGGCTACACCAVCCGATCCT 4920
Db CCTCTTTCGAGCTGCGCGGCTGATCAAGCTGTCCGCGAGGCTACACCAVCCGATCCT 4906
QY GCTGTGGAACCTTTGTCAGTCTTCAAGGCCCTGCCCCACGTGTCTCAATGCCAT 4980
Db GCTGTGGAACCTTTGTCAGTCTTCAAGGCCCTGCCCCACGTGTCTCAATGCCAT 4966
QY GCTGTTCCTTCATCTACGCCATCATCGGATGAGGTGTTTGGGAATATTCCTCGATGA 5040
Db GCTGTTCCTTCATCTACGCCATCATCGGATGAGGTGTTTGGGAATATTCCTCGATGA 5026

Db	7000	CTGCATGCAGCAGGCGTGTGTCCAGTGGATGAGTTTATCATCCACAGCGGCAGTCGG	7059
Qy	7261	CCCTCGGGGGAGGCCCTTCCCCACCTTCGGTCAGAGCTCTGTGCGCCCTCCCTCCGCCCTCT	7320
Db	7060	CCCTCGGGGGAGGCCCTTGCCACCTTGGTCAGAGCTCTGTGCGCCCTCCCTCCGCCCTCT	7119
Qy	7321	CCGCTCTTTTACTCTAGACGACGAAAGACCCCTGTGCTTGAGTGTACGTACCGC	7376
Db	7120	CCGCTCTTTTACTCTAGACGACGAAAGACCCCTGTGCTTGAGTGTACGTACCGC	7175

RESULT 14	
AAD39956	
ID	AAD39956 standard; DNA; 7175 BP.
XX	
XX	AAD39956;
XX	
XX	
DT	22-OCT-2002 (first entry)
XX	
DE	Human calcium channel alpha 1B-2 protein encoding DNA.
XX	
XX	Human; calcium channel protein; therapeutic; autoimmune disease;
KW	diagnosis; Lambert Eaton Syndrome; alpha 1B-2 protein; splice variant;
KW	gene. GS.

CC polynucleotides encoding such proteins. The invention also relates to
CC eukaryotic cells expressing a functional heterologous human calcium
CC channel alpha 1, alpha 2, beta and gamma subunits. The eukaryotic cells
CC are useful for screening for potential calcium channel antagonists or
CC agonists to select compounds that have potential as disease or tissue-
CC specific therapeutic agents. The subunits may be used in diagnostic
CC assays for the autoimmune disease Lambert Eaton Syndrome. The present
CC sequence is a DNA encoding human calcium channel alpha 1B subunit splice
CC variant, alpha 1B-2 protein
XX Sequence 7175 BP: 1415 A: 2197 C: 2168 G: 1395 T: A. H. A. October

|||||
Db 839 TGCCATCCTCATGTTTGGCCATCATTTGGCTTGGAGTTCTACATGGCAAGTTCCACAAGGC 898
Qy 901 CTGTTTCCCAACAGACAGATGCGAGCCCGTGGTGACTTCCCTGTGGCAAGAGGC 960
Db 899 CTGTTTCCCAACAGACAGATGCGAGCCCGTGGTGACTTCCCTGTGGCAAGAGGC 958
Qy 961 CCCAGCCGGCTGTGCGAGGCGGACACTGAGTGC CGGAGTACTTGGCCAGGACCCAACTT 1020
Db 959 CCCAGCCGGCTGTGCGAGGCGGACACTGAGTGC CGGAGTACTTGGCCAGGACCCAACTT 1018
Qy 1021 TGGCATCACCAACTTTGACATATCCTGTTTGGCATCTTGACGTTGTTCCAGTGCATCAC 1080
Db 1019 TGGCATCACCAACTTTGACAAATCCTGTTTGGCATCTTGACGTTGTTCCAGTGCATCAC 1078
Qy 1081 CATGGAGGGCTGGACTGACATCCTCTATATAAACAAGATGCGGCCGGCAACACTCGAA 1140
Db 1079 CATGGAGGGCTGGACTGACATCCTCTATATAAACAAGATGCGGCCGGCAACACTCGAA 1138
Qy 1141 CTGGCTCTACTTCACTCCCTCTCATCATCATCGGCTCCTTTATGCTCAACTGTTGCT 1200
Db 1139 CTGGCTCTACTTCACTCCCTCTCATCATCATCGGCTCCTTTATGCTCAACTGTTGCT 1198
Qy 1201 GGGCGTCTCTCGGGGAGTTTGCAGAGGCGAGAGGGTGAGAACCGCGCGCTT 1260
Db 1199 GGGCGTCTCTCGGGGAGTTTGCAGAGGCGAGAGGGTGAGAACCGCGCGCTT 1258
Qy 1261 CCTGAAGCTGCGCGGAGCAGCAGATCGAGCGAGAGCTCAACGGGTACCTTGAAGTGGAT 1320
Db 1259 CCTGAAGCTGCGCGGAGCAGCAGATCGAGCGAGAGCTCAACGGGTACCTTGAAGTGGAT 1318
Qy 1321 CTTCAAGCGGAGGAATGCTATGTGCGGAGGAGGACAGGAATGCAGAGGAGAAGTCCCC 1380
Db 1319 CTTCAAGCGGAGGAATGCTATGTGCGGAGGAGGACAGGAATGCAGAGGAGAAGTCCCC 1378
Qy 1381 TTTTGGAGTCTGAAGAGAGCGGCCACCAAGAGAGCAGAATGACCTGATCCACGCAGA 1440
Db 1379 TTTTGGAGTCTGAAGAGAGCGGCCACCAAGAGAGCAGAATGACCTGATCCACGCAGA 1438
Qy 1441 GGAGGAGAGGACCGGTTTGAGATCTCTGTGCTGTTGGATGCCCTTTCGCGCGCGCAG 1500
Db 1439 GGAGGAGAGGACCGGTTTGAGATCTCTGTGCTGTTGGATGCCCTTTCGCGCGCGCAG 1498
Qy 1501 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCACTTCCGAGGGAAGAGAGATGTTCCG 1560
Db 1499 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCACTTCCGAGGGAAGAGAGATGTTCCG 1558
Qy 1561 GTTTTTTATCCGGCGCATGTTGAAGGCTCAGAGCTTCTACTGGGTGTTGCTGCGTGGT 1620
Db 1559 GTTTTTTATCCGGCGCATGTTGAAGGCTCAGAGCTTCTACTGGGTGTTGCTGCGTGGT 1618
Qy 1621 GGCCCTGAACACACTGTGTGGCCATGTTGTCATTACAAACAGCGCGCGGCTTACCAC 1680
Db 1619 GGCCCTGAACACACTGTGTGGCCATGTTGTCATTACAAACAGCGCGCGGCTTACCAC 1678
Qy 1681 GACCTGTATTTTGCAGAGTTGTTTTCCTGGTCTCTTCTCAAGAGATGTTCCCTGAA 1740
Db 1679 GACCTGTATTTTGCAGAGTTGTTTTCCTGGTCTCTTCTCAAGAGATGTTCCCTGAA 1738
Qy 1741 GATGTATGGCTGGGCGCCAGAGCTACTTCCGTCCTCTTCAACTGCTTCGACTTTGG 1800
Db 1739 GATGTATGGCTGGGCGCCAGAGCTACTTCCGTCCTCTTCAACTGCTTCGACTTTGG 1798
Qy 1801 GGTCACTGTGGGAGCGTCTTTGAAGTGGTCTGGGCGGCATCAAGCGCGGAAGCTCCTT 1860
Db 1799 GGTCACTGTGGGAGCGTCTTTGAAGTGGTCTGGGCGGCATCAAGCGCGGAAGCTCCTT 1858
Qy 1861 TGGGATCAGTGTGTCGGGCGCTCCGCTGCTGAGGATCTTCAAGTACAGAGTACTG 1920
Db 1859 TGGGATCAGTGTGTCGGGCGCTCCGCTGCTGAGGATCTTCAAGTACAGAGTACTG 1918
Qy 1921 GAGCTCCCTGGGAACCTGTGTGTGCTCCCTGCTGAACTCAGTGAAGTCCATCATCAGCCT 1980
|||||

Db 1919 GAGCTCCCTGCGGAACCTGTGTGTGCTCCCTGTGAACTCCATGAAGTCCATCATCAGCCT 1978
Qy 1981 GCTCTTTCTTGTCTCTTCTGTTCATTTGTGTGCTTCGCCCTGCTGGGGATGAGCTGTTTG 2040
Db 1979 GCTCTTTCTTGTCTCTTCTGTTCATTTGTGTGCTTCGCCCTGCTGGGGATGAGCTGTTTG 2038
Qy 2041 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTCCACACCTTCCCTGCGGC 2100
Db 2039 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCAACTTCCACACCTTCCCTGCGGC 2098
Qy 2101 CATCTCTACCTGTCTCCAGATCTGACGGGAGGAGTGGAAATGCAGTGTATCACGG 2160
Db 2099 CATCTCTACCTGTCTCCAGATCTGACGGGAGGAGTGGAAATGCAGTGTATCACGG 2158
Qy 2161 GATCGAATCGCAAGCGGCGTCAAGAAAGCATGTTCTCGTCTCTTTTACTTTCATTTGCT 2220
Db 2159 GATCGAATCGCAAGCGGCGTCAAGAAAGCATGTTCTCGTCTCTTTTACTTTCATTTGCT 2218
Qy 2221 GACACTGTTTCGGAACCTACACTCTGCTGTAATGTTCTTCTGGCCATCGCTGTGACAACT 2280
Db 2219 GACACTGTTTCGGAACCTACACTCTGCTGTAATGTTCTTCTGGCCATCGCTGTGACAACT 2278
Qy 2281 GGCACACGCCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAGAGAGCAGCCAAATCAGAA 2340
Db 2279 GGCACACGCCCAAGAGCTGACCAAGATGAAGAGGAGATGGAAGAGAGCAGCCAAATCAGAA 2338
Qy 2341 GCTTGTCTCTGCAAAAGGCCAAAGAGTGGCTGAAGTCAGCCCCATGTTCTGCCGCGAACAT 2400
Db 2339 GCTTGTCTCTGCAAAAGGCCCAAGAGTGGCTGAAGTCAGCCCCATGTTCTGCCGCGAACAT 2398
Qy 2401 CTCATCTGCGCCAGCAGCAGCAAACTCGGCCAAGGCGCGTCTGCTGTGAGGAGCAGCGGC 2460
Db 2399 CTCATCTGCGCCAGCAGCAGCAAACTCGGCCAAGGCGCGTCTGCTGTGAGGAGCAGCGGC 2458
Qy 2461 CAGCAGCTACGCTCGCAGAACCTCGCGGCCAGCTCGAGCGCTGTATACAGCGAGATGGA 2520
Db 2459 CAGCAGCTACGCTCGCAGAACCTCGCGGCCAGCTCGAGCGCTGTATACAGCGAGATGGA 2518
Qy 2521 CCCCGAGGAGCGCTCGCTTTCGCCACTAGCGCCACCTTCGCGCCGACATGAAGACGCA 2580
Db 2519 CCCCGAGGAGCGCTCGCTTTCGCCACTAGCGCCACCTTCGCGCCGACATGAAGACGCA 2578
Qy 2581 CTTGGAACGGCCCTGTGTGTGTGAGCTGGGCGCGGACGGCGCGCGGGGCGCTGTGGAGG 2640
Db 2579 CTTGGAACGGCCCTGTGTGTGTGAGCTGGGCGCGGACGGCGCGCGGGGCGCTGTGGAGG 2638
Qy 2641 CAAGCCGACCTGAGGCTGCGGAGCGCCCGGAGGCGTCACTTCGCGCAGGCGCACCA 2700
Db 2639 CAAGCCGACCTGAGGCTGCGGAGCGCCCGGAGGCGTCACTTCGCGCAGGCGCACCA 2698
Qy 2701 CCGGCACCGCGACAAGGACAAGACCCCGCGCGGGGACAGGACCGAGCAGAGGCGCC 2760
Db 2699 CCGGCACCGCGACAAGGACAAGACCCCGCGCGGGGACAGGACCGAGCAGAGGCGCC 2758
Qy 2761 GAAGCGGAGAGCGGGAGCGCTCGGTGCTCGGAGGAGCGGCGCGCGCGCACCGCAGC 2820
Db 2759 GAAGCGGAGAGCGGGAGCGCGGTGCTCGGAGGAGCGGCGCGCGCACCGCAGC 2818
Qy 2821 CAGCAAGGAGCGCGGGCGCCCGGAGCGCGAGCGCGCGCGAGCGCGCCAGGCGCC 2880
Db 2819 CAGCAAGGAGCGCGGGCGCCCGGAGCGCGAGCGCGCGCGAGCGCGCCAGGCGCC 2878
Qy 2881 CGAGGCGCGCGGCGCACCAACCGCGCGGCTTCCCGAGGAGGCGGCGCGCGAGCGG 2940
Db 2879 CGAGGCGCGCGGCGCACCAACCGCGCGGCTTCCCGAGGAGGCGCGCGCGAGCGG 2938
Qy 2941 CCGACCGCACCGCGCGCACCGGCAACAGGATCCGAGCAAGAGTGCCTCGCGCGCCAGGG 3000
Db 2939 CCGACCGCACCGCGCGCACCGGCAACAGGATCCGAGCAAGAGTGCCTCGCGCGCCAGGG 2998
Qy 3001 CGAGCGCGCGCGCGCACCGGCGCGCCCGCGAGCGGGCGCCCGGAGCGCGAGCGG 3060
Db 2999 CGAGCGCGCGCGCGCACCGGCGCGCCCGCGAGCGGGCGCCCGGAGCGCGAGCGG 3058

Db	5207		CGTCTCCTTCAATCTCTCTGTGCTCCTTCTTGATGTGAACCTCTTTGTGGCTGTGATCAT	5266
Qy	5281		GGACAAATTTTGGTACCTTCACGCGGAGCTCTTCCATCCTAGGTCTCTCACACATTTGGATGA	5340
Db	5267		GGACAAATTTTGGTACCTTCACGCGGAGCTCTTCCATCCTAGGTCTCTCACACATTTGGATGA	5326
Qy	5341		GTTTCATCCGGTCTGGGCTGAATACGACCCGGCTCGGTGTGGGCGCATTCAGTTTCAATGA	5400
Db	5327		GTTTCATCCGGTCTGGGCTGAATACGACCCGGCTCGGTGTGGGCGCATTCAGTTTCAATGA	5386
Qy	5401		CATGTTTGGATGCTGAAACACATGTCCTCCGCTCTGGGCTGGGGAAGAAATGCCCTGC	5460
Db	5387		CATGTTTGGATGCTGAAACACATGTCCTCCGCTCTGGGCTGGGGAAGAAATGCCCTGC	5446
Qy	5461		TCGAGTTGCTTACAAGCGCTGGTTGCGATGAACATGCCATCTCCAAACAGAGACATGCAC	5520
Db	5447		TCGAGTTGCTTACAAGCGCTGGTTGCGATGAACATGCCATCTCCAAAGGAGACATGCAC	5506
Qy	5521		TGTTCACTTCACGTCACGCTGATGGCCCTCATCCGACGGCACTGGAGATCAAGCTGGC	5580
Db	5507		TGTTCACTTCACGTCACGCTGATGGCCCTCATCCGACGGCACTGGAGATCAAGCTGGC	5566
Qy	5581		CCGAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCCGTTGT	5640
Db	5567		CCGAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCCGTTGT	5626
Qy	5641		GTGGGCCAATCTGCCCCAGAAAGACTTTTGGACTTCTGTGATCCACCCCATTAAGCCTGATGA	5700
Db	5627		GTGGGCCAATCTGCCCCAGAAAGACTTTTGGACTTCTGTGATCCACCCCATTAAGCCTGATGA	5686
Qy	5701		GATGACAGTGGGGAAGTTTATGACGCTCTGATGATATTTGACTTCTACAAGCAGAAACAA	5760
Db	5687		GATGACAGTGGGGAAGTTTATGACGCTCTGATGATATTTGACTTCTACAAGCAGAAACAA	5746
Qy	5761		AACACACAGACACAGATGACGAGGCTCTTGAGGCTCTCCAGATGGTCTCTGTGTC	5820
Db	5747		AACACACAGACACAGATGACGAGGCTCTTGAGGCTCTCCAGATGGTCTCTGTGTC	5806
Qy	5821		CCTGTTCCACCCTCTGAAGGCCACCTTGAGCAGACACAGCCGCTGTGCTCCGAGGAGC	5880
Db	5807		CCTGTTCCACCCTCTGAAGGCCACCTTGAGCAGACACAGCCGCTGTGCTCCGAGGAGC	5866
Qy	5881		CCGGTTTTCTTCGACAGAAAGTTTCACTCTCCTCAGCAATCGCGGGCCATACAAAA	5940
Db	5867		CCGGTTTTCTTCGACAGAAAGTTTCCACCTCCTCAGCAATCGCGGGCCATACAAAA	5926
Qy	5941		CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC	6000
Db	5927		CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC	5986
Qy	6001		CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTTCCACAGAGATCCTGTGGGGCGGTC	6060
Db	5987		CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTTCCACAGAGATCCTGTGGGGCGGTC	6046
Qy	6061		AGGAGCACTGGCTGTGGACGTTTCAGATGACAGATTAACCCGAGGGGCCCTGTATGGGGA	6120
Db	6047		AGGAGCACTGGCTGTGGACGTTTCAGATGACAGATTAACCCGAGGGGCCCTGTATGGGGA	6106
Qy	6121		GCCCCAGCTGGGCTGGAGACCCAGGTCGAGCGGCTCTCATGCCCGGCTTGGCGCCGA	6180
Db	6107		GCCCCAGCTGGGCTGGAGACCCAGGTCGAGCGGCTCTCATGCCCGGCTTGGCGCCGA	6166
Qy	6181		GACTCAGCCGTCACAGATGCCAGCCCATGAAGGCTTCCATCTCCAGCTGGGCCACGCG	6240
Db	6167		GACTCAGCCGTCACAGATGCCAGCCCATGAAGGCTTCCATCTCCAGCTGGGCCACGCG	6226
Qy	6241		GCCCCGTGGGACTCATCTTTGACGACCAACCCGAGACCGCCACCCCTAGCCAGGCGTC	6300
Db	6227		GCCCCGTGGGACTCATCTTTGACGACCAACCCGAGACCGCCACCCCTAGCCAGGCGTC	6286
Qy	6301		GTCCGACCAACCAACCAACCCGCTGCGCACCGCGGACGAGGAGCGAGGTCCTCTGGA	6360

RESULT 15
AAQ37818

AAQ37818 standard; cDNA; 7175 BP.
AAQ37818;
25-MAR-2003 (revised)
30-JUN-1993 (first entry)
Sequence encoding the alpha 1B-2 human calcium channel subunit.
Human calcium channel subunit; diagnosis; agonist; antagonist;
Lambert Eaton syndrome; ss.
Homo sapiens.
Key Location/Qualifiers
CDS 144..6857
/*tag= a
WO9304083-A1.
04-MAR-1993.
14-AUG-1992; 92WO-US006903.
15-AUG-1991; 91US-00745206.
10-APR-1992; 92US-00868354.
(SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
Harold MM, Ellis SB, Williams ME, Feldman DH, McCue AF;
Brenner R;
WPI; 1993-093936/11.
P-PSDB; AARJ3550.
DNA encoding specific human calcium channel sub-units - used for
identifying calcium channel agonists and antagonists and diagnosing
Lambert Eaton syndrome.
Disclosure; Page 120-128; 150pp; English.
DNA encoding the alpha 1B subunit was isolated by screening a human basal
ganglia cDNA library with fragments of the rabbit skeletal muscle calcium
channel alpha 1 subunit-encoding cDNA. A portion of one of the positive
clones was used to screen an IMR32 cell cDNA library. Clones that
hybridized to the basal ganglia DNA prove were used to further screen an
IMR32 cell cDNA library to identify overlapping clones that in turn were
used to screen a human hippocampus cDNA library. In this way, a
sufficient series of clones to span nearly the entire length of the
nucleotide sequence encoding the human alpha 1B subunit was obtained. PCR
amplification of specific regions of the IMR32 cell alpha 1B mRNA yielded
additional segments of the alpha 1B coding sequence. A full-length alpha
1B DNA clone was constructed by ligating portions of the partial cDNA
clones (see AAQ37817, AAQ37818). Alpha 1B-1 and alpha 1B-2 are derived by
alternative splicing of the alpha 1B subunit transcript. (Updated on 25-
MAR-2003 to correct PN field.)
Sequence 7175 BP; 1415 A; 2204 C; 2162 G; 1394 T; 0 U; 0 Other;
Query Match 93.7%; Score 6913.2; DB 2; Length 7175;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 7162; Conservative 13; Indels 201; Gaps 4;
QY 1 GCGGCGGCGGTGCGGCGGTGGGCGGCGAGTCCGCTCGGTTCGCGGCGGTCCGCTG 60
DB 1 GCGGCGGCGGTGCGGCGGTGGGCGGCGGCGAGTCCG-TGCGGTTCGCGGCGGTCCGCTG 59
QY 61 GCTGCTCCGCTCTGAGCCCTTGGCGCGCCCGCGCCCTCCCTGCGGCGCGCTGGGCGG 120
DB 60 GCTGCTCCGCTCTGAGCCCTTGGCGCGCCCGCGCCCTCCCTGCGGCGCGCTGGGCGG 118
QY 121 GGGATGCACGCGGCGCGGAGCGATGGTCCGCTTCGGGACAGCTGGGCGCGCGCTA 180
|||||

119 GGGATGCACGCGGCGCGGAGCCATGCTCCGCTTCGGGACAGCTGCGGCGCGCTA 178
181 TGGAGGCGCGCGGCGGAGAGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGC 240
179 TGGAGGCGCGCGGCGGAGAGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGC 238
241 GGGTCCCGGCGGCGGTGCGAGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
239 GGGTCCCGGCGGCGGTGCGAGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 298
301 CGCGCGGACCATGGCGGTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACGTC 360
299 CGCGCGGACCATGGCGGTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACGTC 358
361 CCGCTCGCTCTTTCGCTTCAGCGGAGGACAGTCTCGGCAATACCGGAGCGCATCAC 420
359 CCGCTCGCTCTTTCGCTTCAGCGGAGGACAGTCTCGGCAATACCGGAGCGCATCAC 418
421 CGAGTGGCTCCATTTCGAGTATATGATCTGGGCACCATCATCGCCAACTGCATCGTGT 480
419 CGAGTGGCTCCATTTCGAGTATATGATCTGGGCACCATCATCGCCAACTGCATCGTGT 478
481 GGCCCTCGAGAGCACCTCCCTGATGGGACAAAACGCCCATGTCGAGCGGTGAGACGA 540
479 GGCCCTCGAGAGCACCTCCCTGATGGGACAAAACGCCCATGTCGAGCGGTGAGACGA 538
541 CACGAGGCGCTATTTCATCGGATCTTTTTCGAGGCGAGGATCAAAATCATCGCTCT 600
539 CACGAGGCGCTATTTCATCGGATCTTTTTCGAGGCGAGGATCAAAATCATCGCTCT 598
601 GGGCTTTGCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 660
599 GGGCTTTGCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 658
661 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 720
659 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 718
721 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 780
719 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 778
781 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 840
779 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 838
841 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 900
839 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 898
901 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 960
899 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 958
961 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 1020
959 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 1018
1021 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 1080
1019 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 1078
1081 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 1140
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1141 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 1200
1139 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 1198
1201 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 1260
1199 GGTCTCTTCCACAAGGCGCTTACCTGCGGAACGGCTGGAAGCTCATGAGCTTCGT 1258

QY 1261 CCTGAAAGCTGCGCGGACAGCAGATCGACGAGAGCTCAACGGGTACTCTGGAGTGGAT 1320
DB 1259 CCTGAAAGCTGCGCGGACAGCAGATCGACGAGAGCTCAACGGGTACTCTGGAGTGGAT 1318
QY 1321 CTTCAAGCGGAGGAGTCACTGCTGGCGGAGGAGCAGGAAATCGAGGAGAGTCCCC 1380
DB 1319 CTTCAAGCGGAGGAGTCACTGCTGGCGGAGGAGCAGGAAATCGAGGAGAGTCCCC 1378
QY 1381 TTTTGAACGTGCTGAAGAGAGCGGCCACCAAGAAGAGCAGAAATGACCTGTATCCACGCAGA 1440
DB 1379 TTTTGAACGTGCTGAAGAGAGCGGCCACCAAGAAGAGCAGAAATGACCTGTATCCACGCAGA 1438
QY 1441 GGAAGGAGAGAACCGGTTTGAGATCTCTGTGCTGTGGATGCCCTTGGCCCGCGCAG 1500
DB 1439 GGAAGGAGAGAACCGGTTTGAGATCTCTGTGCTGTGGATGCCCTTGGCCCGCGCAG 1498
QY 1501 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCATACCTCCGGAGGAAGAGAGATGTTCCG 1560
DB 1499 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCATACCTCCGGAGGAAGAGAGATGTTCCG 1558
QY 1561 GTTTTTTATCCGGCGCATGTTGAAGGCTCAGAGCTTCTACTGGGTGCTGTGCTGCTGGT 1620
DB 1559 GTTTTTTATCCGGCGCATGTTGAAGGCTCAGAGCTTCTACTGGGTGCTGTGCTGCTGGT 1618
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QY 1741 GATGTATGGCTGGGGCCAGAACTACTTCCGGTCTCTTCAACTGCTTCGACTTTGG 1800
DB 1739 GATGTATGGCTGGGGCCAGAACTACTTCCGGTCTCTTCAACTGCTTCGACTTTGG 1798
QY 1801 GGTCACTGTGGGAGCGTCTTTGAAGTGTCTGGCGGCCATCAAGCCGGGAAGCTCCTT 1860
DB 1799 GGTCACTGTGGGAGCGTCTTTGAAGTGTCTGGCGGCCATCAAGCCGGGAAGCTCCTT 1858
QY 1861 TGGGATCAGTGTGTGGGGCCCTCCGCTGCTCAGGATCTTCAAGTCAAGAGTACTG 1920
DB 1859 TGGGATCAGTGTGTGGGGCCCTCCGCTGCTCAGGATCTTCAAGTCAAGAGTACTG 1918
QY 1921 GAGCTCCTGCGGAACCTGTGTGTCTCCTGTGAACTTCAATGAAGTCCATCATCAGCCT 1980
DB 1919 GAGCTCCTGCGGAACCTGTGTGTCTCCTGTGAACTTCAATGAAGTCCATCATCAGCCT 1978
QY 1981 GCTCTTCTGTCTTCTCTGTTTCAATGTGTCTTCCGCTGCTGGGGATGAGCTGTTTGG 2040
DB 1979 GCTCTTCTGTCTTCTCTGTTTCAATGTGTCTTCCGCTGCTGGGGATGAGCTGTTTGG 2038
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QY 2281 GGCCAAACGCCAAGAGCTGACCAAGGATGAAGAGAGATGGAAGAACGCCAATCAGAA 2340
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QY 2401 CTCATCGCCGCGCAGGAGCAGAACTCGGCCAAAGGCGCGCTCGGTGTGGAGACGCGGGC 2460
DB 2399 CTCATCGCCGCGCAGGAGCAGAACTCGGCCAAAGGCGCGCTCGGTGTGGAGACGCGGGC 2458
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DB 2819 CAGCAAGAGAGCGCGGGGCGCCCGAGGCGCGCGAGCGCGCGCGCGCGCCAGGCCCC 2878
QY 2881 CGAGGGCGCGCGCGGCAACAACCGGCGCGCTCCCGGAGGAGCGCGCGCGCGGAGGCG 2940
DB 2879 CGAGGGCGCGCGCGGCAACAACCGGCGCGCTCCCGGAGGAGCGCGCGCGCGGAGGCG 2938
QY 2941 CCAGCCACCGCGCGCACCGCGCACCGAGATCCGAGCAAGAGTGCAGAGAGTGCAGAGG 3000
DB 2939 CCAGCCACCGCGCGCACCGCGCACCGAGATCCGAGCAAGAGTGCAGAGAGTGCAGAGG 2998
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DB 2999 CGAGCGCGCGCGCGCACCGCGCGCGCCCGCGAGCGGGCGCCCGGAGGCGCGAGAGCGG 3058
QY 3061 GGAGGAGCGCGCGCGCGCACCGCGCGCGGCAAAAGCGCAGCCTGCTCACGAGGCTGT 3120
DB 3059 GGAGGAGCGCGCGCGCGCACCGCGCGCGGCAAAAGCGCAGCCTGCTCACGAGGCTGT 3118
QY 3121 GGAGAGGAGACCAACGAGAGAGGAGGCCACGAGAGAGGAGGCTGAGATAGTGAAGCGGA 3180
DB 3119 GGAGAGGAGACCAACGAGAGAGGAGGCCACGAGAGAGGAGGCTGAGATAGTGAAGCGGA 3178
QY 3181 CAAAGGAAAAGAGAGCTCCGGAAACCAACAGCCCGCGGAGCCACACTGTGACCTCGAGAGCAG 3240
DB 3179 CAAAGGAAAAGAGAGCTCCGGAAACCAACAGCCCGCGGAGCCACACTGTGACCTCGAGAGCAG 3238
QY 3241 TGGGACTGTGACTGTGGGTCCCATGACACACTGCCCAGCACTGTCTCCAGAAAGTGGGA 3300
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QY 3361 AGACCCGGAACACTATTTGTATCATATCCAGTGTGAGCGGGCCCTCTTTGGGGAAGCCAC 3420
DB 3359 AGACCCGGAACACTATTTGTATCATATCCAGTGTGAGCGGGCCCTCTTTGGGGAAGCCAC 3418
QY 3421 GGTCTTCCAGTGGTAACTGTGACCTTGGAAAGCCAAAGCAGAGGGGAAGAGGAGTGGGA 3480

Db 3419 GGTCTGTTCCAGTGGTAAAGCTGGAGCTGGAAGCCAGAGGGGAAAGAGAGGTGGA 3478
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Db 3479 AGCGGATGACGTGATGAGAGAGGGCCCCGGGCTATCGTCCCATACAGCTCCCATCTTG 3538
QY 3541 TTTAAGCCCAACCAACTGCTCGCGCGCTTCTGCCACTACATCGTGACCATGAGGTACTT 3600
Db 3539 TTTAAGCCCAACCAACTGCTCGCGCGCTTCTGCCACTACATCGTGACCATGAGGTACTT 3598
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Db 3659 AGTGGCAGAGACTCGCCCAAGAACAAACGCTCTGAAATACCTGGATTACATTTTCACTGG 3718
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GenCore version 5.1.6
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Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	7316.4	99.2	7362	2	US-08-193-078B-7
5	7316.4	99.2	7362	2	US-08-223-305C-7
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8	7316.4	99.2	7362	3	US-08-450-562-7
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ALIGNMENTS

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; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7376
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7174
US-09-268-163-3

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RESULT 2
US-09-268-163-5
; Sequence 5, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER FILING DATE: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
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; SEQ ID NO 5
; LENGTH: 7364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146...7162
US-09-268-163-5

Query Match          99.5%; Score 7342; DB 4; Length 7364;
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Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

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Db 1141 CTGGCTCTACTTCTCATCTCATCATCTGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
Qy 1201 GGGCGTCTCTCTCGGGGAGTTTCCCAAGGAGCAGAGAGGTTGGAGAACCGCGCGCTT 1260
Db 1201 GGGCGTCTCTCTCGGGGAGTTTCCCAAGGAGCAGAGAGGTTGGAGAACCGCGCGCTT 1260
Qy 1261 CCTGAAGCTGCGCGCGCAGCAGATCGAGAGAGCTCAACGGGTACTCGGAGTGGAT 1320
```

	Db	 CCTGAAGCTGCGCCGGCAGCAGATCGACGAGACTCAACGGGTACTCTGGAGTGGAT 	1261
	Qy	 CTTTAAGCGCGGAAAGTCATGCTGGCCGAGGAGACAAGGAATGCAGAGAGAAGTCCCC 	1380
	Db	 CTTTAAGCGCGGAAAGTCATGCTGGCCGAGGAGACAGGNATCGAGAGAGAAGTCCCC 	1380
	Qy	 TTTTGACGTGCTGAAGAGAGCGGCCAACAAAGAGAGAAAATGACTGATCCACGCGAGA 	1440
	Db	 TTTTGACGTGCTGAAGAGAGCGGCCAACAAAGAGAGAAAATGACTGATCCACGCGAGA 	1440
	Qy	 GGAGGAGAGCACGGTTTGACAGATCTCTGCTGTTTGGATCCCCTTCCCGCGCGCCAG 	1500
	Db	 GGAGGAGAGACCGTTTGACAGATCTCTGCTGTTTGGATCCCCTTCCCGCGCGCCAG 	1500
	Qy	 CCTCAAGAGCGGGAAGACAGAGACTCGTCTCATATCTCCGAGGAGAGAGAAGATGTTCCG 	1560
	Db	 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCTCATATCTCCGAGGAGAGAGAAGATGTTCCG 	1560
	Qy	 GTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGTGCGTGGT 	1620
	Db	 GTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTGGGTGGTGTGTGCGTGGT 	1620
	Qy	 GGCCCTGAACACTGTGTGTGGCCATGTGTGCATTACAACAGCGCGCGCGGTACCAC 	1680
	Db	 GGCCCTGAACACTGTGTGTGGCCATGTGTGCATTACAACAGCGCGCGCGGTACCAC 	1680
	Qy	 GACCTGTATTTTCAGAGTTTGTTTTCTGGGTCCTCTCTCACAGAGATGTCCTGAA 	1740
	Db	 GACCTGTATTTTCAGAGTTTGTTTTCTGGGTCCTCTCTCACAGAGATGTCCTGAA 	1740
	Qy	 GATGTATGGCCTGGGGCCAGAACTACTTCCGGTCTCTCAACTGCCTTCAGCTTTGG 	1800
	Db	 GATGTATGGCCTGGGGCCAGAACTACTTCCGGTCTCTCAACTGCCTTCAGCTTTGG 	1800
	Qy	 GGTCATCGTGGGAGCGTCTTTGAAGTGTGTCTGGGCGCCATCAAGCCGGAAAGTCCTT 	1860
	Db	 GGTCATCGTGGGAGCGTCTTTGAAGTGTGTCTGGGCGCCATCAAGCCGGAAAGTCCTT 	1860
	Qy	 TGGGATCAGTGTGCTCGGGCCCTCCGCCCTGTGAGGATCTTCAAAGTCACGAAGTACTG 	1920
	Db	 TGGGATCAGTGTGCTCGGGCCCTCCGCCCTGTGAGGATCTTCAAAGTCACGAAGTACTG 	1920
	Qy	 GAGTTCCTCGGAACTCGTGTGTCTCTGCTGAACTCCAATGAAGTCCATCATCAGCCT 	1980
	Db	 GAGTTCCTCGGAACTCGTGTGTCTCTGCTGAACTCCAATGAAGTCCATCATCAGCCT 	1980
	Qy	 GCTCTTCTGCTCTTCTGTTTCATTGTTGTCTTCCGCTTCTGGGATCGAGCTTTGG 	2040
	Db	 GCTCTTCTGCTCTTCTGTTTCATTGTTGTCTTCCGCTTCTGGGATCGAGCTTTGG 	2040
	Qy	 GGGACAGTTCAACTTCAGGATGAGACTCCCAACCAACTTCGCACACCTTCCTGCGCG 	2100
	Db	 GGGACAGTTCAACTTCAGGATGAGACTCCCAACCAACTTCGCACACCTTCCTGCGCG 	2100
	Qy	 CATCTTCATCTTCCAGATCTGACGGGAGAGGACTGGAATGCAGTGTATCACGG 	2160
	Db	 CATCTTCATCTTCCAGATCTGACGGGAGAGGACTGGAATGCAGTGTATCACGG 	2160
	Qy	 GATCGAATCGAAGCGCGCTCAGCAAGGCATGTTCTCGTCTCTTTTACTTCATTGTCT 	2220
	Db	 GATCGAATCGAAGCGCGCTCAGCAAGGCATGTTCTCGTCTCTTTTACTTCATTGTCT 	2220
	Qy	 GACACTGTTCCGAAACTACACTCTGCTGTAATGCTTTCTGGCCATCGCTGTGGACAACCT 	2280
	Db	 GACACTGTTCCGAAACTACACTCTGCTGTAATGCTTTCTGGCCATCGCTGTGGACAACCT 	2280
	Qy	 GGCCAA CGCCCAAGACTGACCAAGGATGAAGAGGAGATGGAGAGACGACCAATCAGAA 	2340
	Db	 GGCCAA CGCCCAAGACTGACCAAGGATGAAGAGGAGATGGAGAGACGACCAATCAGAA 	2340
	Qy	 GTTTGTCTGTCAAAAGGCCAAAGAGTGGCTGAAGTCAGCCCCTATGTCTGTCCGCGAACAT 	2400

Db	2341	GCTTGCTCTGCAAAAGGCCAAGAAGTGGCTGAAGTCAGCCCCATGTCTCTCCGCGAACAT	2400
Qy	2401	CTCCATCGCGCCAGGCAGCAGAACTCGGCCAAAGGCGCGCTCGGTCTGGACGACAGCGGC	2460
Db	2401	CTCCATCGCGCCAGGCAGCAGAACTCGGCCAAAGGCGCGCTCGGTCTGGACGACAGCGGC	2460
Qy	2461	CAGCCAGCTACGGTTGCGTGCAGAACCTTGGGGGCCAGCTCGAGGCGCTGTACTAGCAGATGGA	2520
Db	2461	CAGCCAGCTACGGTTGCGTGCAGAACCTTGGGGGCCAGCTCGAGGCGCTGTACTAGCAGATGGA	2520
Qy	2521	CCCAGAGAGCGGCTGCGCTTCGCCACTACGCGCCACCTGCGGCCCGCACGTAGAACGCGCA	2580
Db	2521	CCCAGAGAGCGGCTGCGCTTCGCCACTACGCGCCACCTGCGGCCCGCACGTAGAACGCGCA	2580
Qy	2581	CCTGGACC CGGCGCTGTTGTTGGAGCTGGGCCCGCGACGCGCGCGGGGGCCCGTGGGAGG	2640
Db	2581	CCTGGACC CGGCGCTGTTGTTGGAGCTGGGCCCGCGACGCGCGCGGGGGCCCGTGGGAGG	2640
Qy	2641	CAAAAGCCGACCTGAGGCTTCGGAGAGGCCCGGAGGGCGTGCACCTCCGCGAGGACCA	2700
Db	2641	CAAAAGCCGACCTGAGGCTTCGGAGAGGCCCGGAGGGCGTGCACCTCCGCGAGGACCA	2700
Qy	2701	CCGSCACCGCGCAAAAGACAAGACCCCGCGCGGGGGACCAAGGACCCAGACAGAGGCCCC	2760
Db	2701	CCGSCACCGCGCAAAAGACAAGACCCCGCGCGGGGGACCAAGGACCCAGACAGAGGCCCC	2760
Qy	2761	GAAGGCGGAGAGCGGGAGGCCCGGTCCGCGGAGGAGCGGCCCGCGCACCGCAGCCA	2820
Db	2761	GAAGGCGGAGAGCGGGAGGCCCGGTCCGCGGAGGAGCGGCCCGCGCACCGCAGCCA	2820
Qy	2821	CAGCAAGAGGCGCGCGGGGCCCGGAGCGCGGAGCGAGCGCGCGAGGCCCAAGGCC	2880
Db	2821	CAGCAAGAGGCGCGCGGGGCCCGGAGCGCGGAGCGAGCGCGCGAGGCCCAAGGCC	2880
Qy	2881	CGAAGGCGCGCGCGGACCAACCGGCGCGGCTCCCGGAGGAGCGGCCCGAGCGGGAGCC	2940
Db	2881	CGAAGGCGCGCGCGGACCAACCGGCGCGGCTCCCGGAGGAGCGGCCCGAGCGGGAGCC	2940
Qy	2941	CCGACGCCACCGCGCGCACCGGCACACAGANTCCGACGAGGAGTGGCGCGGCCCAAGGG	3000
Db	2941	CCGACGCCACCGCGCGCACCGGCACACAGANTCCGACGAGGAGTGGCGCGGCCCAAGGG	3000
Qy	3001	CGAGCGCGCGCGCGCACCGCGGGCGGCCCGCGAGCGGGGCCCGCGGAGCGGAGAGCGG	3060
Db	3001	CGAGCGCGCGCGCGCACCGCGGGCGGCCCGCGAGCGGGGCCCGCGGAGCGGAGAGCGG	3060
Qy	3061	GGAGGAGCGCGCGCGCGCACCGGGCCCGGCACAAAGCGCGACCTGTCTACGAGGCTGT	3120
Db	3061	GGAGGAGCGCGCGCGCGCACCGGGCCCGGCACAAAGCGCGACCTGTCTACGAGGCTGT	3120
Qy	3121	GGAGAGGAGGACCAACCGAGAGGAGGCGCACCGAGAGGAGGCTGAGTAGTGAAGCCGA	3180
Db	3121	GGAGAGGAGGACCAACCGAGAGGAGGCGCACCGAGAGGAGGCTGAGTAGTGAAGCCGA	3180
Qy	3181	CAGAGAAAAGAGGACTCCGAAACCAACAGCCCCCGGAGGCCACACTGTGACCTGGAGACCAG	3240
Db	3181	CAGAGAAAAGGAGCTCCGAAACCAACAGCCCCCGGAGGCCACACTGTGACCTGGAGACCAG	3240
Qy	3241	TGGACTGTGACTGTGGGTCCCATGCACACACTGCCACGACCTGTCTCCAGAGGCTGA	3300
Db	3241	TGGGACTGTGACTGTGGGTCCCATGCACACACTGCCACGACCTGTCTCCAGAGGCTGA	3300
Qy	3301	GGAAACGACAGGAGTGCAGACAAATCAGCGGAACTGCTCGACTGGGCATCTCAGCCCCC	3360
Db	3301	GGAAACGACAGGAGTGCAGACAAATCAGCGGAACTGCTCGACTGGGCATCTCAGCCCCC	3360
Qy	3361	AGACCCGACACTATTGTACATATCCAGTGNATGCTGACGGGCCCTCTTGGAGGCCAC	3420
Db	3361	AGACCCGACACTATTGTACATATCCAGTGNATGCTGACGGGCCCTCTTGGAGGCCAC	3420
Qy	3421	GGTCTGTCCAGTGGTAAACGTGGACCTGGAAAGCCCAAGCAGAGGGGGAAGAAGGAGTGA	3480
Db	3421	GGTCTGTCCAGTGGTAAACGTGGACCTGGAAAGCCCAAGCAGAGGGGGAAGAAGGAGTGA	3480

Qy	3481	AGCGGATGACGTGATGAGGAGCGGCCCGCCCTATCGTCCCATACAGCTCCATGTTCTG	3540
Db	3481	AGCGGATGACGTGATGAGGAGCGGCCCGCCCTATCGTCCCATACAGCTCCATGTTCTG	3540
Qy	3541	TTTAAAGCCCCACCAACCTGCTCCGCGCGTTCTGCCACTACATCGTGCACATGAGGTACTTT	3600
Db	3541	TTTAAAGCCCCACCAACCTGCTCCGCGCGTTCTGCCACTACATCGTGCACATGAGGTACTTT	3600
Qy	3601	CGAGGTGGTCAATCTCCGTGGTTCATCGCTTTGAGCAGCATCGCCCTGGCTGCTCAGAGACCC	3660
Db	3601	CGAGGTGGTCAATCTCCGTGGTTCATCGCTTTGAGCAGCATCGCCCTGGCTGCTCAGAGACCC	3660
Qy	3661	AGTGGGCACAGACTGCGCCAGGAACAACGCTCTGAATACTCTGGATTACATTTTCACTGG	3720
Db	3661	AGTGGGCACAGACTGCGCCAGGAACAACGCTCTGAATACTCTGGATTACATTTTCACTGG	3720
Qy	3721	TGTCCTTTACCTTTGAGATGGTGATTAAGATGATCGACTTGGGACTGCTTCAACCTGG	3780
Db	3721	TGTCCTTTACCTTTGAGATGGTGATTAAGATGATCGACTTGGGACTGCTTCAACCTGG	3780
Qy	3781	AGGCTATTTCCGGGACTTTGTGGAACTTCTGGACTTCATTTGTGTGCTAGTGGCGCCCTGGT	3840
Db	3781	AGGCTATTTCCGGGACTTTGTGGAACTTCTGGACTTCATTTGTGTGCTAGTGGCGCCCTGGT	3840
Qy	3841	GGCGTTTGTCTTCTCGAGCTTCTGTGGGAGGATCCAAAGGGAAAGACATCAATACCATCAA	3900
Db	3841	GGCGTTTGTCTTCTC-----AGGATCCAAAGGGAAAGACATCAATACCATCAA	3888
Qy	3901	GTCTCTGAGAGTCTCTCGTGTCTGGCGGCCCTCAAGACCATCAACGGCTGCCCAAGCT	3960
Db	3889	GTCTCTGAGAGTCTCTCGTGTCTGGCGGCCCTCAAGACCATCAACGGCTGCCCAAGCT	3948
Qy	3961	CAAGGCTGTGTTGACGTGTGGTGAACTCCCTGAAGAAATGCTCTCAACATCTTGATTGT	4020
Db	3949	CAAGGCTGTGTTGACGTGTGGTGAACTCCCTGAAGAAATGCTCTCAACATCTTGATTGT	4008
Qy	4021	CTACATGCTCTTCAATGTTTCATATTGCGCGTCATTGCGGTGACGCTCTTCAAGGGGAAGTT	4080
Db	4009	CTACATGCTCTTCAATGTTTCATATTGCGCGTCATTGCGGTGACGCTCTTCAAGGGGAAGTT	4068
Qy	4081	TTTCTACTGCACAGATGAATCCAAAGAGCTGAGAGGGAATGCAAGGGGTCAAGTATTGGGA	4140
Db	4069	TTTCTACTGCACAGATGAATCCAAAGAGCTGAGAGGGAATGCAAGGGGTCAAGTATTGGGA	4128
Qy	4141	TTATGAAAGGAGGAAGTGGAGCTCAGCCAGCGAGTGAAGAAATACACATTTTCACTA	4200
Db	4129	TTATGAAAGGAGGAAGTGGAGCTCAGCCAGCGAGTGAAGAAATACACATTTTCACTA	4188
Qy	4201	CGACAAATGTGCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCAAGGGGAAGGCTGGCC	4260
Db	4189	CGACAAATGTGCTCTGGGCTCTGCTGACGCTGTTTCAAGTGTCCAAGGGGAAGGCTGGCC	4248
Qy	4261	CATGGTGTGAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAGCCCTGGGTA	4320
Db	4249	CATGGTGTGAAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAAGCCCTGGGTA	4308
Qy	4321	CCGCATGGAGCTGTCCATCTTCTACGTGGTCTACTTTGTGGTCTTTCCTTCTTCTCGT	4380
Db	4309	CCGCATGGAGCTGTCCATCTTCTACGTGGTCTACTTTGTGGTCTTTCCTTCTTCTCGT	4368
Qy	4381	CAACATCTTTGTGGCTTTTGATCATCATCACTTCCAGGAGCAGGGGACAAGGTGATGTC	4440
Db	4369	CAACATCTTTGTGGCTTTTGATCATCATCACTTCCAGGAGCAGGGGACAAGGTGATGTC	4428
Qy	4441	TGAAATGACGCTGGAGAAGAACGAGAGGGCTTGCAATTGACTTCGCCATCAGCGCCAAACC	4500
Db	4429	TGAAATGACGCTGGAGAAGAACGAGAGGGCTTGCAATTGACTTCGCCATCAGCGCCAAACC	4488
Qy	4501	CCTGACACGGGTACATGCCCCCAAAACCGGCGAGTGTCTTCCAGTATAAGACGTGGACATTTGT	4560
Db	4489	CCTGACACGGGTACATGCCCCCAAAACCGGCGAGTGTCTTCCAGTATAAGACGTGGACATTTGT	4548

Qy	4561	GGTCTCCCGCCCTTTGAAATCACTTCATCATGCGCCATGATAGCCCTCAACACTGTGGTGCCT	4620
Db	4549	GGTCTCCCGCCCTTTGAAATCACTTCATCATGCGCCATGATAGCCCTCAACACTGTGGTGCCT	4608
Qy	4621	GATGATGAAGTCTTATGATGACACCCCTATGATGACGAGCTGATGCTGGAATGCCTCGAAT	4680
Db	4609	GATGATGAAGTCTTATGATGACACCCCTATGATGACGAGCTGATGCTGGAATGCCTCGAAT	4668
Qy	4681	CGTGTTCACATCCATGTTCTTCATGGAATCGTGCTGAAGATCATCGCCCTTTGGGGTGCCT	4740
Db	4669	CGTGTTCACATCCATGTTCTTCATGGAATCGTGCTGAAGATCATCGCCCTTTGGGGTGCCT	4728
Qy	4741	GAACATTTTCAGAGATGCCCTGGAAATGCTTTTGACTTTGTCACTGTGTGGGAAGTATTAC	4800
Db	4729	GAACATTTTCAGAGATGCCCTGGAAATGCTTTTGACTTTGTCACTGTGTGGGAAGTATTAC	4788
Qy	4801	TGATATTTTATGTAACAGAGATTCGGGAAACGAACTTTCATCAACCTCAGCTTCCTCCG	4860
Db	4789	TGATATTTTATGTAACAGAGATTCGGGAAACGAACTTTCATCAACCTCAGCTTCCTCCG	4848
Qy	4861	CCTCTTTCGAGCTGCGCGCTGATCAAGCTGCTCCGCGAGGGCTACACCATCCGATCCCT	4920
Db	4849	CCTCTTTCGAGCTGCGCGCTGATCAAGCTGCTCCGCGAGGGCTACACCATCCGATCCCT	4908
Qy	4921	GCGTGGACCTTTGTTCAGTCTCTTCAAGGCCCTGCCCTACGTFGTCTGCTCATGTCCAT	4980
Db	4909	GCGTGGACCTTTGTTCAGTCTCTTCAAGGCCCTGCCCTACGTFGTCTGCTCATGTCCAT	4968
Qy	4981	GCGTGTTCTTCATCTACGCCATCATCGGCATGCGAGTGTTTTGGGAATATTCGCTGGATGA	5040
Db	4969	GCGTGTTCTTCATCTACGCCATCATCGGCATGCGAGTGTTTTGGGAATATTCGCTGGATGA	5028
Qy	5041	TGACACAGCATCAACCGGCCACAACTTCCGAGCGTTTTTTCGAAAGCCCTGATGCTGCT	5100
Db	5029	TGACACAGCATCAACCGGCCACAACTTCCGAGCGTTTTTTCGAAAGCCCTGATGCTGCT	5088
Qy	5101	GTTTCAGAGCGCCACGCGGGAGGCTGGCACGAGATCATGCTGCTGCTGAGCAACCA	5160
Db	5089	GTTTCAGAGCGCCACGCGGGAGGCTGGCACGAGATCATGCTGCTGCTGAGCAACCA	5148
Qy	5161	GGCTGTGATGAGGAGGCCAATGGCACCGAGTGTGGAAAGTGACTTTCGCTACTTCTACTT	5220
Db	5149	GGCTGTGATGAGGAGGCCAATGGCACCGAGTGTGGAAAGTGACTTTCGCTACTTCTACTT	5208
Qy	5221	CGTCTCCTTCATCTTCTGTGCTCTTCTTCATGATGTTGAACTCTTTTGTGCTGTGATCAT	5280
Db	5209	CGTCTCCTTCATCTTCTGTGCTCTTCTTCATGATGTTGAACTCTTTTGTGCTGTGATCAT	5268
Qy	5281	GGACAAATTTTGAATCACTCACGCGGACTCTTCATCTAGTGCTCACCATTTGGATGA	5340
Db	5269	GGACAAATTTTGAATCACTCACGCGGACTCTTCATCTAGTGCTCACCATTTGGATGA	5328
Qy	5341	GTTTCATCGGGTCTGGGCTGAATACGACCCGGCTGCGTGTGGGGCATCAGTTTCAATGA	5400
Db	5329	GTTTCATCGGGTCTGGGCTGAATACGACCCGGCTGCGTGTGGGGCATCAGTTTCAATGA	5388
Qy	5401	CATGTTTGAATGCTGTAACACATGTCCTCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460
Db	5389	CATGTTTGAATGCTGTAACACATGTCCTCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5448
Qy	5461	TCGAGTTGCTTACAAGCGCTGGTTTCGATGAACATGCCCATCTCCAAAGGAGCATGCAC	5520
Db	5449	TCGAGTTGCTTACAAGCGCTGGTTTCGATGAACATGCCCATCTCCAAAGGAGCATGCAC	5508
Qy	5521	TGTTCACTTCACTGTCATGATGGCCCTCATCCCGACGGCATCTGAGATCAAGCTGGC	5580
Db	5509	TGTTCACTTCACTGTCATGATGGCCCTCATCCCGACGGCATCTGAGATCAAGCTGGC	5568
Qy	5581	CCGAGCTGGACAAAGCAGCATCAGTGTGACGGAGTTGAGGAAAGGATTTCCGTTGT	5640
Db	5569	CCGAGCTGGACAAAGCAGCATCAGTGTGACGGAGTTGAGGAAAGGATTTCCGTTGT	5628
Qy	5641	GTGGGCCAAATCTGCCCCAGAAACTTTTGGACTTTGTGTTGATCACCACCCCATTAAGCTGATGA	5700

Db 5629 GTGGGCAATTCGCCAGAACTTTGACTTGTGTTACACCCCATTAAGCCTGATGA 5688
QY 5701 GATGACAGTGGGAAGGTTTATGACGCTCTGATGATATTGACTTCTTCAAGACGAACAA 5760
Db 5689 GATGACAGTGGGAAGGTTTATGACGCTCTGATGATATTGACTTCTTCAAGACGAACAA 5748
QY 5761 AACACACAGAGACACAGATCAGAGAGGCTCTCTGGAGGCTTCTCCAGATGGGTCCTGTGTC 5820
Db 5749 AACACACAGAGACACAGATCAGAGAGGCTCTCTGGAGGCTTCTCCAGATGGGTCCTGTGTC 5808
QY 5821 CTTGTTCCACCTCTGAAGGCCACCTTGAGCAGACAGACCGGCTGTGCTCCGAGGAGC 5880
Db 5809 CTTGTTCCACCTCTGAAGGCCACCTTGAGCAGACAGACCGGCTGTGCTCCGAGGAGC 5868
QY 5881 CCGGGTTTTCTTTCGACAGAAAGTTTCCACCTTCCAGCAATGGCGGGCCATACAAAA 5940
Db 5869 CCGGGTTTTCTTTCGACAGAAAGTTTCCACCTTCCAGCAATGGCGGGCCATACAAAA 5928
QY 5941 CCAAGAGATGGGATCAAAAGATCTGTCTCTGGGGCACTCAAGGACCCAGGATGCACC 6000
Db 5929 CCAAGAGATGGGATCAAAAGATCTGTCTCTGGGGCACTCAAGGACCCAGGATGCACC 5988
QY 6001 CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGCGGTC 6060
Db 5989 CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGCGGTC 6048
QY 6061 AGGAGCACTGGCTGTGGAGCTTCAGATGCAGAGCATAAACCGAGGGCCCTGTATGGGGA 6120
Db 6049 AGGAGCACTGGCTGTGGAGCTTCAGATGCAGAGCATAAACCGAGGGCCCTGTATGGGGA 6108
QY 6121 GCCCCAGCTGGCTGGAGAGCAGGGTGCAGCGGCTCCATGCCCCGCTTGGGGCCGA 6180
Db 6109 GCCCCAGCTGGCTGGAGAGCAGGGTGCAGCGGCTCCATGCCCCGCTTGGGGCCGA 6168
QY 6181 GACTCAGCCGTCACAGATGCCAGGCCCATGAAGCGCTCCATCTCCACGCTGGCCAGCG 6240
Db 6169 GACTCAGCCGTCACAGATGCCAGGCCCATGAAGCGCTCCATCTCCACGCTGGCCAGCG 6228
QY 6241 GCCCGTGGGACTCATTTTGCAGACCAACCCCGGACCGCCACCCCTAGCCAGGGGCTC 6300
Db 6229 GCCCGTGGGACTCATTTTGCAGACCAACCCCGGACCGCCACCCCTAGCCAGGGGCTC 6288
QY 6301 GTCGACACACACACACCGCTGCACCGCGGAGGAGACAGGAGGTCCTCTGGA 6360
Db 6289 GTCGACACACACACACCGCTGCACCGCGGAGGAGACAGGAGGTCCTCTGGA 6348
QY 6361 GAAGGGGCCAGCTGTCTGCGGATATGATGGGSCACCAAGCAGTGTGTGGGSCCGG 6420
Db 6349 GAAGGGGCCAGCTGTCTGCGGATATGATGGGSCACCAAGCAGTGTGTGGGSCCGG 6408
QY 6421 GCTGCCCCGGAGAGGGCCCTACAGGCTGCCGGGGAACGAGAGCGCGCGGAGGAGCG 6480
Db 6409 GCTGCCCCGGAGAGGGCCCTACAGGCTGCCGGGGAACGAGAGCGCGCGGAGGAGCG 6468
QY 6481 GGGCCGGTCCAGAGCGGAGGAGCCCTCATCTCTCTCCGAGAGAGCGCTCTTA 6540
Db 6469 GGGCCGGTCCAGAGCGGAGGAGCCCTCATCTCTCTCCGAGAGAGCGCTCTTA 6528
QY 6541 CTCCTCGACCGCTTTGGGGCCGCTGAGCCCGGAGCCCAAGCCCTCCCTCAGCAGCA 6600
Db 6529 CTCCTCGACCGCTTTGGGGCCGCTGAGCCCGGAGCCCAAGCCCTCCCTCAGCAGCA 6588
QY 6601 CCCAACGTCCGCAACAGCTGGCCAGGAGCCGGGACCCCAACCCAGGGCAGTGGTTCCGT 6660
Db 6589 CCCAACGTCCGCAACAGCTGGCCAGGAGCCGGGACCCCAACCCAGGGCAGTGGTTCCGT 6648
QY 6661 GAATGGGAGCCCTTGTCTCAATCTGGTGTAGACACCCCGCGCGGTGGGCGGAG 6720
Db 6649 GAATGGGAGCCCTTGTCTCAATCTGGTGTAGACACCCCGCGCGGTGGGCGGAG 6708
QY 6721 GCAGTCCCGCAGAGCCGCTGACTCCCGCGCCACAGATACCTTACAGAGCGGCAACTC 6780

Db 6709 GCAGTCCCGCAGAGCGCCCTGACTCCCGCCAGCATCACCTACAAGAAGGCAACTC 6768
QY 6781 CTCACCATCCACTTTCGCGGGGCTCAGACAGCTCCCTGCTTCTCCCGAGGCGGCT 6840
Db 6769 CTCACCATCCACTTTCGCGGGGCTCAGACAGCTCCCTGCTTCTCCCGAGGCGGCT 6828
QY 6841 CAGCCGTGGGCTTTCCGAAACACAGCCCTGTCTGACAGAGAGACCCCTCAGCCAGCCCT 6900
Db 6829 CAGCCGTGGGCTTTCCGAAACACAGCCCTGTCTGACAGAGAGACCCCTCAGCCAGCCCT 6888
QY 6901 GGGCCCTGGCTCTCGAATTTGGCTTACCTTACCTGGGGCAGGCTGTGACAGTAGGC 6960
Db 6889 GGGCCCTGGCTCTCGAATTTGGCTTACCTTACCTGGGGCAGGCTGTGACAGTAGGC 6948
QY 6961 CTCTGTCCACGCGCTGTGAGGACAGCTCAGCTTTTCGAGAGGCTGTGCGCCAACTC 7020
Db 6949 CTCTGTCCACGCGCTGTGAGGACAGCTCAGCTTTTCGAGAGGCTGTGCGCCAACTC 7008
QY 7021 GGGCCGCTCTCCAGGACTTCTTACGCTCTCCCTGACCTCCAGTCTCACCTCTCTCG 7080
Db 7009 GGGCCGCTCTCCAGGACTTCTTACGCTCTCCCTGACCTCCAGTCTCACCTCTCTCG 7068
QY 7081 CCGGTCGCCCAACGGTTTACCACTGCACCCCTGGGACTCAGCTCGGGTGGCGGAGCGCA 7140
Db 7069 CCGGTCGCCCAACGGTTTACCACTGCACCCCTGGGACTCAGCTCGGGTGGCGGAGCGCA 7128
QY 7141 CAGTACACACACCTTGACCAAGACCACTGCTGCTAGCTGACCGTACCGCTCAGACGC 7200
Db 7129 CAGTACACACACCTTGACCAAGACCACTGCTGCTAGCTGACCGTACCGCTCAGACGC 7188
QY 7201 CTGATGACAGAGCGCTGTGTTCCAGTGGATAGTTTTATCATCCACAGGCGAGTCGG 7260
Db 7189 CTGATGACAGAGCGCTGTGTTCCAGTGGATAGTTTTATCATCCACAGGCGAGTCGG 7248
QY 7261 CCCTCGGGGAGCGCTTGGCCACCTTGGTGGAGCTCTGTGGCCCTCTCCCTCCCTCT 7320
Db 7249 CCCTCGGGGAGCGCTTGGCCACCTTGGTGGAGCTCTGTGGCCCTCTCCCTCCCTCT 7308
QY 7321 CCCTCTTTTACTCTAGACGACGAATAAGCCCTGTGTTGAGTGTAGCTACCGC 7376
Db 7309 CCCTCTTTTACTCTAGACGACGAATAAGCCCTGTGTTGAGTGTAGCTACCGC 7364

RESULT 3

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; Sequence 7, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
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APPLICATION NUMBER: 07/868,354
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APPLICATION NUMBER: US 07/745,206
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
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APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..7163
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 7161..7362
US-08-455-543A-7

Query Match 99.2%; Score 7316.4; DB 1; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

Qy 1 GCGGCGGGCTGCGGCTGGGCGGGGCGGCGGCTCGCTCGGTCGCGGCGGCTCGGTG 60
Db 1 GCGGCGGGCTGCGGCGGCTGGGCGGGGCGGCGGCTCGGTCGCGGCTCGGTG 59
Qy 61 GCTGCTCGCTCTGAGCGCTTGGGCGGCGGCGGCGGCTCGCTCGGCGGCGGCTGGGCGG 120
Db 60 GCTGCTCGCTCTGAGCGCTTGGGCGGCGGCGGCGGCTCGCTCGGCGGCGGCTGGGCGG 118
Qy 121 GGGATGACGCGGGCGGCGGAGCCATGCTCGCTTTCGGGAGCAGATGCGGCGGCGGCTA 180
Db 119 GGGATGACGCGGGCGGCGGAGCCATGCTCGCTTTCGGGAGCAGATGCGGCGGCGGCTA 178
Qy 181 TGGAGGCGGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 179 TGGAGGCGGCGGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 238
Qy 241 GGGTCCGGGGGGCTGACGCGGCGGCGGCGGCTTCTTACAGCAATCGATCGGCGGCGG 300
Db 239 GGGTCCGGGGGGCTGACGCGGCGGCGGCGGCTTCTTACAGCAATCGATCGGCGGCGG 298
Qy 301 GCGCGGAGCCATGGCGCTGTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAA 360

Db 299 CGCGCGGACCATGGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAA 358
Qy 361 CGCTCGCTCTTCTGCTCTTCTAGCGGAGGACAAACGCTCGTCCGCAAAATAGCGAAGCGCATCAC 420
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Qy 421 CGAGTGGCCCTCCATTCGAGTATATGATCTCTGGCCACCATCATCGCCAACTGCAATCGTGTCT 480
Db 419 CGAGTGGCCCTCCATTCGAGAAATATGATCTCTGGCCACCATCATCGCCAACTGCAATCGTGTCT 478
Qy 481 GGCCCTGGAGCAGCAGCTCCCTCATGGGACAAAACGCCCATCTCCGAGCGGCTGGACGA 540
Db 479 GGCCCTGGAGCAGCAGCTCCCTCATGGGACAAAACGCCCATCTCCGAGCGGCTGGACGA 538
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Db 959 CCCAGCCCGCTGTCGAGGCGGACACTGAGTCCCGGAGTACTGCGCAGAGACCCAACTT 1018
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QY 1921 GAGTCCCTCGGAACTCGTGTGTCTGCTGAAGTCCATGAAGTCCATCATCAGCT 1980
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QY 2041 GGGACAGTTCACCTCCAGGATGAGCTCCCAACCAACTTCGACACTTCCTTCGCGC 2100
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QY 3421 GGTGTTCCAGTGTGTAACTGTGAACTGTGAAAGCAAGCAGAGGGGGAAGAGAGGTGA 3480
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Db 6947 CTCTGTCCAGCCCTGCTGTAGGACACGCTCACCTTTCGAGAGGCTGTGGCCACCACTC 7006
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Db 7007 GGGCCGTCTCTCCAGGACTTCTTACGTCTCTCCCTGACCTCCAGCTCTCACCTCTCCG 7066
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Qy 7201 CTGATCGAGAGCGCTGTCTTCCAGTGGATGATTTTATCATCCACACGCGGCGAGTCGG 7260
Db 7187 CTGATCGAGAGCGCTGTCTTCCAGTGGATGATTTTATCATCCACACGCGGCGAGTCGG 7246
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Db 7247 CCCTCGGGGAGCGCTTGGCCACCTTGGTGAGGCTCTGTGGCCCTTCCCTCCCTCTCT 7306
Qy 7321 CCCCTCTTTTACTCTAGACGACGAATAAGCCCTTGTGTGTAGTGTACGTACCGC 7376
Db 7307 CCCCTCTTTTACTCTAGACGACGAATAAGCCCTTGTGTGTAGTGTACGTACCGC 7362

RESULT 4

US-08-193-078B-7
; Sequence 7, Application US/08193078B
; Patent No. 5846757
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
; STREET: 1660 UNION STREET
; CITY: SAN DIEGO
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,078B
; FILING DATE: 07-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/868,354
; FILING DATE: 10-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-53607

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 7362 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 144..7163

FEATURE:

NAME/KEY: 5'UTR

LOCATION: 1..143

FEATURE:

NAME/KEY: 3'UTR

LOCATION: 7161..7362

US-08-193-078B-7

Query Match 99.2%; Score 7316.4; DB 2; Length 7362;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

Qy	1	GCGCGCGCGGTGCGCGGTCGGGCGCGGCGGAGGTCCGCTCGCGTCCCGCGGCTCCGCTG	60
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Qy	61	GCTGCTCGCTCTGAGCGCTTGGCGCGCCCGCGCGCTTCCCTGCGCGGCGCGCTGGGCGG	120
Db	60	GCTGCTCGCTCTGAGCGCTT-GCGCGCGCGCGCGCTTCCCTGCGCGGCGCGCTGGGCGG	118
Qy	121	GGGATGCACGCGGCGCGGAGCCATGGTCCGCTTCGGGACAGCTGGCGCGCGCTA	180
Db	119	GGGATGCACGCGGCGCGGAGCCATGGTCCGCTTCGGGACAGCTGGCGCGCGCTA	178
Qy	181	TGGAGGCCCCCGCGCGGAGAGCGGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG	240
Db	179	TGGAGGCCCCCGCGCGGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	238
Qy	241	GGGTCCCGGGGGCTGCAGCCCGCGAGCGGGTCTCTAAGAATCGATCGCGGAGCG	300
Db	239	GGGTCCCGGGGGCTGCAGCCCGCGAGCGGGTCTCTAAGAATCGATCGCGGAGCG	298
Qy	301	CGCGCGACCATGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTACCGGTCAA	360
Db	299	CGCGCGACCATGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTACCGGTCAA	358
Qy	361	CCGCTCGCTCTTCTTTCAGCAGGACAAAGTCCGCGCAATACGCGAAGCGCATCAC	420
Db	359	CCGCTCGCTCTTCTTTCAGCAGGACAAAGTCCGCGCAATACGCGAAGCGCATCAC	418
Qy	421	CGAGTGGCTCCATTCGAGTATATGATCTTGGGCCAATCATCGCCAACTGCATCGTCT	480
Db	419	CGAGTGGCTCCATTCGAGTATATGATCTTGGGCCAATCATCGCCAACTGCATCGTCT	478
Qy	481	GGCCCTGGAGCAGCACTCCCTGATGGGACAAACCGCCCATGTCCGAGCGGCTGGACGA	540
Db	479	GGCCCTGGAGCAGCACTCCCTGATGGGACAAACCGCCCATGTCCGAGCGGCTGGACGA	538
Qy	541	CACGAGCCCTATTTTCATCGGGATCTTTTGTCTCGAGCGGGATCAAAATCATCGCTCT	600
Db	539	CACGAGCCCTATTTTCATCGGGATCTTTTGTCTCGAGCGGGATCAAAATCATCGCTCT	598
Qy	601	GGGCTTTGTCTTCCAAAGGCTCTTACTTCGGAACCGGTGGAAAGTCAATGGAATTCGT	660
Db	599	GGGCTTTGTCTTCCAAAGGCTCTTACTTCGGAACCGGTGGAAAGTCAATGGAATTCGT	658
Qy	661	GGTGTCTTACAGGGATCTTGGCAGCGGTGGAACTGACTTCGACCTTCGGAACACTGAG	720
Db	659	GGTGTCTTACAGGGATCTTGGCAGCGGTGGAACTGACTTCGACCTTCGGAACACTGAG	718

Qy	721	GGCTGTGCTGTGCTGAGGCCCCCTGAAGCTGGTGTCTGGGATTCGAAGTTTGCAGGTGGT	780
Db	719	GGCTGTGCTGTGCTGAGGCCCCCTGAAGCTGGTGTCTGGGATTCGAAGTTTGCAGGTGGT	778
Qy	781	GCTCAAGTCCATCATGAAGGCCATGGTTCACCTCTGCAGATTGGGCTGCTCTCTTCTT	840
Db	779	GCTCAAGTCCATCATGAAGGCCATGGTTCACCTCTGCAGATTGGGCTGCTCTCTTCTT	838
Qy	841	TGCCATCTCATGTTTGGCCATCATTTGGCCCTGGAGTCTACATGGGCAAGTTTCCAAGGC	900
Db	839	TGCCATCTCATGTTTGGCCATCATTTGGCCCTGGAGTCTACATGGGCAAGTTTCCAAGGC	898
Qy	901	CTGTTTCCCAACAGCACAGATGCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	960
Db	899	CTGTTTCCCAACAGCACAGATGCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	958
Qy	961	CCAGCCCGGCTGTGCGAGGGCGACACTGAGTGCAGGAGTACTGGGCCAGGACCCAACTT	1020
Db	959	CCAGCCCGGCTGTGCGAGGGCGACACTGAGTGCAGGAGTACTGGGCCAGGACCCAACTT	1018
Qy	1021	TGGCATCACCAACTTTGACAAATATCTGTTTGCCATCTTGACGCTGTTCCAGTGCATCAC	1080
Db	1019	TGGCATCACCAACTTTGACAAATATCTGTTTGCCATCTTGACGCTGTTCCAGTGCATCAC	1078
Qy	1081	CATGGAGGGCTGGACTGACATCTCTATAATAAACAACGATGCGGCCCGGCAACACTTGGAA	1140
Db	1079	CATGGAGGGCTGGACTGACATCTCTATAATAAACAACGATGCGGCCCGGCAACACTTGGAA	1138
Qy	1141	CTGGCTCTACTTCTATCCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTCT	1200
Db	1139	CTGGCTCTACTTCTATCCCTCTCATCATCATCGGCTCTTCTTATGCTCAACCTGGTCT	1198
Qy	1201	GGCGTCTCTCGGGGAGTTTGCAGAGGAGCAGAGAGGTGGAGAACCGCGCGGCTT	1260
Db	1199	GGCGTCTCTCGGGGAGTTTGCAGAGGAGCAGAGAGGTGGAGAACCGCGCGGCTT	1258
Qy	1261	CCTGAAGCTCGCGCGCAGCAGATCGAGCGAGAGCTCAAGCGGTACCTGGAGTGGAT	1320
Db	1259	CCTGAAGCTCGCGCGCAGCAGATCGAGCGAGAGCTCAAGCGGTACCTGGAGTGGAT	1318
Qy	1321	CTTCAAGCGGAGGAAGTCACTGCTGGCCGAGGAGCAGGAATGCAGAGAGAGTCCCC	1380
Db	1319	CTTCAAGCGGAGGAAGTCACTGCTGGCCGAGGAGCAGGAATGCAGAGAGAGTCCCC	1378
Qy	1381	TTTGGACGCTCTCAAGAGAGCGCGCACCAAGAGAGCAGAAATGACCTGATCCACGAGA	1440
Db	1379	TTTGGACGCTCTCAAGAGAGCGCGCACCAAGAGAGCAGAAATGACCTGATCCACGAGA	1438
Qy	1441	GGAGGAGAGGACCGGTTTCAGATCTCTGTGCTTGGATGCCCTTCCGCCCGCGCCAG	1500
Db	1439	GGAGGAGAGGACCGGTTTCAGATCTCTGTGCTTGGATGCCCTTCCGCCCGCGCCAG	1498
Qy	1501	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATATCTTCGAGGAGGAAGAGATGTTCCG	1560
Db	1499	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATATCTTCGAGGAGGAAGAGATGTTCCG	1558
Qy	1561	GTTTTTTATCCGCGCATGTGAGGCTCAGAGCTTACTTGGGTGGTGTGCTGCGTGGT	1620
Db	1559	GTTTTTTATCCGCGCATGTGAGGCTCAGAGCTTACTTGGGTGGTGTGCTGCGTGGT	1618
Qy	1621	GGCCCTGAAACACACTGTGTGGCCATGGTGCATTACAACAGCCCGCGCGGCTTACCAC	1680
Db	1619	GGCCCTGAAACACACTGTGTGGCCATGGTGCATTACAACAGCCCGCGCGGCTTACCAC	1678
Qy	1681	GACCTGTATTTCAGAGTTTGTTCCTGGGTCTTCTTCTCAGAGATGTCCTGAA	1740
Db	1679	GACCTGTATTTCAGAGTTTGTTCCTGGGTCTTCTTCTCAGAGATGTCCTGAA	1738
Qy	1741	GATGTATGGCTCGGGCCCAAGAGTACTTCCGCTCTCTCTCAACTGCTTCCACTTTGG	1800
Db	1739	GATGTATGGCTCGGGCCCAAGAGTACTTCCGCTCTCTCTCAACTGCTTCCACTTTGG	1798

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1919 GAGCTCCCTCGGAACTCTGGTGTGTCCCTGTCTGAATCTCATGAAGTCAATCAGCCT 1978
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2041 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACAACTTCGACACCTTCCCTGCCGC 2100
2039 GGGACAGTTCAACTTCCAGGATGAGACTCCCAACAACTTCGACACCTTCCCTGCCGC 2098
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2639 CAAAGCCGCACTGAGGCTGCGGAGGCCCGCGAGGCGTCAACCTTCGCGCAGGCAACA 2698
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2939 CGAGCGCACCGCGCGCACCGGCACACAGATCCAGCAAGAGATGCGCGCGCCAAAGG 2998
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3121 GGAGAGGAGACACAGGAGAAAGAGGCCACAGGAGAGGCTGAGATAGTGGAAAGCGGA 3180
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3181 CAAGGAAAGGAGCTCCGGAAACCAACAGCCCGGAGCCACACTGTGACCTGGAGACCA 3240
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DB	6767	CTCACCATTCACTTCCCGGGGCTCAGACGAGCGCTCCCTGCTCTCCCGCAGCGCGCT	6826
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; Sequence 7, Application US/082233305C			
; Patent No. 5851824			
; GENERAL INFORMATION:			
; APPLICANT: Harpold, Michael			
; APPLICANT: Ellis, Steven			
; APPLICANT: Williams, Mark			
; APPLICANT: Feldman, Daniel			
; APPLICANT: McCue, Ann			
; APPLICANT: Bremer, Robert			
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND			
; TITLE OF INVENTION: METHODS			
; NUMBER OF SEQUENCES: 57			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Brown, Martin, Haller & McClain			
; STREET: 1660 Union Street			
; CITY: San Diego			
; STATE: California			
; COUNTRY: USA			
; ZIP: 92101-2926			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSeq Version 1.5			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/223,305C			
; FILING DATE: April 4, 1994			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 07/868,354			
; FILING DATE: April 10, 1992			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/745,206			
; FILING DATE: 15-AUG-1991			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/620,250			
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; FILING DATE: 04-APR-1989			
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; APPLICATION NUMBER: US 07/176,899			
; FILING DATE: 04-APR-1988			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Seidman, Stephanie L.			
; REGISTRATION NUMBER: 33,779			
; REFERENCE/DOCKET NUMBER: 52516 (P519739)			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (619)238-0999			
; TELEFAX: (619)238-0062			
; INFORMATION FOR SEQ ID NO: 7:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 7362 base pairs			
; TYPE: nucleic acid			
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[illegible]

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6601 CCCAAGCTGCGCAACAGCTGGCCAGAGCGGGAGCCCAACCCACAGAGGAGTGGTTCGGT 6660
6587 CCCAAGCTGCGCAACAGCTGGCCAGAGCGGGAGCCCAACCCACAGAGGAGTGGTTCGGT 6646
6661 GAATGGAGCCCTTGTCTGTAACATCTGTGCTAGCAGCCCGGCGGGTGGGGGAG 6720
6647 GAATGGAGCCCTTGTCTGTAACATCTGTGCTAGCAGCCCGGCGGGTGGGGGAG 6706
6721 GAGCTCCCCAGAGCGCCCTGACTCCCCCGCCCCAGCATCACTACAAGAGCGCCAACTC 6780
6707 GAGCTCCCCAGAGCGCCCTGACTCCCCCGCCCCAGCATCACTACAAGAGCGCCAACTC 6766
6781 CTCACCATCCACTTCCCGGGGCTCAGACAGCCCTCTGCTTCTCCAGAGCGGCT 6840
6767 CTCACCATCCACTTCCCGGGGCTCAGACAGCCCTCTGCTTCTCCAGAGCGGCT 6826
6841 CAGCCGTGGGCTTTCCGAACACAGCGCCCTGCTGAGAGAGACCCCTCAGCCAGCCCT 6900
6827 CAGCCGTGGGCTTTCCGAACACAGCGCCCTGCTGAGAGAGACCCCTCAGCCAGCCCT 6886
6901 GGGCCCTGCTCTGAAATTTGGCTTGAACCTTACCTGGGGAGGCTGTGGACAGTGGG 6960
6887 GGGCCCTGCTCTGAAATTTGGCTTGAACCTTACCTGGGGAGGCTGTGGACAGTGGG 6946
6961 CTCTGTCCAGCGCCCTGCTGAGAGACAGCTCACTTTCAGAGAGGCTGTGGCACCAGTC 7020
6947 CTCTGTCCAGCGCCCTGCTGAGAGACAGCTCACTTTCAGAGAGGCTGTGGCACCAGTC 7006
7021 GGGCCCTCTCTCAGGACTTCTACGTGTCTCTCTGACCTCCAGCTCTCAGCTCTCCG 7080
7007 GGGCCCTCTCTCAGGACTTCTACGTGTCTCTCTGACCTCCAGCTCTCAGCTCTCCG 7066
7081 CCGCTGCCCCACGCTTACCACTGACCTCGGAGTCAAGCTCGGGTGGCCAGCAGGCA 7140
7067 CCGCTGCCCCACGCTTACCACTGACCTCGGAGTCAAGCTCGGGTGGCCAGCAGGCA 7126
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7127 CAGCTACCAACACCTGACCAAGACCACTGGTGTGCTGACCTGACCTGACCTGACAGCG 7186
7201 CTGATGAGCAGGCGTGTGTTCAGTGGATGAGTTTATCATCCACAGGGGAGTGG 7260
7187 CTGATGAGCAGGCGTGTGTTCAGTGGATGAGTTTATCATCCACAGGGGAGTGG 7246
7261 CCCTGGGGAGGCTTCCACCTTGTGAGGCTCTGTGGGCGCTTCTCCCTCCCTCT 7320
7247 CCCTGGGGAGGCTTCCACCTTGTGAGGCTCTGTGGGCGCTTCTCCCTCCCTCT 7306
7321 CCCCTCTTTTACTCTAGACGAGCAATAAGCCCTGTTGCTTGTGAGTGTAGCTACCGC 7376
7307 CCCCTCTTTTACTCTAGACGAGCAATAAGCCCTGTTGCTTGTGAGTGTAGCTACCGC 7362

RESULT 6

US-08-149-097D-7

; Sequence 7, Application US/08149097D

; Patent No. 5874236

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; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 40
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; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; FILING DATE: 04-APR-1989
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; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 144..7163

FEATURE:		5'UTR	
NAME/KEY:		1..143	
LOCATION:			
FEATURE:		3'UTR	
NAME/KEY:		7161..7362	
LOCATION:			
US-08-149-097D-7			
Query Match			
Best Local Similarity 99.2%; Score 7316.4; DB 2; Length 7362;			
Matches 7361, Conservative 0; Mismatches 1; Indels 14; Gaps 3;			
Qy	1	CGCGCGCGGCTGCGCGGTGGGCGGCGAGTCCGCTGCGGTCCGCGGCGTCCGCTG	60
Db	1	CGCGCGCGGCTGCGCGGTGGGCGGCGAGTCCG-TGCGGTCCCGCGGCTCCGCTG	59
Qy	61	GCTGCTCCGCTCAGCGCCTGGCGCGCCCGCGCCCTCCCTGCGCGGCGCTGGGCGG	120
Db	60	GCTGCTCCGCTCAGCGCCT-GCGCGCCCGCGCCCTCCCTGCGCGGCGCTGGGCGG	118
Qy	121	GGGATGCACCGCGGCGCGGAGCCATGCTCCGCTTCGGGACGAGCTGGGCGGCGCTA	180
Db	119	GGGATGCACCGCGGCGCGGAGCCATGCTCCGCTTCGGGACGAGCTGGGCGGCGCTA	178
Qy	181	TGGAGGCCCGCGCGGCGAGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGCC	240
Db	179	TGGAGGCCCGCGCGGCGAGCGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGCC	238
Qy	241	GGGTCCCGGGGGCTGCAGCCCGGCGAGCGGCTCTTACAAAGCAATCGATCGCGAGCG	300
Db	239	GGGTCCCGGGGGCTGCAGCCCGGCGAGCGGCTCTTACAAAGCAATCGATCGCGAGCG	298
Qy	301	CGCGCGGACCATGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	360
Db	299	CGCGCGGACCATGCGCTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA	358
Qy	361	CGGCTCGCTCTTCTTACGAGGAGCAAGCTCGTCCGCAATACGCGAAGCGCATCAC	420
Db	359	CGGCTCGCTCTTCTTACGAGGAGCAAGCTCGTCCGCAATACGCGAAGCGCATCAC	418
Qy	421	CGAGTGGCTCCATTCGAGTATATGATCTGGCCACCATCATCGCCAACTGCATCGTGT	480
Db	419	CGAGTGGCTCCATTCGAGTATATGATCTGGCCACCATCATCGCCAACTGCATCGTGT	478
Qy	481	GGCCCTGGAGCAGCACTCCCTGATGGGCAAAAACGCCATGTCGAGCGGCTGGACGA	540
Db	479	GGCCCTGGAGCAGCACTCCCTGATGGGCAAAAACGCCATGTCGAGCGGCTGGACGA	538
Qy	541	CACGAGCCCTATTTTCATCGGGATCTTTTGTTCGAGCGGAGATCAAAATCATCGCTCT	600
Db	539	CACGAGCCCTATTTTCATCGGGATCTTTTGTTCGAGCGGAGATCAAAATCATCGCTCT	598
Qy	601	GGGCTTTGTCTTCCAAAGGCTCTTACCTGCGGAAAGGCTGGAACTGATGGACTTCGT	660
Db	599	GGGCTTTGTCTTCCAAAGGCTCTTACCTGCGGAAAGGCTGGAACTGATGGACTTCGT	658
Qy	661	GGTCTCTCTCACAGGATCTTTGCAAGGCTGGAACTGACTTCGACCTGGAACTGAG	720
Db	659	GGTCTCTCTCACAGGATCTTTGCAAGGCTGGAACTGACTTCGACCTGGAACTGAG	718
Qy	721	GGCTGCGGTGTGAGGCGCCCTGAAAGTGGTGTCTGGGATTCGAAAGTTGAGGTGGT	780
Db	719	GGCTGCGGTGTGAGGCGCCCTGAAAGTGGTGTCTGGGATTCGAAAGTTGAGGTGGT	778
Qy	781	GCTCAAGTCCATCATGAGGCCATGTTCCACTCTCGAGATGGGCTGCTTCTTCTT	840
Db	779	GCTCAAGTCCATCATGAGGCCATGTTCCACTCTCGAGATGGGCTGCTTCTTCTT	838
Qy	841	TGCCATCTCATGTTTGGCATATGGCTGGAGTTCTACATGGGCAAGTTCCAAAGGC	900
Db	839	TGCCATCTCATGTTTGGCATATGGCTGGAGTTCTACATGGGCAAGTTCCAAAGGC	898
Qy	901	CTGTTTTCCCAACAGCAGATCGGAGCCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	960

Db	899	CTGTTTTCCCAACAGCACAGATCGGAGCCGTGGGTGACTTCCCTGTGGCAAGGAGGC	958
Qy	961	CCCAGCCCGCTGTGCGAGGGCGACACTGAGTCCCGGAGTACTTGGCCAGACCCAACTT	1020
Db	959	CCCAGCCCGCTGTGCGAGGGCGACACTGAGTCCCGGAGTACTTGGCCAGACCCAACTT	1018
Qy	1021	TGGCATCACCAACTTTTGACAATATCCTGTTTGGCATCTTTCAGCGGTGTTTCAGTGCATCAC	1080
Db	1019	TGGCATCACCAACTTTTGACAATATCCTGTTTGGCATCTTTCAGCGGTGTTTCAGTGCATCAC	1078
Qy	1081	CATGGAGGCTGACATGACATCTCTATATACAAACGATGCGGCGGCAACCTGGAA	1140
Db	1079	CATGGAGGCTGACATGACATCTCTATATACAAACGATGCGGCGGCAACCTGGAA	1138
Qy	1141	CTGGCTCTACTCTCATCTCTCATCATCGGCTCTTCTTATGCTCAACCTGGTGTCT	1200
Db	1139	CTGGCTCTACTCTCATCTCTCATCATCGGCTCTTCTTATGCTCAACCTGGTGTCT	1198
Qy	1201	GGCGCTGCTCTCGGGGAGTTTGCACAGGAGCGAGAGGGTGGAGAACCGCGCGCTT	1260
Db	1199	GGCGCTGCTCTCGGGGAGTTTGCACAGGAGCGAGAGGGTGGAGAACCGCGCGCTT	1258
Qy	1261	CCTGAAGCTCGCGCGGCGAGCAGATCGAGCGAGAGCTCAACGGGTACCTGGAGTGGAT	1320
Db	1259	CCTGAAGCTCGCGCGGCGAGCAGATCGAGCGAGAGCTCAACGGGTACCTGGAGTGGAT	1318
Qy	1321	CTTCAAGGCGGAGAACTCATGCTGCGCGAGGAGCAGGAAATGCGAGGAGAAAGTCCCC	1380
Db	1319	CTTCAAGGCGGAGAACTCATGCTGCGCGAGGAGCAGGAAATGCGAGGAGAAAGTCCCC	1378
Qy	1381	TTTGGACGTGCTCAAGAGAGCGGCCAACAAAGAGAGCAGAAATGACTGATCAACGAGA	1440
Db	1379	TTTGGACGTGCTCAAGAGAGCGGCCAACAAAGAGAGCAGAAATGACTGATCAACGAGA	1438
Qy	1441	GGAGGAGAGGACCGGTTTGCAGATCTCTGCTGTGTTGGATCCCTTCCGCGCGGCGAG	1500
Db	1439	GGAGGAGAGGACCGGTTTGCAGATCTCTGCTGTGTTGGATCCCTTCCGCGCGGCGAG	1498
Qy	1501	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATACTTCCGAGGAAGAGAGAGATGTTCCG	1560
Db	1499	CCTCAAGAGCGGGAAGACAGAGAGCTGTCATACTTCCGAGGAAGAGAGAGATGTTCCG	1558
Qy	1561	GTMTTTTATCCGCGCATGGTGAAGCTCAGAGCTTCTACTGGGTGGTGTGCTGCTGGT	1620
Db	1559	GTMTTTTATCCGCGCATGGTGAAGCTCAGAGCTTCTACTGGGTGGTGTGCTGCTGGT	1618
Qy	1621	GGCCCTGAACACACTGTGTGTGSCCATGTTGATTAACAACAGCCGCGGCTTACCAC	1680
Db	1619	GGCCCTGAACACACTGTGTGTGSCCATGTTGATTAACAACAGCCGCGGCTTACCAC	1678
Qy	1681	GACCTGTATTTTGCAGAGTTTCTTTTCTGGGTCTCTTCTCCTCACAGAGATGTCCTGAA	1740
Db	1679	GACCTGTATTTTGCAGAGTTTCTTTTCTGGGTCTCTTCTCCTCACAGAGATGTCCTGAA	1738
Qy	1741	GATGTATGGCTCGGGGCCCAAGAGTACTTCCGGTCTCTCTTCAACTGTCTCGACTTTGG	1800
Db	1739	GATGTATGGCTCGGGGCCCAAGAGTACTTCCGGTCTCTCTTCAACTGTCTCGACTTTGG	1798
Qy	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCCGCGGAAGCTCTT	1860
Db	1799	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCCATCAAGCCGCGGAAGCTCTT	1858
Qy	1861	TGGGATCAGTGTCTCGGGCCCTCCGCTGTGAGGATCTTCAAAGTACAGAGTACTG	1920
Db	1859	TGGGATCAGTGTCTCGGGCCCTCCGCTGTGAGGATCTTCAAAGTACAGAGTACTG	1918
Qy	1921	GAGCTCCCTCGGAACTCGTGGTGTCCCTGTGTGAATCCATGAAGTCCATCATAGCCT	1980
Db	1919	GAGCTCCCTCGGAACTCGTGGTGTCCCTGTGTGAATCCATGAAGTCCATCATAGCCT	1978
Qy	1981	GCTCTCTTGTCTCTCTGTGTTCAATGTGTGCTTTCGCCCTGTCTGGGATGAGCTGTTGG	2040

QY 4201 CGACAAATGTGCTCTGGGCTCTGTGACGCTGTTTCAAGTGTCCACGGGAAAGCGCTGGCC 4260
DB 4187 CGACAAATGTGCTCTGGGCTCTGTGACGCTGTTTCAAGTGTCCACGGGAAAGCGCTGGCC 4246
QY 4261 CATGGTCTGAAACACTCCGTTGGATGCCACTATGAGAGCAGGGTCCAAAGCCCTGGGTA 4320
DB 4247 CATGGTCTGAAACACTCCGTTGGATGCCACTATGAGAGCAGGGTCCAAAGCCCTGGGTA 4306
QY 4321 CCGCATGGAGCTGTCCATCTTTCTACGTGGTCTACTTTTGTGGTCTTTTCCCTTCTTCTTCGT 4380
DB 4307 CCGCATGGAGCTGTCCATCTTTCTACGTGGTCTACTTTTGTGGTCTTTTCCCTTCTTCTTCGT 4366
QY 4381 CAACATCTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGCAAGGTGATGTC 4440
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DB 4427 TGAATGAGCTGTGAGAAAGAACGAGAGGGCTTGCAATTGACTTGCCTCATAGCGCCAAACC 4486
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DB 4547 GGTCTCCCCGCCCTTTGAATACTTTCATCATGAGGCCATGATAGCCCTCAACACTGTGGTGTCT 4606
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QY 4741 GAACATATTCAGAGATGCCATGATGTTTGTGACTTTGTCACTGTGTGTGGAGATATTAC 4800
DB 4727 GAACATATTCAGAGATGCCATGATGTTTGTGACTTTGTCACTGTGTGTGGAGATATTAC 4786
QY 4801 TGATATTTTATGTAACAGAGATTCGGGAAACGAAACAATTTTCATCAACCTCAGCTTCTCCG 4860
DB 4787 TGATATTTTATGTAACAGAGATTCGGGAAACGAAACAATTTTCATCAACCTCAGCTTCTCCG 4846
QY 4861 CCTCTTTTCGAGCTGCGCGGTGATCAAGCTGCTCCGCGAGGGCTACACCATCCGCACTCCT 4920
DB 4847 CCTCTTTTCGAGCTGCGCGGTGATCAAGCTGCTCCGCGAGGGCTACACCATCCGCACTCCT 4906
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DB 5087 GTTCAGAGCGCCACCGGGGAGGCTGTGGACAGATCATGCTGTCTGCTGAGCAACCA 5146
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QY 5221 CGTCTCTTCATCTTCTGTGCTCTTCTTGATGTTGAACTCTTTTGTGGCTGTGATCAT 5280
DB 5207 CGTCTCTTCATCTTCTGTGCTCTTCTTGATGTTGAACTCTTGTGTGCTGTGATCAT 5266
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QY 5401 CATGTTTGAATGCTGAAACACATGTCCTCGCTCTGGGGCTGGGGAAGAAATGCGCTGC 5460
DB 5387 CATGTTTGAATGCTGAAACACATGTCCTCGCTCTGGGGCTGGGGAAGAAATGCGCTGC 5446
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QY 5761 AACACACAGAGACAGATGCAGCAGCTCTCTGAGGCCCTCTCCAGATGGGTCTCTGTGTC 5820
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QY 6361 GAAGGGGCCAGGCTGTCTGCGCATGATGATGGCGCCACCAAGCAGTGTGTGGGGCCGG 6420

[illegible]

1259	Db	CCTGAAGCTGCGCGGCAGCAGCAGATCGAGCGAGAGCTCAACGGGTACTTGGAGTGGAT	1318
1321	Qy	CTTCAAGCGCGAGGAAGTCAATGCTGGCGCAGGAGGACAGGAATGCACAGAGAAAGTCCCC	1380
1319	Db	CTTCAAGCGCGAGGAAGTCAATGCTGGCGCAGGAGGACAGGAATGCACAGGAGAAAGTCCCC	1378
1381	Qy	TTTGGACGTGCTGAAGAGAGCGGCCACCAAGAAAGAGCAGAAATGACTGATCCACGCAGA	1440
1379	Db	TTTGGACGTGCTGAAGAGAGCGGCCACCAAGAAAGAGCAGAAATGACTGATCCACGCAGA	1438
1441	Qy	GGAGGAGAGGACCGGTTTCAGATCTCTGCTGTGTGGATCCCCCTTCCGCCCGCGGCAG	1500
1439	Db	GGAGGAGAGGACCGGTTTCAGATCTCTGCTGTGTGGATCCCCCTTCCGCCCGCGGCAG	1498
1501	Qy	CCTCAAGAGCGGGAAGACAGAGAGCTCGTCACTCTCCGAGGAAGAGAAAGATGTTCCG	1560
1499	Db	CCTCAAGAGCGGGAAGACAGAGAGCTCGTCACTCTCCGAGGAAGAGAAAGATGTTCCG	1558
1561	Qy	GTTTTTTATCCGGCGCATGTTGAAGGCTCAGAGCTTCTACTTGGGTGTTGCTGCTGCGTGGT	1620
1559	Db	GTTTTTTATCCGGCGCATGTTGAAGGCTCAGAGCTTCTACTTGGGTGTTGCTGCTGCGTGGT	1618
1621	Qy	GGCCCTGAAACACTGTGTGTGCGCATGTGTCAATTACAAACAGCCGCGCGGCTTACCAC	1680
1619	Db	GGCCCTGAAACACTGTGTGTGCGCATGTGTCAATTACAAACAGCCGCGCGGCTTACCAC	1678
1681	Qy	GACCCTGATTTTGGACAGAGTTGTTTTCCCTGGGTCTCTTCTCCTCACAGAGATGTCCTGAA	1740
1679	Db	GACCCTGATTTTGGACAGAGTTGTTTTCCCTGGGTCTCTTCTCCTCACAGAGATGTCCTGAA	1738
1741	Qy	GATGTATGGCTCGGGGCCAAGAGCTACTTCCGGTCTCTCTTCAAATGCTTCGACTTTTGG	1800
1739	Db	GATGTATGGCTCGGGGCCAAGAGCTACTTCCGGTCTCTCTTCAAATGCTTCGACTTTTGG	1798
1801	Qy	GGTCATCGTGGGAGCGTCTTTGAAGTGGTCTGGCGGGCCATCAAGCCGCGGAAGCTCCTT	1860
1799	Db	GGTCATCGTGGGAGCGTCTTTGAAGTGGTCTGGCGGGCCATCAAGCCGCGGAAGCTCCTT	1858
1861	Qy	TGGGATCAGTGTGCTGCGGGCCCTCCGCCCTGCTGAGGATCTTCAAAGTCACGAAGTACTG	1920
1859	Db	TGGGATCAGTGTGCTGCGGGCCCTCCGCCCTGCTGAGGATCTTCAAAGTCACGAAGTACTG	1918
1921	Qy	GAGCTCCCTCGGAAACCTGGTGGTGTCCCTGCTGAATCCATGAAGTCCATCATCAGCCT	1980
1919	Db	GAGCTCCCTCGGAAACCTGGTGGTGTCCCTGCTGAATCCATGAAGTCCATCATCAGCCT	1978
1981	Qy	GCTCTCTTGTCTTCTCTGTTTCAATTTGTGTTCTTCGCCCTGCTGGGATGAGCTGTTTGG	2040
1979	Db	GCTCTCTTGTCTTCTCTGTTTCAATTTGTGTTCTTCGCCCTGCTGGGATGAGCTGTTTGG	2038
2041	Qy	GGGACAGTTCAACTTCCAGGATGAGACTCCCAACAACCAACTTTCGACACCTTCCCTGCGCG	2100
2039	Db	GGGACAGTTCAACTTCCAGGATGAGACTCCCAACAACCAACTTTCGACACCTTCCCTGCGCG	2098
2101	Qy	CATCTCTCACTGTCTTCCAGATCTCTGACGGGAGAGGACTGGAATGCAGTGTATCACGG	2160
2099	Db	CATCTCTCACTGTCTTCCAGATCTCTGACGGGAGAGGACTGGAATGCAGTGTATCACGG	2158
2161	Qy	GATCGAATCGAAGCGGCGTTCAGCAAAAGCATGTTCTCGTCTCTTTTACTTTCATTGTCTCT	2220
2159	Db	GATCGAATCGAAGCGGCGTTCAGCAAAAGCATGTTCTCGTCTCTTTTACTTTCATTGTCTCT	2218
2221	Qy	GACACTGTTCCGAAACTPACACTCTGCTGTAATGTTCTTTTCGCCCATCGCTGTGGACAACCT	2280
2219	Db	GACACTGTTCCGAAACTPACACTCTGCTGTAATGTTCTTTTCGCCCATCGCTGTGGACAACCT	2278
2281	Qy	GGCCACCGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAAGACGCCCAATCAGAA	2340
2279	Db	GGCCACCGCCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAAGACGCCCAATCAGAA	2338
2341	Qy	GCTTGTCTTCGAAAAGGCCAAAGAGTGGCTGAAGTCAGCCCCCATGTTCTCCGCGGAACAT	2400
2339	Db	GCTTGTCTTCGAAAAGGCCAAAGAGTGGCTGAAGTCAGCCCCCATGTTCTCCGCGGAACAT	2398

QY 2401 CTCCATCGCGCCGAGCAGCAGAACTCGGCCAAGGCGCGCTCGGTGTGGGAGCAGCGGC 2460
DB |||||
QY 2399 CTCATCGCGCCGAGGAGCAGAGAACTCGGCCAAGGCGCGCTCGGTGTGGGAGCAGCGGC 2458
DB |||||
QY 2461 CAGCAGCTACGGCTCGAGAACTCGCGGGCAGCTCGGAGGCGCTGTGACAGCGAGATGA 2520
DB |||||
QY 2459 CAGCCAGCTACGGCTCGAGAACTCGCGGGCAGCTCGGAGGCGCTGTGACAGCGAGATGA 2518
DB |||||
QY 2521 CCCGAGGAGCGGCTCGCTTCGCCACTACGCGCCACCTGCGGCCCGGACATCAAGACCA 2580
DB |||||
QY 2519 CCCGAGGAGCGGCTCGCTTCGCCACTACGCGCCACCTGCGGCCCGGACATCAAGACCA 2578
DB |||||
QY 2581 CTTGAGACCGCGCTCGTGTGTGAGCTGGGCGCGGACCGCGCGCGCGGCGCGCTGGGAGG 2640
DB |||||
QY 2579 CTTGAGACCGCGCTCGTGTGTGAGCTGGGCGCGGACCGCGCGCGCGGCGCGCTGGGAGG 2638
DB |||||
QY 2641 CAAAGCCGACCTGAGGCTCGGAGGCGCCCGGAGGCGCTGACACCTTCGCGCAGGACCA 2700
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QY 2639 CAAAGCCGACCTGAGGCTCGGAGGCGCCCGGAGGCGCTGACACCTTCGCGCAGGACCA 2698
DB |||||
QY 2701 CCGGACCCGCGACAGGACAAAGACCCCGCGCGGGGACAGGACCGGAGAGGCGCC 2760
DB |||||
QY 2699 CCGGACCCGCGACAGGACAAAGACCCCGCGCGGGGACAGGACCGGAGAGGCGCC 2758
DB |||||
QY 2761 GAAAGCGGAGAGCGGGGAGCCCGGTGCCCGGAGGAGGCGCGCGCGCCACCGCAGCCA 2820
DB |||||
QY 2759 GAAAGCGGAGAGCGGGGAGCCCGGTGCCCGGAGGAGGCGCGCGCGCCACCGCAGCCA 2818
DB |||||
QY 2821 CAGCAAGGAGGCGCGGGGCGCCCGGAGCGCGGAGCGCGCGCGCCACCGCAGGCC 2880
DB |||||
QY 2819 CAGCAAGGAGGCGCGGGGCGCCCGGAGCGCGGAGCGCGCGCGCCACCGCAGGCC 2878
DB |||||
QY 2881 CGAGGCGCGCGCGCGCACACCGCGCGCGCTCCCGAGGAGGCGCGCGCGGAGCC 2940
DB |||||
QY 2879 CGAGGCGCGCGCGCGCACACCGCGCGCGCTCCCGAGGAGGCGCGCGCGGAGCC 2938
DB |||||
QY 2941 CCGACGCGACCGCGCGCACCGGACACAGGATCCGAGCAGAGGAGTGCGCGCGCGCAAGGG 3000
DB |||||
QY 2939 CCGACGCGACCGCGCGCACCGGACACAGGATCCGAGCAGAGGAGTGCGCGCGCGCAAGGG 2998
DB |||||
QY 3001 CGAGCGCGCGCGCGCACCGCGCGCGCCCGCGAGCGGGCGCGCGCGGAGCGG 3060
DB |||||
QY 2999 CGAGCGCGCGCGCGCACCGCGCGCGCCCGCGAGCGGGCGCGCGCGGAGCGG 3058
DB |||||
QY 3061 GGAGAGCGCGCGCGCGCACCGCGCGCGGACAAAGCGCGAGCGCTGCTCAAGAGGCTGT 3120
DB |||||
QY 3059 GGAGAGCGCGCGCGCGCACCGCGCGCGGACAAAGCGCGAGCGCTGCTCAAGAGGCTGT 3118
DB |||||
QY 3121 GGAGAGGAGCACCGGAGAGGAGGCCACCGAGAGGAGGCTGAGATAGTGGAGCGCA 3180
DB |||||
QY 3119 GGAGAGGAGCACCGGAGAGGAGGCCACCGAGAGGAGGCTGAGATAGTGGAGCGCA 3178
DB |||||
QY 3181 CAAGGAAAAGGAGCTCCGGAAACCAACCGCGGAGGCCACACTGTGACCTGGAGACCA 3240
DB |||||
QY 3179 CAAGGAAAAGGAGCTCCGGAAACCAACCGCGGAGGCCACACTGTGACCTGGAGACCA 3238
DB |||||
QY 3241 TGGGACTGTGAGTGTGGTTCATGCAACACTGCGCCAGCACACTGTCTCCAGAGGTTGA 3300
DB |||||
QY 3239 TGGGACTGTGAGTGTGGTTCATGCAACACTGCGCCAGCACACTGTCTCCAGAGGTTGA 3298
DB |||||
QY 3301 GGACAGCGCAGAGGATGAGACATACGCGGACGTCACTCGCATGGCAGTCAAGCCCC 3360
DB |||||
QY 3299 GGACAGCGCAGAGGATGAGACATACGCGGAAAGTCACTCGCATGGCAGTCAAGCCCC 3358
DB |||||
QY 3361 AGACCCGAACACTATTGTACATATCCCAAGTATGCTGACGGGCGCTCTTGGGGAGGCC 3420
DB |||||
QY 3359 AGACCCGAACACTATTGTACATATCCCAAGTATGCTGACGGGCGCTCTTGGGGAGGCC 3418
DB |||||
QY 3421 GGTGTTCCAGTGTGATGAGCTGGAAAGCCCAAGAGGAGGAGGAGGTTGA 3480
DB |||||
QY 3419 GGTGTTCCAGTGTGATGAGCTGGAAAGCCCAAGAGGAGGAGGAGGTTGA 3478

QY 3481 AGCGGATGACGTGATGAGGAGCGGCCCGGCGCTATCGTCCATACAGCTCATGTTCTG 3540
DB |||||
QY 3479 AGCGGATGACGTGATGAGGAGCGGCCCGGCGCTATCGTCCATACAGCTCATGTTCTG 3538
DB |||||
QY 3541 TTTAAGCCCCAACCTGTCTCGGCCCTTCTGCCACTACATCGTGACCATGAGGTACTT 3600
DB |||||
QY 3539 TTTAAGCCCCAACCTGTCTCGGCCCTTCTGCCACTACATCGTGACCATGAGGTACTT 3598
DB |||||
QY 3601 CGAGGTGTCATCTTCGTGTCATCGGCTTGAGCAGCATCGCCCTGCTGCTGAGGACCC 3660
DB |||||
QY 3599 CGAGGTGTCATCTTCGTGTCATCGGCTTGAGCAGCATCGCCCTGCTGCTGAGGACCC 3658
DB |||||
QY 3661 AGTCGCGACAGACTCGGCCAGGAAACAGCTCTGAAATACCTGGAATACATTTTCACTGG 3720
DB |||||
QY 3659 AGTCGCGACAGACTCGGCCAGGAAACAGCTCTGAAATACCTGGAATACATTTTCACTGG 3718
DB |||||
QY 3721 TGTCTTTACCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780
DB |||||
QY 3719 TGTCTTTACCTTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3778
DB |||||
QY 3781 AGCCTATTTCCGGGACTTGTGGACATTTCTGGACTTCAATTTGTTGTTGTTGTTGTTGTTGTT 3840
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QY 3779 AGCCTATTTCCGGGACTTGTGGACATTTCTGGACTTCAATTTGTTGTTGTTGTTGTTGTTGTT 3838
DB |||||
QY 3841 GGCCTTTGCTTTCTCGAGCTTCTGCGGAGGATCCAAAGGAGGAAAGACATCAATACCATCAA 3900
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QY 3839 GGCCTTTGCTTTCTC-----AGGATCCAAAGGAGGAAAGACATCAATACCATCAA 3886
DB |||||
QY 3901 GTCTCTGAGAGTCTTCTGTTCTCTGCGGCCCTTCAGAGCATCAAAAGGCTGCGCCAAAGCT 3960
DB |||||
QY 3887 GTCTCTGAGAGTCTTCTGTTCTCTGCGGCCCTTCAGAGCATCAAAAGGCTGCGCCAAAGCT 3946
DB |||||
QY 3961 CAAGGCTGTCTTTGACTGTGTGTGAACTCCCTGAAAGAAATGCTCAAACTTTGATGTT 4020
DB |||||
QY 3947 CAAGGCTGTCTTTGACTGTGTGTGAACTCCCTGAAAGAAATGCTCAAACTTTGATGTT 4006
DB |||||
QY 4021 CTACATGCTCTTTCATGTTTCATATTTCCGCTCATTTGCGGTGACGCTCTTCAAGGGAAGTT 4080
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QY 4007 CTACATGCTCTTTCATGTTTCATATTTCCGCTCATTTGCGGTGACGCTCTTCAAGGGAAGTT 4066
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QY 4081 TTTCTACTGACAGATGAATCCAAAGAGCTGGAGAGGAGCTGAGGGGCTGATTTTGA 4140
DB |||||
QY 4067 TTTCTACTGACAGATGAATCCAAAGAGCTGGAGAGGAGCTGAGGGGCTGATTTTGA 4126
DB |||||
QY 4141 TTATGAGAGGAGGAGTGAAGCTCAGCCAGGCTGGAAGAAATACGCTTTTCACTA 4200
DB |||||
QY 4127 TTATGAGAGGAGGAGTGAAGCTCAGCCAGGCTGGAAGAAATACGCTTTTCACTA 4186
DB |||||
QY 4201 CGAATATGCTCTGCGGCTCTGCTGACGCTGTTTCAAGTGTCCACGCGGAGAGGCTGGCC 4260
DB |||||
QY 4187 CGAATATGCTCTGCGGCTCTGCTGACGCTGTTTCAAGTGTCCACGCGGAGAGGCTGGCC 4246
DB |||||
QY 4261 CATGGTGTGAACACTCCGTGGATGCGACCTATGAGGAGGAGGCTGGAAGGCTGGCTGGCT 4320
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QY 4247 CATGGTGTGAACACTCCGTGGATGCGACCTATGAGGAGGAGGCTGGAAGGCTGGCTGGCT 4306
DB |||||
QY 4321 CCGCATGAGGCTGTCCACTCTTACCTGCTGCTACTTTGTTGTTGTTTCCCTTCTTCTTCTG 4380
DB |||||
QY 4307 CCGCATGAGGCTGTCCACTCTTCTACGCTGCTACTTTTGTGTTTCTTCTTCTTCTTCTG 4366
DB |||||
QY 4381 CAACATCTTTGTTGCTTTGATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4440
DB |||||
QY 4367 CAACATCTTTGTTGCTTTTGTATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 4426
DB |||||
QY 4441 TGAATCAGCTGGAGAGAAAGAGAGGCTTGTGATTTGACTTTCGCCATCAGCGCCAAACC 4500
DB |||||
QY 4427 TGAATCAGCTGGAGAGAAAGAGAGGCTTGTGATTTGACTTTCGCCATCAGCGCCAAACC 4486
DB |||||
QY 4501 CTTGACACCGGTATGTCGCCCAAAACCGGAGCTGTTTCCAGTATAAGACGTGAGCACTTTGT 4560
DB |||||
QY 4487 CTTGACACCGGTATGTCGCCCAAAACCGGAGCTGTTTCCAGTATAAGACGTGAGCACTTTGT 4546
DB |||||
QY 4561 GGTCTCCCGCCCTTTGTAATCTTTCATCATGCGCCATGATAGCCCTCAACACTGTGTGTGCT 4620

Db	4547		GGTCTCCCCGCCCTTTGAATACCTTCATCATGCCCATGATGCCCTCAACACTGFGTGCT	4606
Qy	4621		GATGATGAAGTCTTATGATGACACCTATGATGACGCTGATGCTGAAATGCCTGAACAT	4680
Db	4607		GATGATGAAGTCTTATGATGACACCTATGATGACGCTGATGCTGAAATGCCTGAACAT	4666
Qy	4681		CGTGTTCACATCCATGTTCTCATGGAATGCGTCTGAAGATCATCGCTTTGGGGTGCT	4740
Db	4667		CGTGTTCACATCCATGTTCTCATGGAATGCGTCTGAAGATCATCGCTTTGGGGTGCT	4726
Qy	4741		GAACTATTTACAGATCGCTGGAATGCTTTGACTTTGCTCACTGTGTTGGGAAGTATTAC	4800
Db	4727		GAACTATTTACAGATCGCTGGAATGCTTTGACTTTGCTCACTGTGTTGGGAAGTATTAC	4786
Qy	4801		TGATATTTTATGATAACAGAGATTTGGGAAACGAAACAAATTTATCAACCTCAGCTTCCTCCG	4860
Db	4787		TGATATTTTATGATAACAGAGATTTGGGAAACGAAACAAATTTATCAACCTCAGCTTCCTCCG	4846
Qy	4861		CCTCTTTGAGCTCGCGGCTGATCAAGCTGCTCCGCCAGGGCTACACCATTCGCATCCT	4920
Db	4847		CCTCTTTGAGCTCGCGGCTGATCAAGCTGCTCCGCCAGGGCTACACCATTCGCATCCT	4906
Qy	4921		GCTGTGACCTTTTGCAGTCCCTCAAGGCCCTGCCCTACGTGTGCTGCTCATTTGCCAT	4980
Db	4907		GCTGTGACCTTTTGCAGTCCCTCAAGGCCCTGCCCTACGTGTGCTGCTCATTTGCCAT	4966
Qy	4981		GCTGTCTTCTATCTACGCCATCATCGGCATCGAGTGTGTTGGGAATATTTGCCCTGGATGA	5040
Db	4967		GCTGTCTTCTATCTACGCCATCATCGGCATCGAGTGTGTTGGGAATATTTGCCCTGGATGA	5026
Qy	5041		TGACACAGCATCAACGCCCAACAACTTCCCGACGTTTTTGAAGCCCTGATGTGCT	5100
Db	5027		TGACACAGCATCAACGCCCAACAACTTCCCGACGTTTTTGAAGCCCTGATGTGCT	5086
Qy	5101		GTTTCAGGAGCCCAAGGGGAGGCTGGCAGAGATCATGTGTGCTGCTGAGCAACCA	5160
Db	5087		GTTTCAGGAGCCCAAGGGGAGGCTGGCAGAGATCATGTGTGCTGCTGAGCAACCA	5146
Qy	5161		GGCTGTGTATGAGCAGGCGCAATGCCACCGAGTGTGGAAGTACATTTGCTACTTCTACTT	5220
Db	5147		GGCTGTGTATGAGCAGGCGCAATGCCACCGAGTGTGGAAGTACATTTGCTACTTCTACTT	5206
Qy	5221		CGTCTCCTTCTATCTTCCTGTGCTCCTTTCTGATGTTGAACCTCTTTGTGGCTGATCAT	5280
Db	5207		CGTCTCCTTCTATCTTCCTGTGCTCCTTTCTGATGTTGAACCTCTTTGTGGCTGATCAT	5266
Qy	5281		GGACAAATTTTGAATACCTCAGCGGGACTCTTCCATCTAGGTCTCACCACCTTGGATGA	5340
Db	5267		GGACAAATTTTGAATACCTCAGCGGGACTCTTCCATCTAGGTCTCACCACCTTGGATGA	5326
Qy	5341		GTTTCATCCGGTCTGGGCTGAATACGACCCGGCTCGTGTGGGCGCATCAGTTACAATGA	5400
Db	5327		GTTTCATCCGGTCTGGGCTGAATACGACCCGGCTCGTGTGGGCGCATCAGTTACAATGA	5386
Qy	5401		CATGTTTGAATGCTGAAACACATGTCCCCGCCCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460
Db	5387		CATGTTTGAATGCTGAAACACATGTCCCCGCCCTCTGGGGCTGGGGAAGAAATGCCCTGC	5446
Qy	5461		TCGAGTTGCTTTAAGAGCCCTGGTTCCGATGAACATGCCCATCTCCAACCGAGGACATGAC	5520
Db	5447		TCGAGTTGCTTTAAGAGCCCTGGTTCCGATGAACATGCCCATCTCCAACCGAGGACATGAC	5506
Qy	5521		TGTTTCACTTCAGTCCAGCTGATGGCCCTCATCCGAGCGCATCTGGAGATCAAGCTGGC	5580
Db	5507		TGTTTCACTTCAGTCCAGCTGATGGCCCTCATCCGAGCGCATCTGGAGATCAAGCTGGC	5566
Qy	5581		CCCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCCGTTGT	5640
Db	5567		CCCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCCGTTGT	5626
Qy	5641		GTGGGCCATCTGCCCCGAAAGACTTTTGGACTTGTGCTAGTGATCCACCCCATTAAGCCTGATGA	5700

Db	5627		GTGGGCCAATCTGCCCCAGAGACTTTTGGACTTGTGCTGGTACCACCCCATTAAGCCTGATGA	5686
Qy	5701		GATGACAGTGGGAAAGTTTTATCAGCTCTGATGATATTTTGACTTTTACAAAGCAGAACAA	5760
Db	5687		GATGACAGTGGGAAAGTTTTATCAGCTCTGATGATATTTTGACTTTTACAAAGCAGAACAA	5746
Qy	5761		AACCAACAGAGACACAGATGACAGCAGGCTCCTGAGAGGCTTCTCCAGATGGGTCTGTGTC	5820
Db	5747		AACCAACAGAGACACAGATGACAGCAGGCTCCTGAGAGGCTTCTCCAGATGGGTCTGTGTC	5806
Qy	5821		CCTGTTTCCACCTCTGAAGGCCACCTTGAGAGCAGACACAGCCGGCTGTCTCCGAGGAGC	5880
Db	5807		CCTGTTTCCACCTCTGAAGGCCACCTTGAGAGCAGACACAGCCGGCTGTCTCCGAGGAGC	5866
Qy	5881		CCGGGTTTTCTTCGACAGAAAGTTCACCTCCCTCAGCAATGGGGGGGCCATACAAAA	5940
Db	5867		CCGGGTTTTCTTCGACAGAAAGTTCACCTCCCTCAGCAATGGGGGGGCCATACAAAA	5926
Qy	5941		CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC	6000
Db	5927		CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAAGGACCCAGGATGCACC	5986
Qy	6001		CCATGAGGCCAGGCCACCCCTGAGAGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6060
Db	5987		CCATGAGGCCAGGCCACCCCTGAGAGTGGCCACTCCACAGAGATCCCTGTGGGGCGGTC	6046
Qy	6061		AGGAGCACTGGCTGTGTGACGTTTCAGATGACAGATCAACCCGGAGGGGCCCTTGATGGGA	6120
Db	6047		AGGAGCACTGGCTGTGTGACGTTTCAGATGACAGATCAACCCGGAGGGGCCCTTGATGGGA	6106
Qy	6121		GCCCCAGCTTGGGCTTGAGAGCCAGGGTTCAGAGGCTCCATGCTGCGGCCCTTGGGGCCGA	6180
Db	6107		GCCCCAGCTTGGGCTTGAGAGCCAGGGTTCAGAGGCTCCATGCTGCGGCCCTTGGGGCCGA	6166
Qy	6181		GACTCAGCCGCTCACAGATGCCAGCCCATGAAGCGCTCCATCTTCCACGCTGGCCACGCG	6240
Db	6167		GACTCAGCCGCTCACAGATGCCAGCCCATGAAGCGCTCCATCTTCCACGCTGGCCACGCG	6226
Qy	6241		GCCCCGTGGGACTCATCTTTTGACAGCACACCCCGGACCGGCCACCCCTTAGCCAGGCGTC	6300
Db	6227		GCCCCGTGGGACTCATCTTTTGACAGCACACCCCGGACCGGCCACCCCTTAGCCAGGCGTC	6286
Qy	6301		GTCGCACACACACACACACCGCTGCCACCGCCGAGGGACAGGAGCAGAGTCCCTGGA	6360
Db	6287		GTCGCACACACACACACACCGCTGCCACCGCCGAGGGACAGGAGCAGAGTCCCTGGA	6346
Qy	6361		GAAGGGSCCAGAGCTGTCTGCCGATATGATGCGCACCAAGCAGTCTCTGTGGGGCCGGG	6420
Db	6347		GAAGGGSCCAGAGCTGTCTGCCGATATGATGCGCACCAAGCAGTCTCTGTGGGGCCGGG	6406
Qy	6421		GCTGCCCCCGGAGAGGGGCTTACAGGCTGCCCGCGGGAACGAGAGCGCCGCGAGGAGCG	6480
Db	6407		GCTGCCCCCGGAGAGGGGCTTACAGGCTGCCCGCGGGAACGAGAGCGCCGCGAGGAGCG	6466
Qy	6481		GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCTCTCGGAGAAAGCAGCGCTTCTA	6540
Db	6467		GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCTCTCGGAGAAAGCAGCGCTTCTA	6526
Qy	6541		CTCTCTGACCGCTTTGGGGCGCTGAGCCCCCGAGGCCCAAGCCCTCCCTCAGCAGCCCA	6600
Db	6527		CTCTCTGACCGCTTTGGGGCGCTGAGCCCCCGAGGCCCAAGCCCTCCCTCAGCAGCCCA	6586
Qy	6601		CCCAACGCTCCCAACAGCTGGCCAGGAGCGGACCCCAACCCACAGGGCAGTGGTTCGCT	6660
Db	6587		CCCAACGCTCCCAACAGCTGGCCAGGAGCGGACCCCAACCCACAGGGCAGTGGTTCGCT	6646
Qy	6661		GAATGGAGGCCCTTGTGTCAACATCTGTGTGTAGCACCCCCGGCCGCGGTTGGGGGAG	6720
Db	6647		GAATGGAGGCCCTTGTGTCAACATCTGTGTGTAGCACCCCCGGCCGCGGTTGGGGGAG	6706
Qy	6721		GCAGCTCCCCCAGACGCCCTGACTCCCCGCCCCAGCATCACCTACAAAGACGCCAACTC	6780
Db	6707		GCAGCTCCCCCAGACGCCCTGACTCCCCGCCCCAGCATCACCTACAAAGACGCCAACTC	6766

FEATURE:									
NAME/KEY: 3'UTR									
LOCATION: 7161...7362									
US-08-450-562-7									
Query Match 99.2%; Score 7316.4; DB 3; Length 7362;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;									
Qy	1	GC	GC	GC	GC	GC	GC	GC	GC
Db	1	GC	GC	GC	GC	GC	GC	GC	GC
Qy	61	GCT	GCT	CGCT	CGCT	CGCT	CGCT	CGCT	CGCT
Db	60	GCT	GCT	CGCT	CGCT	CGCT	CGCT	CGCT	CGCT
Qy	121	GGG	ATG	CAC	GGG	GGG	GGG	GGG	GGG
Db	119	GGG	ATG	CAC	GGG	GGG	GGG	GGG	GGG
Qy	181	TGA	AGG	CCC	CGG	CGG	CGG	CGG	CGG
Db	179	TGA	AGG	CCC	CGG	CGG	CGG	CGG	CGG
Qy	241	GGG	TC	CGG	GGG	GGG	GGG	GGG	GGG
Db	239	GGG	TC	CGG	GGG	GGG	GGG	GGG	GGG
Qy	301	CGG	CGG	ACCAT	GGG	GGG	GGG	GGG	GGG
Db	299	CGG	CGG	ACCAT	GGG	GGG	GGG	GGG	GGG
Qy	361	CGG	TC	CGCT	CGG	CGG	CGG	CGG	CGG
Db	359	CGG	TC	CGCT	CGG	CGG	CGG	CGG	CGG
Qy	421	CGA	GTG	CCCT	CGA	GTG	CCCT	CGA	GTG
Db	419	CGA	GTG	CCCT	CGA	GTG	CCCT	CGA	GTG
Qy	481	GGC	CTT	GGG	GGG	GGG	GGG	GGG	GGG
Db	479	GGC	CTT	GGG	GGG	GGG	GGG	GGG	GGG
Qy	541	CAC	GGG	CCCT	ATG	ATG	ATG	ATG	ATG
Db	539	CAC	GGG	CCCT	ATG	ATG	ATG	ATG	ATG
Qy	601	GGG	CTT	GGT	CTT	GGT	CTT	GGT	CTT
Db	599	GGG	CTT	GGT	CTT	GGT	CTT	GGT	CTT
Qy	661	GCT	CGT	CGT	CGT	CGT	CGT	CGT	CGT
Db	659	GCT	CGT	CGT	CGT	CGT	CGT	CGT	CGT
Qy	721	GGT	GTG	GGT	GTG	GGT	GTG	GGT	GTG
Db	719	GGT	GTG	GGT	GTG	GGT	GTG	GGT	GTG
Qy	781	GCT	CAAGT	CCAT	CAAGT	CCAT	CAAGT	CCAT	CAAGT
Db	779	GCT	CAAGT	CCAT	CAAGT	CCAT	CAAGT	CCAT	CAAGT
Qy	841	TGC	CAAT	CGT	CGT	CGT	CGT	CGT	CGT
Db	839	TGC	CAAT	CGT	CGT	CGT	CGT	CGT	CGT
Qy	901	CTG	TTT	CCC	AAAG	CCG	CCG	CCG	CCG
Db	899	CTG	TTT	CCC	AAAG	CCG	CCG	CCG	CCG

Qy	961	CCC	AGC	CGG	CTG	CGA	GGG	CGA	CACT
Db	959	CCC	AGC	CGG	CTG	CGA	GGG	CGA	CACT
Qy	1021	TGC	ATC	CAAC	CTT	TGA	CAAT	CTC	TGT
Db	1019	TGC	ATC	CAAC	CTT	TGA	CAAT	CTC	TGT
Qy	1081	CAT	GAG	GGG	CTG	CAAT	CTC	TAT	ATA
Db	1079	CAT	GAG	GGG	CTG	CAAT	CTC	TAT	ATA
Qy	1141	CTG	CTT	CAAT	CTC	TAT	ATA	CAAA	CGAT
Db	1139	CTG	CTT	CAAT	CTC	TAT	ATA	CAAA	CGAT
Qy	1201	GGG	CGT	GGT	CTT	CGG	GGG	AGT	TTG
Db	1199	GGG	CGT	GGT	CTT	CGG	GGG	AGT	TTG
Qy	1261	CCT	GAA	AGT	CGC	CGC	CGC	CGC	CGC
Db	1259	CCT	GAA	AGT	CGC	CGC	CGC	CGC	CGC
Qy	1321	CTT	CAAG	CGG	AGG	AGT	CAAT	CGG	AGG
Db	1319	CTT	CAAG	CGG	AGG	AGT	CAAT	CGG	AGG
Qy	1381	TTT	GGA	CGT	GGT	CTT	CGG	GGG	AGT
Db	1379	TTT	GGA	CGT	GGT	CTT	CGG	GGG	AGT
Qy	1441	GGA	GGG	AGG	AGT	CGG	GGT	CTT	CGG
Db	1439	GGA	GGG	AGG	AGT	CGG	GGT	CTT	CGG
Qy	1501	CCT	CAAG	CGG	AGG	AGT	CAAT	CGG	AGG
Db	1499	CCT	CAAG	CGG	AGG	AGT	CAAT	CGG	AGG
Qy	1561	GTG	TTT	ATC	CGG	CGG	CGG	CGG	CGG
Db	1559	GTG	TTT	ATC	CGG	CGG	CGG	CGG	CGG
Qy	1621	GGC	CTT	GAA	CAC	ACT	GTG	GGT	GGT
Db	1619	GGC	CTT	GAA	CAC	ACT	GTG	GGT	GGT
Qy	1681	GAC	CTT	GAT	TTT	TGA	AGT	TTG	TTG
Db	1679	GAC	CTT	GAT	TTT	TGA	AGT	TTG	TTG
Qy	1741	GAT	GAT	GGC	CTT	GGG	CGG	CGG	CGG
Db	1739	GAT	GAT	GGC	CTT	GGG	CGG	CGG	CGG
Qy	1801	GGT	CAT	CGT	GGG	AGG	AGT	CTT	CTT
Db	1799	GGT	CAT	CGT	GGG	AGG	AGT	CTT	CTT
Qy	1861	TGG	GAT	CAG	TGT	CGT	CGG	CGG	CGG
Db	1859	TGG	GAT	CAG	TGT	CGT	CGG	CGG	CGG
Qy	1921	GAC	CTT	CGG	AGG	AGT	CTT	CGG	AGG
Db	1919	GAC	CTT	CGG	AGG	AGT	CTT	CGG	AGG
Qy	1981	GCT	CTT	CTT	CTT	CTT	CTT	CTT	CTT
Db	1979	GCT	CTT	CTT	CTT	CTT	CTT	CTT	CTT
Qy	2041	GGG	ACG	ATT	CAACT	TCG	AGG	ATG	AGG
Db	2038	GGG	ACG	ATT	CAACT	TCG	AGG	ATG	AGG

Db	2039	GGGACAGTTCAA	CTTCCAGGATGAG	ATCCCAACAACAA	CTTCGACACCTT	CCCTGCGCG	2098
Qy	2101	CATCCTCACTGT	CTTCTCCAGATC	CTGACGGGAGAG	AGACTGGAATGC	AGTGTATCACGG	2160
Db	2099	CATCCTCACTGT	CTTCTCCAGATC	CTGACGGGAGAG	AGACTGGAATGC	AGTGTATCACGG	2158
Qy	2161	GATCGMATCGA	AGCGGCGCTCAG	CAAAAGGCATG	TTCTGTCCTTTT	TACTTCATTGTCCT	2220
Db	2159	GATCGAATCGA	AGCGGCGGTCAG	CAAAAGGCATG	TTCTGTCCTTTT	TACTTCATTGTCCT	2218
Qy	2221	GACACTGTTTC	GAAACTACACT	CTGCTGAAATG	TTCTTCTGGCCAT	CGCTGTGGACAACCT	2280
Db	2219	GACACTGTTTC	GAAACTACACT	CTGCTGAAATG	TTCTTCTGGCCAT	CGCTGTGGACAACCT	2278
Qy	2281	GGCCAAAGCC	CAAGAGCTGAC	CAAGGATGAAG	AGGAGATGAAGA	AGAGCCCAATCAGAA	2340
Db	2279	GGCCAAAGCC	CAAGAGCTGAC	CAAGGATGAAG	AGGAGATGAAGA	AGAGCCCAATCAGAA	2338
Qy	2341	GCTTGTCTCTG	CAAAAGGCCAA	AGAGTGCGT	TGAAGTCAGCC	CATGTCGCCGCAACAT	2400
Db	2339	GCTTGTCTCTG	CAAAAGGCCAA	AGAGTGCGT	TGAAGTCAGCC	CATGTCGCCGCAACAT	2398
Qy	2401	CTCCATCGCG	CCAGGACAGAA	ACTCGGCCAAG	CGCCGCTCGGT	TGGAGCAGCGGGC	2460
Db	2399	CTCCATCGCG	CCAGGACAGAA	ACTCGGCCAAG	CGCCGCTCGGT	TGGAGCAGCGGGC	2458
Qy	2461	CAGCCAGTAC	GGCTGAGACCT	GCGGCGCAGT	GCGAGCGCTG	TACAGCAGATGGA	2520
Db	2459	CAGCCAGTAC	GGCTGAGACCT	GCGGCGCAGT	GCGAGCGCTG	TACAGCAGATGGA	2518
Qy	2521	CCCCAGGAG	CGGCTGGCCACT	TACGCGCAC	CTCGGCGCCG	CACATGAAGACGA	2580
Db	2519	CCCCAGGAG	CGGCTGGCCACT	TACGCGCAC	CTCGGCGCCG	CACATGAAGACGA	2578
Qy	2581	CCTTGGACGG	CGCCGTGTGTG	AGCTTGCGCG	CGCAGCGG	CGGGGGGCCCTGGGAGG	2640
Db	2579	CCTTGGACGG	CGCCGTGTGTG	AGCTTGCGCG	CGCAGCGG	CGGGGGGCCCTGGGAGG	2638
Qy	2641	CAAAAGCCG	ACCTGAGGCT	CGGAGGGCC	CCGAGGGCGT	CGACCTCCGCGCAGGACCA	2700
Db	2639	CAAAAGCCG	ACCTGAGGCT	CGGAGGGCC	CCGAGGGCGT	CGACCTCCGCGCAGGACCA	2698
Qy	2701	CCGGCAACCG	CGCAAAAGCA	ACCCCGCGGG	GGGACCAAGG	ACCGAGCAGAGACCCC	2760
Db	2699	CCGGCAACCG	CGCAAAAGCA	ACCCCGCGGG	GGGACCAAGG	ACCGAGCAGAGACCCC	2758
Qy	2761	GAAGCGGAG	AGCGGGAGCC	CGGTGCCG	CGGAGGAGCG	CGCGCCGACCGCAGCCA	2820
Db	2759	GAAGCGGAG	AGCGGGAGCC	CGGTGCCG	CGGAGGAGCG	CGCGCCGACCGCAGCCA	2818
Qy	2821	CAGCAAGGAG	CGCGGGGCC	CCCGGAGGCG	CGGAGCGAGC	CGCGGCCGAGGCCAGGCC	2880
Db	2819	CAGCAAGGAG	CGCGGGGCC	CCCGGAGGCG	CGGAGCGAGC	CGCGGCCGAGGCCAGGCC	2878
Qy	2881	CGAGGGCGCG	CGCGCACCA	CCGGCGCGCT	CCCCGAGGAG	CGCGCGCGAGCGG	2940
Db	2879	CGAGGGCGCG	CGCGCGCAC	CAACCGCGCGCT	CCCCGAGGAG	CGCGCGCGAGCGG	2938
Qy	2941	CCGACGCCAC	CGCGCGCAC	CCGGCACCA	GAGATCCGAG	CAAGGAGTGGCCGGCCCAAGGG	3000
Db	2939	CCGACGCCAC	CGCGCGCGCAC	CCGGCACCA	GAGATCCGAG	CAAGGAGTGGCCGGCCCAAGGG	2998
Qy	3001	CGAGCGCGCG	CGCGGACCG	CGCGCGGCC	CCCCCGAG	CGGGGCCCGCGGAGCGG	3060
Db	2999	CGAGCGCGCG	CGCGGACCG	CGCGCGGCC	CCCCCGAG	CGGGGCCCGCGGAGCGG	3058
Qy	3061	GGAGGAGCCG	CGCGCGGAC	CCGGGCCCGG	CACAAAGGCG	CAGCTGTCTCACAGAGGCTGT	3120
Db	3059	GGAGGAGCCG	CGCGCGGAC	CCGGGCCCGG	CACAAAGGCG	CAGCTGTCTCTCACAGAGGCTGT	3118
Qy	3121	GGAGAGGAG	ACCAAGGAGG	CCACGGAGAG	AGGAGGTGA	TATAGTGAAGCCGA	3180

3119	GGAGAACGAGACACCGAGAGGAGGCCACGAGAAAGAGGCTGAGATAGTGGAAGCCGA	3179
3181	CAAGGAAAAGGAGCTCGGGAACACACGAGCCCCGGGAGCCACACTGTGACCTGGAGACCCAG	3240
3179	CAAGGAAAAGGAGCTCGGGAACACACGAGCCCCGGGAGCCACACTGTGACCTGGAGACCCAG	3238
3241	TGGGACTGTGACTGTGGGTCCCATGACACACTGCCCCAGCACCTGTCTCCAGNAGGTGA	3300
3239	TGGGACTGTGACTGTGGGTCCCATGACACACTGCCCCAGCACCTGTCTCCAGNAGGTGA	3298
3301	GGAAACGCCAGAGGATGCAGACAATCAGGGGAACGTCACTCGCATGGCAGTCCAGGCCCCC	3360
3299	GGAAACGCCAGAGGATGCAGACAATCAGGGGAACGTCACTCGCATGGGCGAGTTCAGCCCCC	3358
3361	AGACCCGAAACACTATTGTATCATATCCACGTGATGTGACGGGCCCCCTTTGGGAAAGCCAC	3420
3359	AGACCCGAAACACTATTGTATCATATCCACGTGATGTGACGGGCCCCCTTTGGGAAAGCCAC	3418
3421	GGTCGTTCCAGTGTAAAGTGGACCTGGAAGCCAGAGGAGGGAAGAGAGGTGA	3480
3419	GGTCGTTCCAGTGTGTAAAGTGGACCTGGAAGCCAGAGGAGGGAAGAGAGGTGA	3478
3481	AGCGGATGACGTGATGAGGAGCGGCCCGCGGCTATCGTCCCATACAGCTCCCATGTTCTG	3540
3479	AGCGGATGACGTGATGAGGAGCGGCCCGCGGCTATCGTCCCATACAGCTCCCATGTTCTG	3538
3541	TTTTAAGCCCCAACCACTGCTCGCGCGCTTTCGCCNCTACATCATGTGACCATGAGTACTTT	3600
3539	TTTTAAGCCCCAACCACTGCTCGCGCGCTTTCGCCNCTACATCATGTGACCATGAGTACTTT	3598
3601	CGAGGTGGTCAATTCCTCGTGGTCACTCGCCTTGAGCAGCATCGGCCCTGGCTGTGAGGACCC	3660
3599	CGAGGTGGTCAATTCCTCGTGGTCACTCGCCTTGAGCAGCATCGGCCCTGGCTGTGAGGACCC	3658
3661	AGTGGCGACAGACTCCGCCAGGAAACACGCTCTGAATACCTTGGATTACATTTTCACTGG	3720
3659	AGTGGCGACAGACTCCGCCAGGAAACACGCTCTGAATACCTTGGATTACATTTTCACTGG	3718
3721	TGTCTTTACCTTTGAGATGGTGATAAAGATGATCGACTTGGGACATGCTGCTTCAACCTGG	3780
3719	TGTCTTTACCTTTGAGATGGTGATAAAGATGATCGACTTGGGACATGCTGCTTCAACCTGG	3778
3781	AGCCTATTTCCGGGACTTTGTGAAACATTCGCACTTTCATTTGGTCAGTGCGCCCTGGT	3840
3779	AGCCTATTTCCGGGACTTTGTGAAACATTCGCACTTTCATTTGGTCAGTGCGCCCTGGT	3838
3841	GGCGTTGCTTTCTCGAGCTTCGTGGGAGGATCCAAAGGGAAGACATCAATACCATCAA	3900
3839	GGCGTTTGTCTTCTC-----AGGATCCAAAGGGAAGACATCAATACCATCAA	3886
3901	GTCTCTGAGAGTCTTTCGTGCTCGCGGCCCTCAAGACCATCAAAACGCGTCCCAAGCT	3960
3887	GTCTCTGAGAGTCTTTCGTGCTCGCGGCCCTCAAGACCATCAAAACGCGTCCCAAGCT	3946
3961	CAAGGCTGTTTGAAGTGTGGTGAACCTCCTCGAAGATGTCCCTCAACATCTTGATGT	4020
3947	CAAGGCTGTTTGAAGTGTGGTGAACCTCCTCGAAGATGTCCCTCAACATCTTGATGT	4006
4021	CTACATGCTCTTCATGTTTCATATTTGCGGCTCATTCGGGTGACGCTCTTCAAGGAAGTT	4080
4007	CTACATGCTCTTCATGTTTCATATTTGCGGCTCATTCGGGTGACGCTCTTCAAGGAAGTT	4066
4081	TTTCTACTGCAAGATGAATCCAAAGAGCTGGAGAGGACTGCAGGGGTCAAGTATTGGA	4140
4067	TTTCTACTGCAAGATGAATCCAAAGAGCTGGAGAGGACTGCAGGGGTCAAGTATTGGA	4126
4141	TTATGAGAAGGAGGAAGTGGAGACTCAGCCCCAGGAGTGGGAAGAAATACGACTTTCACTA	4200
4127	TTATGAGAAGGAGGAAGTGGAGACTCAGCCCCAGGAGTGGGAAGAAATACGACTTTCACTA	4186
4201	CGACAAATGTGCTCTGGGCTCTGCTGACCGTGTTCACAGTGTCCACGGGAGAGGCTGCCC	4260
4187	CGACAAATGTGCTCTGGGCTCTGCTGACCGTGTTCACAGTGTCCACGGGAGAGGCTGCCC	4246

QY	4261	CATGGTCTGAAACACACTCCGTGGATGCCACCTATGAGGACAGGGTCCAAGCCCTGGGTA	4320
Db	4247	CATGGTCTGAAACACACTCCGTGGATGCCACCTATGAGGACAGGGTCCAAGCCCTGGGTA	4306
QY	4321	CCGCATGGAGCTGTCATCTCTACGTGGTGTACTTTGTGGTCTTTCCCTCTCTTCGT	4380
Db	4307	CCGCATGGAGCTGTCATCTCTACGTGGTGTACTTTGTGGTCTTTCCCTCTCTTCGT	4366
QY	4381	CAACATCTTTGTGGCTTTGATCATCATCACCTCCAGGAGCAGGGGACAAGGTGATGTC	4440
Db	4367	CAACATCTTTGTGGCTTTGATCATCATCACCTCCAGGAGCAGGGGACAAGGTGATGTC	4426
QY	4441	TGAATGAGCCTGGAGAAGAACGAGAGGGCTTGCAATTGACTTGCCTATCAGCGCCAAACC	4500
Db	4427	TGAATGAGCCTGGAGAAGAACGAGAGGGCTTGCAATTGACTTGCCTATCAGCGCCAAACC	4486
QY	4501	CCTGACACGGTACATGCCCCCAAAACCGGCAGTGGTTCAGTATTAAGACGGTGAATTGT	4560
Db	4487	CCTGACACGGTACATGCCCCCAAAACCGGCAGTGGTTCAGTATTAAGACGGTGAATTGT	4546
QY	4561	GGTCTCCCGCCCTTTGAATACTTTCAATCATGCGCCATGATAGCCCTCAACACTGTGGTGCT	4620
Db	4547	GGTCTCCCGCCCTTTGAATACTTTCAATCATGCGCCATGATAGCCCTCAACACTGTGGTGCT	4606
QY	4621	GATGATGAAGTTCATGATGCACCTATGATGATGATGATGATGATGATGATGATGATGAT	4680
Db	4607	GATGATGAAGTTCATGATGCACCTATGATGATGATGATGATGATGATGATGATGATGAT	4666
QY	4681	CGTGTTCACATCCATGTTCTCCATGGAATGGGTGCTGAAGATCATGCGCCTTTGGGGTGCT	4740
Db	4667	CGTGTTCACATCCATGTTCTCCATGGAATGGGTGCTGAAGATCATGCGCCTTTGGGGTGCT	4726
QY	4741	GAACATATTCAGAGATGCCCTGGAATGCTTTGACTTTGTCACTGTGTGGGAAGTATTAC	4800
Db	4727	GAACATATTCAGAGATGCCCTGGAATGCTTTGACTTTGTCACTGTGTGGGAAGTATTAC	4786
QY	4801	TGATATTTTATGATAACAGAGATTCGGGAACGAAACAAATTTTCATCAACCTCAGCTTCCTCCG	4860
Db	4787	TGATATTTTATGATAACAGAGATTCGGGAACGAAACAAATTTTCATCAACCTCAGCTTCCTCCG	4846
QY	4861	CCTCTTTCGAGCTGCGGGCTGATCAAGCTGTCTCCGCGAGGGCTACACCATCGCATCCT	4920
Db	4847	CCTCTTTCGAGCTGCGGGCTGATCAAGCTGTCTCCGCGAGGGCTACACCATCGCATCCT	4906
QY	4921	GCTGTGACCTTTGTCCAGTCCCTTCAAGGCCCTGSCCTACGTGTGTCTCATTTGCCAT	4980
Db	4907	GCTGTGACCTTTGTCCAGTCCCTTCAAGGCCCTGSCCTACGTGTGTCTCATTTGCCAT	4966
QY	4981	GCTGTCTTCATCTACGCCATCATCGGCATGCGAGTGTGTTGGGAATATTGCCCTGGATGA	5040
Db	4967	GCTGTCTTCATCTACGCCATCATCGGCATGCGAGTGTGTTGGGAATATTGCCCTGGATGA	5026
QY	5041	TGACACAGATCATACCGCCACAAACAACTTCGCGAGCTTTTGGAGCCCTGATGTGCT	5100
Db	5027	TGACACAGATCATACCGCCACAAACAACTTCGCGAGCTTTTGGAGCCCTGATGTGCT	5086
QY	5101	GTTTCAGAGCGCCACGGGGAGGCTGCGACGAGATCATGCTGCTGCTGAGCAACCA	5160
Db	5087	GTTTCAGAGCGCCACGGGGAGGCTGCGACGAGATCATGCTGCTGCTGAGCAACCA	5146
QY	5161	GGCCTGTGATGAGCAGGCCCAATGCGACCGAGTGTGGAAAGTGACTTTTGCCTACTTTACTTT	5220
Db	5147	GGCCTGTGATGAGCAGGCCCAATGCGACCGAGTGTGGAAAGTGACTTTTGCCTACTTTACTTT	5206
QY	5221	CGTCTCCTCATCTTCTGTGCTCTTTCTGATGATGATGATGATGATGATGATGATGATGAT	5280
Db	5207	CGTCTCCTCATCTTCTGTGCTCTTTCTGATGATGATGATGATGATGATGATGATGATGAT	5266
QY	5281	GGACAAATTTTGAATACCTCAGCGGGACTCTTCCATCTAGGTGCTCACCACCTGGATGA	5340
Db	5267	GGACAAATTTTGAATACCTCAGCGGGACTCTTCCATCTAGGTGCTCACCACCTGGATGA	5326

QY	5341	GTTTCATCCGGTCTGGGCTGGAATACGACCGGCTGCGTGTGGCGCATCAGTTTACAATGA	5400
Db	5327	GTTTCATCCGGTCTGGGCTGGAATACGACCGGCTGCGTGTGGCGCATCAGTTTACAATGA	5386
QY	5401	CATGTTTGAGATGCTCAAAACACATGTCCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460
Db	5387	CATGTTTGAGATGCTCAAAACACATGTCCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5446
QY	5461	TCGAGTTGCTTACAAGCGCCTGGTTTCGCGATGAATGCCCATCTCCAAACGAGGACATGAC	5520
Db	5447	TCGAGTTGCTTACAAGCGCCTGGTTTCGCGATGAATGCCCATCTCCAAACGAGGACATGAC	5506
QY	5521	TGTTCACTTCACTGTCACGCTGATGGCCCTCATCCCGAAGCGGACCTGAGAGTCAAGCTGGC	5580
Db	5507	TGTTCACTTCACTGTCACGCTGATGGCCCTCATCCCGAAGCGGACCTGAGAGTCAAGCTGGC	5566
QY	5581	CCGAGCTGGGACAAACGACATCAGTGTGACGCGGAGTTGAGGAAGAGATTTCCGTTGT	5640
Db	5567	CCGAGCTGGGACAAACGACATCAGTGTGACGCGGAGTTGAGGAAGAGATTTCCGTTGT	5626
QY	5641	GTGGGCAATCTGCCCCAGAAAGACTTTTGGACTTTGGTATGCTTGAATTTGATCTTCAAGCAGAACAA	5700
Db	5627	GTGGGCAATCTGCCCCAGAAAGACTTTTGGACTTTGGTATGCTTGAATTTGATCTTCAAGCAGAACAA	5686
QY	5701	GATGACAGTGGGGAAGGTTTATGACGCTCTGATGATATTTGATCTTCAAGCAGAACAA	5760
Db	5687	GATGACAGTGGGGAAGGTTTATGACGCTCTGATGATATTTGATCTTCAAGCAGAACAA	5746
QY	5761	AACCAACAGAGACCATGACGAGGCTCTGAGAGGCTCTCCAGATGGGTCTCTGTGC	5820
Db	5747	AACCAACAGAGACCATGACGAGGCTCTGAGAGGCTCTCTCCAGATGGGTCTCTGTGC	5806
QY	5821	CTGTGTTCCACCTCTGAAAGGCCACCTGGAGACAGACACAGCCCGGCTGTCTCCGAGGAGC	5880
Db	5807	CTGTGTTCCACCTCTGAAAGGCCACCTGGAGACAGACACAGCCCGGCTGTCTCCGAGGAGC	5866
QY	5881	CCGGGTTTTCTTTCGACAGAGATTCACCTCCCTCAGCAATGGCGGGCCATACAATA	5940
Db	5867	CCGGGTTTTCTTTCGACAGAGATTCACCTCCCTCAGCAATGGCGGGCCATACAATA	5926
QY	5941	CCAAGAGATGGCATCAAGAGTCTCTCTGGGGCACTCAAGAGGACCCAGAGATGCACC	6000
Db	5927	CCAAGAGATGGCATCAAGAGTCTCTCTGGGGCACTCAAGAGGACCCAGAGATGCACC	5986
QY	6001	CCATGAGGCGCAGGCCACCTCGAGGCTGCGCACTCCACAGAGATCCCTGTGGGGCGGTC	6060
Db	5987	CCATGAGGCGCAGGCCACCTCGAGGCTGCGCACTCCACAGAGATCCCTGTGGGGCGGTC	6046
QY	6061	AGGAGCACTGGCTGTGGAAGTTCAGATGACAGCATAAACCCGAGGGGCTCTGATGGGGA	6120
Db	6047	AGGAGCACTGGCTGTGGAAGTTCAGATGACAGCATAAACCCGAGGGGCTCTGATGGGGA	6106
QY	6121	GCCTCAGCTTGGCTGGAGAGCCAGGCTGAGCGGCTCCATGCTCCGCTGGGCGCA	6180
Db	6107	GCCTCAGCTTGGCTGGAGAGCCAGGCTGAGCGGCTCCATGCTCCGCTGGGCGCA	6166
QY	6181	GACTCAGCCCGCTCACAGATGCGACCCCATGAAGCGCTCCATCTCCACGCTGCGCCAGCG	6240
Db	6167	GACTCAGCCCGCTCACAGATGCGACCCCATGAAGCGCTCCATCTCCACGCTGCGCCAGCG	6226
QY	6241	GCCTCCTGGGACTCATCTTTTGACGACACACCGCGGACCGGCCACCCCTAGCAGCGCTC	6300
Db	6227	GCCTCCTGGGACTCATCTTTTGACGACACACCGCGGACCGGCCACCCCTAGCAGCGCTC	6286
QY	6301	GTGCAACCAACCAACCAACCGCTGCCACCGCGCAGGAGCAGGAAGCAGAGTCCCTTGA	6360
Db	6287	GTGCAACCAACCAACCAACCGCTGCCACCGCGCAGGAGCAGGAAGCAGAGTCCCTTGA	6346
QY	6361	GAAGGGGCGCAGCGCTCTCTGCGGATATGATGATGATGATGATGATGATGATGATGATGAT	6420
Db	6347	GAAGGGGCGCAGCGCTCTCTGCGGATATGATGATGATGATGATGATGATGATGATGATGAT	6406
QY	6421	GCTGCCCGCGGAGAGGGGCTTACAGGCTGCGCGGGGAACGAGAGCGCGGAGAGCG	6480

Db 359 CCGCTCGCTCTTCTGCTTTCACGAGGACAACTGCTCGGCAAAATACCGGAAGCCCATCAC 418
Qy 421 CGAGTGGCCTCCATTCGAGTATATGATCCTGGCCACCACCATCATCGCCAACTGTCATCGTGCT 480
Db 419 CGAGTGGCCTCCATTCGAGATATGATCCTGGCCACCACCATCATCGCCAACTGTCATCGTGCT 478
Qy 481 GGCCTCTGAGCAGACACCTCCCTGATGGGACAAAACGCCCATGTCAGAGCGGCTGAGACGA 540
Db 479 GGCCTCTGAGCAGCACCCTCCCTGATGGGACAAAACGCCCATGTCAGAGCGGCTGAGACGA 538
Qy 541 CACGAGCCCTATTTTCATCGGGATCTTTTGCTTCAGGCGAGGATCAAAATCATCGCTCT 600
Db 539 CACGAGCCCTATTTTCATCGGGATCTTTTGCTTCAGGCGAGGATCAAAATCATCGCTCT 598
Qy 601 GGGCTTTGCTTCCACAAGGSCCTTATCTCTCGGAAACGGCTGGAACTGATGAGACTTCGT 660
Db 599 GGGCTTTGCTTCCACAAGGSCCTTATCTCTCGGAAACGGCTGGAACTGATGAGACTTCGT 658
Qy 661 GGTGCTCTCACAGGATCTTGGCACGGCTGGAACTGATGATGACCTTGGAACTGAG 720
Db 659 GGTGCTCTCACAGGATCTTGGCACGGCTGGAACTGATGATGACCTTGGAACTGAG 718
Qy 721 GGCCTGCTGCTGAGGSCCTTGAAGCTGCTCTGGGATTCGAAGTTTGCAGGCTGT 780
Db 719 GGCCTGCTGCTGAGGSCCTTGAAGCTGCTCTGGGATTCGAAGTTTGCAGGCTGT 778
Qy 781 GCTCAAGTCCATCATGAAGSCCTTGAAGCTGCTCTGGGATTCGAAGTTTGCAGGCTGT 840
Db 779 GCTCAAGTCCATCATGAAGSCCTTGAAGCTGCTCTGGGATTCGAAGTTTGCAGGCTGT 838
Qy 841 TGCATCTCATGTTTGCATCATGAGCTGAGTCTTACATGAGGCAAGTTTGCAGAGG 900
Db 839 TGCATCTCATGTTTGCATCATGAGCTGAGTCTTACATGAGGCAAGTTTGCAGAGG 898
Qy 901 CTGTTTCCCAACAGCAGATGCGAGCCGCTGGGTGACTTCCCTGTCGCAAGGAGGC 960
Db 899 CTGTTTCCCAACAGCAGATGCGAGCCGCTGGGTGACTTCCCTGTCGCAAGGAGGC 958
Qy 961 CCCAGCCCGGTGTCGAGGCGCAGACTGAGTGCAGGAGTACTTGGCCAGGACCCAACTT 1020
Db 959 CCCAGCCCGGTGTCGAGGCGCAGACTGAGTGCAGGAGTACTTGGCCAGGACCCAACTT 1018
Qy 1021 TGGCATCACCACTTTGACAAATATCTGTTTGGCCATCTTGAAGTGTTCAGTGCATCAC 1080
Db 1019 TGGCATCACCACTTTGACAAATATCTGTTTGGCCATCTTGAAGTGTTCAGTGCATCAC 1078
Qy 1081 CATGAGGCTGGAATGACATCTCTATATACAAAGATGCGCGCGGCAACCTCGAA 1140
Db 1079 CATGAGGCTGGAATGACATCTCTATATACAAAGATGCGCGCGGCAACCTCGAA 1138
Qy 1141 CTGGCTCTACTTCTCATCTCTCATCATCTCGGCTCTTCTTCTCATGCTCAACCTGGTGCT 1200
Db 1139 CTGGCTCTACTTCTCATCTCTCATCATCTCGGCTCTTCTTCTCATGCTCAACCTGGTGCT 1198
Qy 1201 GGGCGTCTCTCGGGGAGTTTGCAGAGGCGAGAGAGGTTGAGAAACCGCCGCGCTT 1260
Db 1199 GGGCGTCTCTCGGGGAGTTTGCAGAGGCGAGAGAGGTTGAGAAACCGCCGCGCTT 1258
Qy 1261 CCTGAAGCTGCGCGCAGCAGATGTCGAGAGGCTCAACGGGTACCTGGAGTGGAT 1320
Db 1259 CCTGAAGCTGCGCGCAGCAGATGTCGAGAGGCTCAACGGGTACCTGGAGTGGAT 1318
Qy 1321 CTTCAAGCGGAGGAAGTCTATGCTGGCCGAGGAGGACAGGAATGCAGAGGAGAGTCCCC 1380
Db 1319 CTTCAAGCGGAGGAAGTCTATGCTGGCCGAGGAGGACAGGAATGCAGAGGAGAGTCCCC 1378
Qy 1381 TTTTGAAGTGTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACTGTATCCACGAGA 1440
Db 1379 TTTTGAAGTGTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACTGTATCCACGAGA 1438
Qy 1441 GGAGGAGAGAGACCGGTTTGCAGATCTCTGTGCTGTTGGATCCCCCTTCCGCCGCGCAG 1500
Db 1439 GGAGGAGAGAGACCGGTTTGCAGATCTCTGTGCTGTTGGATCCCCCTTCCGCCGCGCAG 1498

Qy 1501 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCATATCTTCCGAGGAAGAGAGATGTTCCG 1560
Db 1499 CCTCAAGAGCGGGAAGACAGAGAGCTCGTCATATCTTCCGAGGAAGAGAGATGTTCCG 1558
Qy 1561 GTTTTTATCCGCGCATGCTGAAGCTCAGAGCTTCTACTGGGTGCTGTGCGTGGT 1620
Db 1559 GTTTTTATCCGCGCATGCTGAAGCTCAGAGCTTCTACTGGGTGCTGTGCGTGGT 1618
Qy 1621 GGCCTTGAAACACACTGTGTGGCCATGCTGATTAACAACAGCGCGCGGCTTACAC 1680
Db 1619 GGCCTTGAAACACACTGTGTGGCCATGCTGATTAACAACAGCGCGCGGCTTACAC 1678
Qy 1681 GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTCTCACAGAGATGCTCCTGAA 1740
Db 1679 GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTCTCACAGAGATGCTCCTGAA 1738
Qy 1741 GATGATGGCTCGGCGCCAGAGACTTCTCCGGTCTCTCTCAACTGCTTCCACTTTGG 1800
Db 1739 GATGATGGCTCGGCGCCAGAGACTTCTCCGGTCTCTCTCAACTGCTTCCACTTTGG 1798
Qy 1801 GGTATCTGCGGAGCGTCTTTGAAGTGTCTGGCGGCCATCAAGCCGGGAAGCTCCTT 1860
Db 1799 GGTATCTGCGGAGCGTCTTTGAAGTGTCTGGCGGCCATCAAGCCGGGAAGCTCCTT 1858
Qy 1861 TGGGATCAGTGTCTCGGCGCCCTCCGCTGTGAGGATCTTCAAGTCAAGAGTACTG 1920
Db 1859 TGGGATCAGTGTCTCGGCGCCCTCCGCTGTGAGGATCTTCAAGTCAAGAGTACTG 1918
Qy 1921 GAGTCTCGTGGGAAACCTGCTGTGCTTCCGCTGTGAGTCTCATGAGTCTCATCAGCCT 1980
Db 1919 GAGTCTCGTGGGAAACCTGCTGTGCTTCCGCTGTGAGTCTCATGAGTCTCATCAGCCT 1978
Qy 1981 GCTCTTCTGCTCTCTCTGTTTCAATTGTGCTTTCGCCCTCTCGGGATGAGCTGTTGG 2040
Db 1979 GCTCTTCTGCTCTCTCTGTTTCAATTGTGCTTTCGCCCTCTCGGGATGAGCTGTTGG 2038
Qy 2041 GGGACAGTTCAACTTCCAGGATGAGATCCCAACAACCACTTCGACACCTTCCCTGCGGC 2100
Db 2039 GGGACAGTTCAACTTCCAGGATGAGATCCCAACAACCACTTCGACACCTTCCCTGCGGC 2098
Qy 2101 CATCTCTGCTTCTTCCAGTCTCTGAGTCCGAGAGAGGATGGAATGCAGTGTATCAGG 2160
Db 2099 CATCTCTGCTTCTTCCAGTCTCTGAGTCCGAGAGAGGATGGAATGCAGTGTATCAGG 2158
Qy 2161 GATCGAATGCAAGCGGCTCAGCAAGGATGTTCTCGTCTCTTTTACTTTCATTTGCTCT 2220
Db 2159 GATCGAATGCAAGCGGCTCAGCAAGGATGTTCTCGTCTCTTTTACTTTCATTTGCTCT 2218
Qy 2221 GACACTGTTTCGGAACCTTACATCTGCTGAAATGTTCTTCTGGCCATCGCTGTGACAACT 2280
Db 2219 GACACTGTTTCGGAACCTTACATCTGCTGAAATGTTCTTCTGGCCATCGCTGTGACAACT 2278
Qy 2281 GGCACAGCCCAAGAGCTGACCAAGATGAAGAGGATGGAAGAGAGAGAGAGAGAGAGAG 2340
Db 2279 GGCACAGCCCAAGAGCTGACCAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2338
Qy 2341 GCTTGTCTTGCAAAAGCCCAAGAGTGGCTGAAGTCAAGCTCAGCCCATGCTCTCCCGCAACAT 2400
Db 2339 GCTTGTCTTGCAAAAGCCCAAGAGTGGCTGAAGTCAAGCTCAGCCCATGCTCTCCCGCAACAT 2398
Qy 2401 CTCATCTCGCGCCAGGACAGCAACTCTCGGCCAAGGGCGCTCGGTGTGGAGAGAGCGGGC 2460
Db 2399 CTCATCTCGCGCCAGGACAGCAACTCTCGGCCAAGGGCGCTCGGTGTGGAGAGAGCGGGC 2458
Qy 2461 CAGCAGCTACGCTCGCAACCTCGCGGCCAGCTCGAGGCGCTGTACAGCAGATGGA 2520
Db 2459 CAGCAGCTACGCTCGCAACCTCGCGGCCAGCTCGAGGCGCTGTACAGCAGATGGA 2518
Qy 2521 CCCCAGGAGGCGCTCGGCTTCCGCTACGCGCCACCTCGCGGCCAGATGAAGAGCA 2580
Db 2519 CCCCAGGAGGCGCTCGGCTTCCGCTACGCGCCACCTCGCGGCCAGATGAAGAGCA 2578

QY 2581 CCTGGAACGGCCGCTGTGTGTGAGCTTGGCCCGACGCGCGCGGGGCCCTCGTGAGG 2640
Db CCTGGAACGGCCGCTGTGTGTGAGCTTGGCCCGACGCGCGCGGGGGCCGCTGGAGG 2638
QY 2641 CAAAGCCCGACCTGAGGCTCGGAGGCCCCCGGAGGGGCTGCACCTTCCGGGCHAGGCACCA 2700
Db CAAAGCCCGACCTGAGGCTCGGAGGCCCCCGGAGGGGCTGCACCTTCCGGCAGGCACCA 2698
QY 2701 CCGSCACCGCGACAAGACACCCCGCGGGGGGACAGGACCGAGCAGAGSCCCC 2760
Db CCGSCACCGCGACNAAGACACCCCGCGGGGGGACAGGACCGAGCAGAGSCCCC 2758
QY 2761 GAAGCGGAGAGCGGGAGCCCCCGTGTCCCGGAGGAGCGCGCCGCGCACCGCAGGCCA 2820
Db GAAGCGGAGAGCGGGAGCCCCCGTGTCCCGGAGGAGCGCGCCGCGCGCACCGCAGGCCA 2818
QY 2821 CAGCAAGAGGCGCGGGCCCCCGGAGCGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 2880
Db CAGCAAGAGGCGCGGGCCCCCGGAGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGG 2878
QY 2881 CGAGGCGGCGCGGCGCACACCGGCGCGCTCCCGGAGGAGCGGCGGCGGCGGCGGCGG 2940
Db CGAGGCGGCGCGGCGCACACCGGCGCGCTCCCGGAGGAGCGGCGGCGGCGGCGGCGG 2938
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RESULT 10

US-08-450-272-7
; Sequence 7, Application US/08450272
; Patent No. 6387696
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Gillespie, Alison
; APPLICANT: Feldman, Daniel
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: US
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,272
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,950
; FILING DATE: 13-MAR-1995
; APPLICATION NUMBER: 08/336,257
; FILING DATE: 7-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/314,083
; FILING DATE: 28-SEPT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/311,363
; FILING DATE: 23-SEPT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/290,012
; FILING DATE: 11-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: 4-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/193,078
; FILING DATE: 07-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/149,097
; FILING DATE: 5-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/105,536
; FILING DATE: 11-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/914,231
; FILING DATE: 13-JULY-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: 10-APR-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06903
; FILING DATE: 14-AUG-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/745,206
; FILING DATE: 15-AUG-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-519812
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; TELEPHONE: (619) 238-0999
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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; LOCATION: 7161..7362
; US-08-450-272-7

Query Match 99.2%; Score 7316.4; DB 4; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

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RESULT 11
US-08-450-273-7
; Sequence 7, Application US/08450273
; Patent No. 6653097
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: McCue, Ann
; APPLICANT: Gillespie, Alison
; APPLICANT: Feldman, Daniel
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: US
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,273
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; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,950
; FILING DATE: 13-MAR-1995
; APPLICATION NUMBER: 08/336,257
; FILING DATE: 7-NOV-1994
; APPLICATION NUMBER: 08/314,083
; FILING DATE: 28-SEPT-1994
; APPLICATION NUMBER: 08/311,363
; FILING DATE: 23-SEPT-1994
; APPLICATION NUMBER: 08/290,012
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 08/223,305
; FILING DATE: 4-APR-1994
; APPLICATION NUMBER: 08/193,078
; FILING DATE: 07-FEB-1994
; APPLICATION NUMBER: 08/149,097
; FILING DATE: 5-NOV-1993
; APPLICATION NUMBER: 08/105,536
; FILING DATE: 11-AUG-1993
; APPLICATION NUMBER: 07/914,231
; FILING DATE: 13-JULY-1992
; APPLICATION NUMBER: 07/868,354
; FILING DATE: 10-APR-1992
; APPLICATION NUMBER: PCT/US92/06903
; FILING DATE: 14-AUG-1992
; APPLICATION NUMBER: 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-519812
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 238-0999
; TELEFAX: (619) 238-0062
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 144..7163
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..143
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 7161..7362
; US-08-450-273-7

Query Match 99.2%; Score 7316.4; DB 4; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

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Qy 2821 CAGCAAGGAGGCGCGGGGCCCCCGAGGCGCGGACGAGCGCGCGCGAGGCCAGGGCC 2880
Db 2819 CAGCAAGGAGGCGCGGGGCCCCCGAGGCGCGGAGCGCGCGCGAGGCCAGGGCC 2878
Qy 2881 CGAGGCGCGCGGCGCACACCGGCGGGTCCCGGAGGAGCGCGCGCGAGGCC 2940
Db 2879 CGAGGCGCGCGGCGCACACCGGCGGGTCCCGGAGGAGCGCGCGCGAGGCC 2938
Qy 2941 CCGAGCCACCGCGCACCGGACACAGATCCGAGCAGGAGTGCGGCGCGCGCAAGGG 3000
Db 2939 CCGAGCCACCGCGCACCGGACACAGATCCGAGCAGGAGTGCGGCGCGCGCAAGGG 2998
Qy 3001 CGAGCGCGCGCGCACCGGCGGGCCCCCGAGCGGGGCCCCCGGAGGCGGAGCGG 3060
Db 2999 CGAGCGCGCGCGCACCGGCGGGCCCCCGAGCGGGGCCCCCGGAGGCGGAGCGG 3058
Qy 3061 GGAGGCGCGCGCGCGCACCGGCGCGGCGGACAAAGCGCGAGCTGTCTACGAGGCTGT 3120
Db 3059 GGAGGCGCGCGCGCGCGCACCGGCGCGGCGGACAAAGCGCGAGCTGTCTACGAGGCTGT 3118
Qy 3121 CGAGAAGGAGACACCGGAGAGGAGGCCACGAGAGGAGGCTGAGATAGTGGAGCCGA 3180
Db 3119 GGAGAAGGAGACACCGGAGAGGAGGCCACGAGAGGAGGCTGAGATAGTGGAGCCGA 3178
Qy 3181 CAAAGAAAGGAGCTCCGGAAACACAGCCCGCGGAGCCACACTGTGACCTGGAGACGAG 3240
Db 3179 CAAAGAAAGGAGCTCCGGAAACACAGCCCGCGGAGCCACACTGTGACCTGGAGACGAG 3238
Qy 3241 TGGGACTGTGACTGTGGGTCCCATGCAACACTGCCAGCACCTGTCTCCAGAGAGTGGA 3300
Db 3239 TGGGACTGTGACTGTGGGTCCCATGCAACACTGCCAGCACCTGTCTCCAGAGAGTGGA 3298
Qy 3301 GGAAACAGCAGAGGATGAGACAAATCAGCGGAACGTCACTCGCATGGGCGAGTCAGCCCC 3360
Db 3299 GGAAACAGCAGAGGATGAGACAAATCAGCGGNAAGTCACTCGCATGGGCGAGTCAGCCCC 3358
Qy 3361 AGACCCGAACACTATTGTACATATCCAGTAGTGTGACGGGCCCTCTTGGGGAAGCCAC 3420
Db 3359 AGACCCGAACACTATTGTACATATCCAGTAGTGTGACGGGCCCTCTTGGGGAAGCCAC 3418
Qy 3421 GGTCTTCCAGTGTACGTGAGCTGGAAAGCCAGCAGAGGGGAGAGAGGTGGA 3480
Db 3419 GGTCTTCCAGTGTACGTGAGCTGGAAAGCCAGCAGAGGGGAGAGAGGTGGA 3478
Qy 3481 AGCGGATGAGTATGAGGAGCGGCCCGCGGCTATCGTCCCATACAGCTCCATGTTCTG 3540

Db 3479 AGCGGATGAGTATGAGGAGCGGCCCGGCGCTATCGTCCCATACAGCTCCATGTTCTG 3538
Qy 3541 TTTAAGCCCAACCAACCTGCTCCGCGCTTCTGCACATACATCTGACCATGAGTACTT 3600
Db 3539 TTTAAGCCCAACCAACCTGCTCCGCGCTTCTGCACATACATCTGACCATGAGTACTT 3598
Qy 3601 CGAGTGTCTCATTTCTCGTGGTTCATCGCTTGAGCAGCATCGCCCTGGCTGCTGAGGACCC 3660
Db 3599 CGAGTGTCTCATTTCTCGTGGTTCATCGCTTGAGCAGCATCGCCCTGGCTGCTGAGGACCC 3658
Qy 3661 AGTGGCAGACAGCTCGCCCGAGGAAACACGCTCTCAAAATACCTGATATACATTTTCACTGG 3720
Db 3659 AGTGGCAGACAGCTCGCCCGAGGAAACACGCTCTCAAAATACCTGATATACATTTTCACTGG 3718
Qy 3721 TGTCTTTACCTTTGAGATGGTGAATAAGATCATCGACTTGGGACTGCTTCAACCTTGG 3780
Db 3719 TGTCTTTACCTTTGAGATGGTGAATAAGATCATCGACTTGGGACTGCTTCAACCTTGG 3778
Qy 3781 AGCCTATTTCCGGGACTTTGTGGAAACATTTCTGGACTTCATTTGTGTGCTAGTGCGGCTTGGT 3840
Db 3779 AGCCTATTTCCGGGACTTTGTGGAAACATTTCTGGACTTCATTTGTGTGCTAGTGCGGCTTGGT 3838
Qy 3841 GCGCTTTGCTTTCTCGAGCTTCGTGGAGGATCCAAAGGGAAAGACATCAATACCATCAA 3900
Db 3839 GCGCTTTGCTTTCTC-----AGGATCCAAAGGGAAAGACATCAATACCATCAA 3886
Qy 3901 GTCTCTCAGAGTCTTCTCGTGTCTCGGCGCCCTCAAGACCATCAAAAGGGCTGCCCAAGCT 3960
Db 3887 GTCTCTCAGAGTCTTCTCGTGTCTCGGCGCCCTCAAGACCATCAAAAGGGCTGCCCAAGCT 3946
Qy 3961 CAAGGCTGTGTTGACTGTGTGTGAACTCCCTGAAAGATGTCTCAACATCTTGTATTTGT 4020
Db 3947 CAAGGCTGTGTTGACTGTGTGTGAACTCCCTGAAAGATGTCTCAACATCTTGTATTTGT 4006
Qy 4021 CTACATGCTCTTCACTGTTTCAATTTTCCGCTCATTTGCGTGCAGCTCTTCAAGAGGAGTT 4080
Db 4007 CTACATGCTCTTCACTGTTTCAATTTTCCGCTCATTTGCGTGCAGCTCTTCAAGAGGAGTT 4066
Qy 4081 TTTCTACTGCACAGATGAATCCCAAGAGCTGGAGAGGAGCTGCAGGGGTCAAGTATTTGGA 4140
Db 4067 TTTCTACTGCACAGATGAATCCCAAGAGCTGGAGAGGAGCTGCAGGGGTCAAGTATTTGGA 4126
Qy 4141 TTAATGAGAGGAGGAGTGGAAAGCTCAGGCCAGGCTGGAAGAAATACGATTTTCACTA 4200
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Qy 4201 CGAATATGCTCTGCGCTCTGCTGACGCTGTTCACAGTGTCCACGGAGAGGCTGGCC 4260
Db 4187 CGAATATGCTCTGCGCTCTGCTGACGCTGTTCACAGTGTCCACGGAGAGGCTGGCC 4246
Qy 4261 CATGGTGTGAAACACTCCGTTGGATGCCACCTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
Db 4247 CATGGTGTGAAACACTCCGTTGGATGCCACCTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4306
Qy 4321 CCGCATGGAGCTGTCCATCTTCTACGTGTCTACTTTTGTGCTTCTTCCCTTCTTCTTCTGT 4380
Db 4307 CCGCATGGAGCTGTCCATCTTCTACGTGTCTACTTTTGTGCTTCTTCCCTTCTTCTTCTGT 4366
Qy 4381 CAACATCTTTTGTGGCTTTGATCATCATCATCTTCCAGGAGCAGGGGACANGGTGATGTC 4440
Db 4367 CAACATCTTTTGTGGCTTTGATCATCATCATCTTCCAGGAGCAGGGGACANGGTGATGTC 4426
Qy 4441 TGAATCGACCTGGAGAAGACGAGAGGCTTGCATTTGACTTTCCGCATCAGCGCCAAACC 4500
Db 4427 TGAATCGACCTGGAGAAGACGAGAGGCTTGCATTTGACTTTCCGCATCAGCGCCAAACC 4486
Qy 4501 CCTGACACGGTACATGCCCCCAAAACCGGCGAGTCTGTTCCAGTATAGACCTGACATTTGT 4560
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Qy 4561 GGTCTCCCCCGCTTTTGAATCTTATCATGTGCCATGATAGCCCTCAACAATTGTGTGTGT 4620
Db 4547 GGTCTCCCCCGCTTTTGAATCTTATCATGTGCCATGATAGCCCTCAACAATTGTGTGTGT 4606

Qy	4621	GATGATGAAGTTCTATGATGACACCTATAGTACGAGCTGATGCTGAAATGCCTGAAACAT	4680
Dd	4607	GATGATGAAGTTCTATGATGACACCTATAGTACGAGCTGATGCTGAAATGCCTGAAACAT	4666
Qy	4681	CGTCTTCACATCCATGTTCTCCATGGAAATGCTGCTGAAGATCATCGCTTTGGGGTGCT	4740
Dd	4667	CGTGTTCACATCCATGTTCTCCATGGAAATGCTGCTGAAGATCATCGCTTTGGGGTGCT	4726
Qy	4741	GAACTATTTTCAGAGATGCTGGAATGCTTTTGACTTTGTCTCACTGTGTTGGGAAGTATTAC	4800
Dd	4727	GAACTATTTTCAGAGATGCTGGAATGCTTTTGACTTTGTCTCACTGTGTTGGGAAGTATTAC	4786
Qy	4801	TGATATTTTAGTAAACAGAGATGCGGAAACGAAACAAATTCATCAACCTCAGCTTCCTCCG	4860
Dd	4787	TGATATTTTAGTAAACAGAGATGCGGAAACGAAACAAATTCATCAACCTCAGCTTCCTCCG	4846
Qy	4861	CCTCTTTGAGCTCGCGGCTGATCAAGCTGCTCCGCCAGGGCTACACCATCCGCATCCT	4920
Dd	4847	CCTCTTTGAGCTCGCGGCTGATCAAGCTGCTCCGCCAGGGCTACACCATCCGCATCCT	4906
Qy	4921	GCTGTGACCTTTGTCTCAGTCCCTTCAAGGCCCTCGCTACGTGTGTCTGCTCATTTGCCAT	4980
Dd	4907	GCTGTGACCTTTGTCTCAGTCCCTTCAAGGCCCTCGCTACGTGTGTCTGCTCATTTGCCAT	4966
Qy	4981	GCTGTCTTCATCTACGCCATCATCGGCATCGAGTGTGTTGGGAATATTGCTCTGGATGA	5040
Dd	4967	GCTGTCTTCATCTACGCCATCATCGGCATCGAGTGTGTTGGGAATATTGCTCTGGATGA	5026
Qy	5041	TGACACAGCATCAACGCCCAACAACTTCGAGACGTTTTTGGAGCCCTGATGCTGCT	5100
Dd	5027	TGACACAGCATCAACGCCCAACAACTTCGAGACGTTTTTGGAGCCCTGATGCTGCT	5086
Qy	5101	GTTTCAGAGCGCCACGGGGAGGCTGGCAGAGATCATGTGTCTGCTCGCTGAGCAACCA	5160
Dd	5087	GTTTCAGAGCGCCACGGGGAGGCTGGCAGAGATCATGTGTCTGCTCGCTGAGCAACCA	5146
Qy	5161	GGCCTGTGATGAGCAGGCCAATCCACCGAGTGTGGAAGTGACTTTGCCTACTTCTACTT	5220
Dd	5147	GGCCTGTGATGAGCAGGCCAATCCACCGAGTGTGGAAGTGACTTTGCCTACTTCTACTT	5206
Qy	5221	CGTCTCTCTCATCTCTCTGTGCTCTTCTTGATGTTGAACCTCTTTGTGGCTGTGATCAT	5280
Dd	5207	CGTCTCTCTCATCTCTCTGTGCTCTTCTTGATGTTGAACCTCTTTGTGGCTGTGATCAT	5266
Qy	5281	GGACAAATTTTCAGTACCTCAACGCGGACTCTTCCATCTAGGTCTCACCACATTGGATGA	5340
Dd	5267	GGACAAATTTTCAGTACCTCAACGCGGACTCTTCCATCTAGGTCTCACCACATTGGATGA	5326
Qy	5341	GTTTCATCCGGTCTGGGCTGAATACGACCCGGCTCGGTGTGGGCGCATCAGTTACAATGA	5400
Dd	5327	GTTTCATCCGGTCTGGGCTGAATACGACCCGGCTCGGTGTGGGCGCATCAGTTACAATGA	5386
Qy	5401	CATGTTTGAATGCTGAAACACATGTCGCCCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460
Dd	5387	CATGTTTGAATGCTGAAACACATGTCGCCCTCTGGGGCTGGGGAAGAAATGCCCTGC	5446
Qy	5461	TCGAGTTGCTTACAAAGCGCTGTTTCGATCAACATGCCATCTCCAAACGAGGACATGAC	5520
Dd	5447	TCGAGTTGCTTACAAAGCGCTGTTTCGATCAACATGCCATCTCCAAACGAGGACATGAC	5506
Qy	5521	TGTTTCACTTCACTCCAGCTGTAGTGGCCCTCATCCGACGGCACTGGAGATCAAGCTGGC	5580
Dd	5507	TGTTTCACTTCACTCCAGCTGTAGTGGCCCTCATCCGACGGCACTGGAGATCAAGCTGGC	5566
Qy	5581	CCCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCCGTTGT	5640
Dd	5567	CCCAGCTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAAGGAGATTTCCGTTGT	5626
Qy	5641	GTGGGCCAAATCTGCCCCAGAGAGATTTGGAGCTTCTGTATCACCCCATCAAGCCCTGATGA	5700
Dd	5627	GTGGGCCAAATCTGCCCCAGAGAGATTTGGAGCTTCTGTATCACCCCATCAAGCCCTGATGA	5686

Qy	5701	GATGACAGTGGGAAAGGTTTATGAGCTCTGATGATATTTTGACTTCTACAAGCAGAACAA	5760
Dd	5687	GATGACAGTGGGAAAGGTTTATGAGCTCTGATGATATTTTGACTTCTACAAGCAGAACAA	5746
Qy	5761	AACACCCAGAGACACAGATGACAGAGCTCTGAGAGGCTCTCCAGATGGTCTCTGTGTC	5820
Dd	5747	AACACCCAGAGACACAGATGACAGAGCTCTGAGAGGCTCTCCAGATGGTCTCTGTGTC	5806
Qy	5821	CCTGTTTCCACCCTCTGAAGGCCACCTTGGAGCAGACACAGCCGGCTGTGTCCGAGGAGC	5880
Dd	5807	CCTGTTTCCACCCTCTGAAGGCCACCTTGGAGCAGACACAGCCGGCTGTGTCCGAGGAGC	5866
Qy	5881	CCGGGTTTTCTTCGACAGAAAGTTCACCTCCCTCAGCAATGGCGGGGCCATACAAAA	5940
Dd	5867	CCGGGTTTTCTTCGACAGAAAGTTCACCTCCCTCAGCAATGGCGGGGCCATACAAAA	5926
Qy	5941	CAAAGAGATGGCATCAAAAGATCTGTCTCTGGGGCACTCAAAGGACCCAGAGATGCACC	6000
Dd	5927	CAAAGAGATGGCATCAAAAGATCTGTCTCTGGGGCACTCAAAGGACCCAGAGATGCACC	5986
Qy	6001	CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGGGGTCT	6060
Dd	5987	CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCCTGTGGGGGGTCT	6046
Qy	6061	AGGAGCATCTGGCTGTGGACGTTCAGATGACAGCATAAACCCGGAGGGGCCCTGATGGGGA	6120
Dd	6047	AGGAGCATCTGGCTGTGGACGTTCAGATGACAGCATAAACCCGGAGGGGCCCTGATGGGGA	6106
Qy	6121	GCCCCAGCTGGGCTGGAGAGCCAGGGTCCAGCGGCTCCATGCCCGCTTCGGGCCGA	6180
Dd	6107	GCCCCAGCTGGGCTGGAGAGCCAGGGTCCAGCGGCTCCATGCCCGCTTCGGGCCGA	6166
Qy	6181	GACTCAGCCCCGTCAACAGATGCCAGCCCCATGAAAGCGCTCCATCTCCAAGCTGGGCCACG	6240
Dd	6167	GACTCAGCCCCGTCAACAGATGCCAGCCCCATGAAAGCGCTCCATCTCCAAGCTGGGCCACG	6226
Qy	6241	GCCCCGTGGAGCTCATCTTTTGGAGCACACCCCGGACCGGCCACCCCTAGCCAGCGGCTC	6300
Dd	6227	GCCCCGTGGAGCTCATCTTTTGGAGCACACCCCGGACCGGCCACCCCTAGCCAGCGGCTC	6286
Qy	6301	GTGCGACCAACACACCCCGCTGCCACCCGCGGACAGGAGCAGGAAGCAGAGTCCCTGGA	6360
Dd	6287	GTGCGACCAACACACCCCGCTGCCACCCGCGGACAGGAGCAGGAAGCAGAGTCCCTGGA	6346
Qy	6361	GAAGGGGCCCCAGCGCTGTCTGCCGATATGGATGGCGCACCAAGCAGTGTCTGTGGGGCCGG	6420
Dd	6347	GAAGGGGCCCCAGCGCTGTCTGCCGATATGGATGGCGCACCAAGCAGTGTCTGTGGGGCCGG	6406
Qy	6421	GCTGCCCCCGGGAGAGGGGCTTACAGGCTGCCGGCGGGAAACGAGAGCGCCGCGGAGAGCG	6480
Dd	6407	GCTGCCCCCGGGAGAGGGGCTTACAGGCTGCCGGCGGGAAACGAGAGCGCCGCGGAGAGCG	6466
Qy	6481	GGGCGGCTCCAGAGCGGAGGAGCCCTCATCTCTCTCGGAGAGCAGCGCTTCTA	6540
Dd	6467	GGGCGGCTCCAGAGCGGAGGAGCCCTCATCTCTCTCGGAGAGCAGCGCTTCTA	6526
Qy	6541	CTCTCTGAGACCGCTTTTGGGGCCGTGAGCCCCCGAAGCCCAAGCCCTCTCTCAGAGCCCA	6600
Dd	6527	CTCTCTGAGACCGCTTTTGGGGCCGTGAGCCCCCGAAGCCCAAGCCCTCTCTCAGAGCCCA	6586
Qy	6601	CCCAAGCTGCCAACAGCTGGCCAGGAGCGGAGACCCCAACAGGGCAGTGGTTCCT	6660
Dd	6587	CCCAAGCTGCCAACAGCTGGCCAGGAGCGGAGACCCCAACAGGGCAGTGGTTCCT	6646
Qy	6661	GAATGGAGGCCCTTCTGTCAACATCTGGTGTAGCACCCCGCGCGCGTGGGGGAG	6720
Dd	6647	GAATGGAGGCCCTTCTGTCAACATCTGGTGTAGCACCCCGCGCGCGTGGGGGAG	6706
Qy	6721	GCAGCTCCCCCAGACGCCCTCTGACTCCCCGCCCCAGCATCACCTACAAGACGGCCAACTC	6780
Dd	6707	GCAGCTCCCCCAGACGCCCTCTGACTCCCCGCCCCAGCATCACCTACAAGACGGCCAACTC	6766
Qy	6781	CTCACCCATCCACTTTCGCGGGGCTCAGACCAAGCTCCCTTCTTCTCCACAGGCGGCT	6840

Db 6767 CTCACCCATCCACTTCGCGGGCTCAGACAGGCTCCCTGCTTCTCCCGAGCGCGCT 6826
Qy 6841 CAGCGTGGGCTTCCGAACAACAGCGCTGCTGCAGAGAGACCCCTCAGCCAGCCCT 6900
Db 6827 CAGCGTGGGCTTCCGAACAACAGCGCTGCTGCAGAGAGACCCCTCAGCCAGCCCT 6886
Qy 6901 GGCCCTGGCTCTCGAATTTGGCTCTGACCCCTTACCTGGGCGAGCGTCTGGACAGTGAGCG 6960
Db 6887 GGCCCTGGCTCTCGAATTTGGCTCTGACCCCTTACCTGGGCGAGCGTCTGGACAGTGAGCG 6946
Qy 6961 CTCTGTCCAGCCCTGCTCAGGACAGCGCTCACTTTCGAGGAGCGTGTGGCCACCAACTC 7020
Db 6947 CTCTGTCCAGCCCTGCTCAGGACAGCGCTCACTTTCGAGGAGCGTGTGGCCACCAACTC 7006
Qy 7021 GGCGCGCTCTCCAGGACTTCTTACGTTGCTCCTCCCTGACCTCCCTCAGCTCACCCTCTCG 7080
Db 7007 GGCGCGCTCTCCAGGACTTCTTACGTTGCTCCTCCCTGACCTCCCTCAGCTCACCCTCTCG 7066
Qy 7081 CGCGTCCCAAGCGTTTACCACTGCACTGCACTGGGACTCAGCTCGGCTGGCGGACGCGCA 7140
Db 7067 CGCGTCCCAAGCGTTTACCACTGCACTGCACTGGGACTCAGCTCGGCTGGCGGACGCGCA 7126
Qy 7141 CAGTACCAACCGCTGACCAAGCACTGGTCTAGCTGCACTGCACTGCACTGCACTGCACTGCA 7200
Db 7127 CAGTACCAACCGCTGACCAAGCACTGGTCTAGCTGCACTGCACTGCACTGCACTGCACTGCA 7186
Qy 7201 CTGATGACGAGCGGTGTTCCAGTGGATGAGTTTATCATCCACAGGCGGAGTGG 7260
Db 7187 CTGATGACGAGCGGTGTTCCAGTGGATGAGTTTATCATCCACAGGCGGAGTGG 7246
Qy 7261 CCTCGGGGAGCGCTTGGCCACTGGTGGAGCTCCTGTGCGCCCTCCCTCCCTCCT 7320
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Qy 7321 CCCTCTTTTACTCTAGACAGCAATAAGCCCTGTGCTGAGTACGTACCG 7376
Db 7307 CCCTCTTTTACTCTAGACAGCAATAAGCCCTGTGCTGAGTACGTACCG 7362

RESULT 12

US-08-713-118-1
; Sequence 1, Application US/08713118
; Patent No. 6040436
; GENERAL INFORMATION:
; APPLICANT: Franco, Rodrigo
; APPLICANT: Sun Chen, Ai Ru
; APPLICANT: Suey, David J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
; TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,118
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mata, Elizabeth W.
; REGISTRATION NUMBER: 38,236
; REFERENCE/DOCKET NUMBER: ACC96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7266 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 92..7102
; US-08-713-118-1

Query Match 97.9%; Score 7223.2; DB 3; Length 7266;
Best Local Similarity 99.7%; Pred. No. 0;

Matches 7263; Conservative 0; Mismatches 3; Indels 18; Gaps 2;

Qy 55 TCCGTGGCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCCCTCCCTGCGGGCGCGCT 114
Db 1 TCCGTGGCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCCCTCCCTGCGGGCGCGCT 60
Qy 115 GGGCCGGGAGTGCACGCGGGGCCCGGAGCCATGGTCCGCTTCGGGACAGCTGGCGG 174
Db 61 GGGCCGGGAGTGCACGCGGGGCCCGGAGCCATGGTCCGCTTCGGGACAGCTGGCGG 120
Qy 175 CCGCTATGGAGGCGCCCGCGCGGAGAGCGGGCCCGGGGCGGCGGCGCGGCGG 234
Db 121 CCGCTATGGAGGCGCCCGCGCGGAGAGCGGGCCCGGGGCGGCGGCGGCGG 180
Qy 235 GGGCCCGGGTCCGCGGGGGCTGCAGCCCGGCGAGCGGGTCTCTACAAGCAATCGATCG 294
Db 181 GGGCCCGGGTCCGCGGGGGCTGCAGCCCGGCGAGCGGGTCTCTACAAGCAATCGATCG 240
Qy 295 GCAGCGCGCGGAGCAATGGCGCTGTACAACCCCATCCCGGTCAAGCAATCTGCTTCA 354
Db 241 GCAGCGCGCGGAGCAATGGCGCTGTACAACCCCATCCCGGTCAAGCAATCTGCTTCA 300
Qy 355 CGTCAACCGCTCTCTGCTCTTTCAGCGAGGACACGTCGTCGCAAAATACGCGAGCG 414
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Qy 415 CATCACCGAGTGCTCCATTCGAGTATATGATCTCTGGCCACCATCATCGCAATGCAAT 474
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Db 421 CGTGTGGCGCTGGAGCAGCACTCCCTGATGGGACAAAACGCCCATGTTCGAGCGGT 480
Qy 535 GGACGACACGAGCGCCCTATTTTCATCGGGATCTTTTGTTCGAGGAGGAGTCAAAATCAT 594
Db 481 GGACGACACGAGCGCCCTATTTTCATCGGGATCTTTTGTTCGAGGAGGAGTCAAAATCAT 540
Qy 595 CGCTCTGGGCTTTGTCTTCCACAAGGGCTTTTACCTGCGGAAACGGCTGGAACGTCATGA 654
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Db 661 ACTGAGGGCTGTGCTGTGCTGAGGCCCTCGAAGCTGGTGTCTGGGATTCGAAATTTGCA 720
Qy 775 GGTGTGTCTCAAGTCCATCATGAAGGCCATGGTTCCTCCTCGAGATGGGCTGCTTCT 834
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Qy 835 CTTCCTTTGCGCATCTCTCATGTTTGCCATCATTTGGCTGGAGTTTACATGGGCAAGTTCCA 894
Db 781 CTTCCTTTGCGCATCTCTCATGTTTGCCATCATTTGGCTGGAGTTTACATGGGCAAGTTCCA 840

Qy 895 CAAGGCGCTGTTTCCCAACAGCAGATGCGGAGCGCCGTGGGTGACTTCCCCTGTGGCAA 954
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955 GGAGGCCCCAGCCGCGTGTGCGAGGGCGACACAGTGGCGGAGTACTGGCCAGGACC 1014
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901 GGAGGCCCCAGCCGCGTGTGCGAGGGCGACACTGAGTGGCGGAGTACTGGCCAGGACC 960
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1021 CATCAACATGAGGGCTGGACTGACATCCTCTATAATAACAAAGATGCGGCGGCAACAC 1080
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1081 CTGGAACCTGGCTTACTTCACTCCCTCATCATCATCGGCTCCTTCTTATGCTCAACCT 1140
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1141 GGTGCTGGGCGTGTCTCGGGGAGTTTGCCAAAGAGCGAGAGGGTGGAGAACCGCCG 1200
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1255 GCGCTTCTGAAGCTGCGCGGCGAGCAGAGATCGAGGAGAGCTCAACGGGTTACTTGGGA 1314
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1261 GTGGATCTTCAAGCGGAGGAAGTCATGCTGGCGGAGGAGACAGGAATGCAGAGGAGAA 1320
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1435 GCGAGAGAGGAGAGGACCGGTTTGAGATCTCTGTGCTTTGGATCCCTTTCGCGCG 1494
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1381 GCGAGAGAGGAGAGGACCGGTTTGAGATCTCTGTGCTTTGGATCCCTTTCGCGCG 1440
Qy |||||
1495 GCGCAGCTCAAGAGCGGAGAGACAGAGAGCTCTCATCTTCGAGGAGGAGAGAGAT 1554
Db |||||
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1555 GTTCCGGTTTTTTATCCGGCGCATGTGTAAGGCTCAGAGCTTCTACTGGGTGTGTGTG 1614
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1501 GTTCCGGTTTTTTATCCGGCGCATGTGTAAGGCTCAGAGCTTCTACTGGGTGTGTGTG 1560
Qy |||||
1615 CGTGGTGCCCTGAACACACTGTGTGTGGCCATGGTGATTAACACAGCGCGGGCGGT 1674
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1561 CGTGGTGCCCTGAACACACTGTGTGTGGCCATGGTGATTAACACAGCGCGGGCGGT 1620
Qy |||||
1675 TACCACGACCTGTATTTTGCAGAGTTGTGTTTCTGGGTCTCTTCTCAAGAGATGTC 1734
Db |||||
1621 TACCACGACCTGTATTTTGCAGAGTTGTGTTTCTGGGTCTCTTCTCAAGAGATGTC 1680
Qy |||||
1735 CCTGAAGATGATGGCTTGGGGCCAGAAAGTACTTCCGGTCTCTCTTCAACTGCTTCGA 1794
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1861 GTACTGAGCTCCCTGCGGAACCTGGTGTGCTCCCTGCTGAACTCCATGAAGTCCATCAT 1920
Qy |||||
1975 CAGCCTGCTCTTCTTCTCTTCTGTTGATGTTGCTTTCGCGCTGTGGGATGACGT 2034

Db |||||
1921 CAGCCTGCTCTTCTTCTCTTCTGTTCACTTG6GTCTTTCGCCCTGCTGGGATGACGT 1980
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1981 GTTTGGGGACAGTTCAACTTCCAGATGAGACTCCACAAACCAACTTCCACACCTTCCC 2040
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2041 TGCCGCCATCTCTCACTGTCTTCCAGATCTCTGACGGGAGGAGACTGGAATGAGTGTGA 2100
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2155 TCAGGGGATCGAATCGAAGGCGGCTCAGCAAGGCACTGTTCTGCTCTTTTACTTTCAT 2214
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2101 TCAGGGGATCGAATCGAAGGCGGCGTCAAGAAAGCATGTTCTGCTCTTTTACTTTCAT 2160
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2281 TCAGAACTTGTCTCTGCAAAAGGCGCAAGAGTGGCTGAAGTCAGCCCATGCTGCGCG 2340
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Db |||||
2341 GAACATCTCATCTCGCGCCAGGAGCAGAACTCGGCCNAGCGCGCTCGGTGTGGGAGCA 2400
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Db |||||
2461 GATGGAACCGGAGAGGCGCTGCGCTTCCGCCACTAGCGCCACTGCGGCGCCGACATGAA 2520
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Db |||||
2521 GAGCGACTTGGACCGCGCTGCTGTGTGGAGCTGGGCGCGCAGCGCGCGCGGGCGCCGT 2580
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Db |||||
2581 GGGAGCAAAAGCCGACCTGAGGCTGGGAGGCGCCCGAGGGCGTGCACCTCGCGCGAG 2640
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2701 GGGCCGGAAGCGGAGAGCGGGAGCGCGGTGCGCGGAGGAGCGCGCGCGCGCACCG 2760
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Qy |||||
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Db 3829 CATCAAGTCTGTGAGTCTTGTGCTCGTGGGCCCTCAAGACCATCAACCGGCTGCC 3888
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DB 5503 GCTGGCCCCAGCTGGGACAAAGCAGCATCAGTGTGACGCGGAGTTGAGGAAGGAGATTTC 5562
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DB 6643 GCGGAGGAGCTCCCGCAGAGCGCCCTGTGACTCCCGCCCGCCAGCATCACCTACAGAGGCG 6702
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RESULT 13

US-09-452-007-1

; Sequence 1, Application US/09452007

; Patent No. 6140485

; GENERAL INFORMATION:

APPLICANT: Franco, Rodrigo
APPLICANT: Sun Chen, Ai Ru
APPLICANT: Suey, David J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
TITLE OF INVENTION: CALCIUM CHANNEL SUBUNITS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/452,007
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/713,118
FILING DATE: 16-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mata, Elizabeth W.
REGISTRATION NUMBER: 38,236
REFERENCE/DOCKET NUMBER: ACC96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7266 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 92..7102
US-09-452-007-1

Query Match 97.9%; Score 7223.2; DB 3; Length 7266;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 7263; Conservative 0; Mismatches 3; Indels 18; Gaps 2;

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DB	61	GGGCGGGGATGACGCGGGGCGGGGAGCATGTGTCGGTTCGGGGACGAGCTGGGGG	120
QY	175	CGCTATGAGGCCCGCGGCGGAGAGCGGGCCCGGGCGGCGGGGCGGGGCGGG	234
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QY	235	GGGCGGGGTCGGGGGGCTGCAGCCCGGCGAGCGGGTCTCTACAGCAATCGATCGC	294
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QY	835	CTTCTTTGCCATCTCATGTTTGGCTGAGGCTGAGTCTTACATGAGGCTGAGTCTCA	894
DB	781	CTTCTTTGCCATCTCATGTTTGGCTGAGGCTGAGTCTTACATGAGGCTGAGTCTCA	840
QY	895	CAAGGCTGTTTCCCAACAGCAGATGCGGAGCGGCTGGGCTGACTTCCCTGTTGGCAA	954
DB	841	CAAGGCTGTTTCCCAACAGCAGATGCGGAGCGGCTGGGCTGACTTCCCTGTTGGCAA	900
QY	955	GGAGGCGCCAGCGGCTGTGCGAGGCGGACACTGAGTGTGCGGAGTACTTGGCAGGACC	1014
DB	901	GGAGGCGCCAGCGGCTGTGCGAGGCGGACACTGAGTGTGCGGAGTACTTGGCAGGACC	960
QY	1015	CAACTTTGGCATCACCAATTTGCAATATCTGTTTGGCTGCTTGGCTGCTTGGCTGCT	1074
DB	961	CAACTTTGGCATCACCAATTTGCAATATCTGTTTGGCTGCTTGGCTGCTTGGCTGCT	1020
QY	1075	CATCACCATGAGGCTGAGCTGACATCTCTATATACAAACGATCGGCTGGCAACAC	1134
DB	1021	CATCACCATGAGGCTGAGCTGACATCTCTATATACAAACGATCGGCTGGCAACAC	1080
QY	1135	CTGGAATGCTGCTTCTCATATCTCTCATCATCGGCTCTTCTTTCATGCTCAACCT	1194
DB	1081	CTGGAATGCTGCTTCTCATATCTCTCATCATCGGCTCTTCTTTCATGCTCAACCT	1140
QY	1195	GGTGTGGGCTGCTCTCGGGGAGTTTCCAGGAGCGGAGAGGCTGAGGCTGAGGCTGAG	1254
DB	1141	GGTGTGGGCTGCTCTCGGGGAGTTTCCAGGAGCGGAGAGGCTGAGGCTGAGGCTGAG	1200
QY	1255	CGCTTTCTGAACTGCGCGGCGGAGAGTCTGAGGAGGAGTCTCAAGCTGAGTCTGGA	1314
DB	1201	CGCTTTCTGAACTGCGCGGCGGAGAGTCTGAGGAGGAGTCTCAAGCTGAGTCTGGA	1260
QY	1315	GTGGATCTTCAAGGCGGAGGAGTCTATGCTGGCGGAGGAGGAGGAGTCTGAGGAGAA	1374
DB	1261	GTGGATCTTCAAGGCGGAGGAGTCTATGCTGGCGGAGGAGGAGGAGTCTGAGGAGAA	1320
QY	1375	GTCCCTCTTGGAGCTCTGAAGAGCGGCGGAGGAGGAGGAGGAGGAGTCTGAGTCTCA	1434
DB	1321	GTCCCTCTTGGAGCTCTGAAGAGCGGCGGAGGAGGAGGAGGAGGAGTCTGAGTCTCA	1380
QY	1435	CGCAGAGGAGGAGGAGGAGGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1494
DB	1381	CGCAGAGGAGGAGGAGGAGGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1440
QY	1495	CGCCAGCTTCAAGAGCGGAGGAGGAGGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCT	1554

Db 1441 GCGCAGCCTCAAGACGGGAAGACAGAGAGCTGTCATATCTTCGGAGGAAGAGAGAT 1500
Qy 1555 GTTCCGGTTTTTTATCCGGCGCATGTTGAAGGCTCAGAGCTTCTACTGGGTGGTCTGTG 1614
Db 1501 GTTCCGGTTTTTTATCCGGCGCATGTTGAAGGCTCAGAGCTTCTACTGGGTGGTCTGTG 1560
Qy 1615 GTGGTGGCCCTGAACACATCTGTGTGTGGCCATGGTGCATTACAACAGCGCGGGCGGCT 1674
Db 1561 CGTGGTGGCCCTGAACACATCTGTGTGTGGCCATGGTGCATTACAACAGCGCGGGCGGCT 1620
Qy 1675 TACCACACCTCTGATTTTTCAGAGATTTTGTTCCTGGGTCTCTTCTCTACAGAGATGTC 1734
Db 1621 TACCACACCTCTGATTTTTCAGAGATTTTGTTCCTGGGTCTCTTCTCTACAGAGATGTC 1680
Qy 1735 CTTGGAAGATGATGGCTGGGGGCCAAGAGCTACTTCCGGTCTCTTCAACTGCTTCGA 1794
Db 1681 CTTGGAAGATGATGGCCCTGGGGGCCAAGAGCTACTTCCGGTCTCTTCAACTGCTTCGA 1740
Qy 1795 CTTTGGGGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGCGGCCATCAAGCCGGAAG 1854
Db 1741 CTTTGGGGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGCGGCCATCAAGCCGGAAG 1800
Qy 1855 CTCCTTTGGGATCAGTGTGCTGGGGCCCTCCGGCTGCTGAGGATCTTCAAAGTCAAGAA 1914
Db 1801 CTCCTTTGGGATCAGTGTGCTGGGGCCCTCCGGCTGCTGAGGATCTTCAAAGTCAAGAA 1860
Qy 1915 GTACTGGAGCTCCTGCGGAACCTGGTGTCTCCTGCTGAATCCATGAAGTCCATCAT 1974
Db 1861 GTACTGGAGCTCCTGCGGAACCTGGTGTCTCCTGCTGAATCCATGAAGTCCATCAT 1920
Qy 1975 CAGCCTGCTCTTCTGCTCTCTCTGTTTCAATGTGGTCTTCCCTGCTGGGATGCAGCT 2034
Db 1921 CAGCCTGCTCTTCTGCTCTCTCTGTTTCAATGTGGTCTTCCCTGCTGGGATGCAGCT 1980
Qy 2035 GTTTGGGGAGAGTTCAACTTCCAGGATGAGACTCCACAAACCAACTTCGACACTTTCCC 2094
Db 1981 GTTTGGGGAGAGTTCAACTTCCAGGATGAGACTCCACAAACCAACTTCGACACTTTCCC 2040
Qy 2095 TGCGGCCATCCTCACTGTTTCCAGATCTCTGACGGGAGAGACTGGAAATGCAATGATGA 2154
Db 2041 TGCGGCCATCCTCACTGTTTCCAGATCTCTGACGGGAGAGACTGGAAATGCAATGATGA 2100
Qy 2155 TCAGGGATGGAATCGGAAGCGCGTTCAGGAAGGCAATGTTCTGTCCTTTTACTTTCAT 2214
Db 2101 TCAGGGATGGAATCGGAAGCGCGTTCAGGAAGGCAATGTTCTGTCCTTTTACTTTCAT 2160
Qy 2215 TGTCTGACACTGTTTCGGAACCTACACTCTGCTGAATGTTCTTCTGSCCATCGTGTGGA 2274
Db 2161 TGTCTGACACTGTTTCGGAACCTACACTCTGCTGAATGTTCTTCTGSCCATCGTGTGGA 2220
Qy 2275 CAACCTGGCCAAACGCCCCAAGAGCTGACCAAGGATGAAGAGAGATGAAGAGCAGCCAA 2334
Db 2221 CAACCTGGCCAAACGCCCCAAGAGCTGACCAAGGATGAAGAGAGATGAAGAGCAGCCAA 2280
Qy 2335 TCAGAACTTGTCTTGCAAAAGGCCAAAGAGTGGCTGAAGTCAAGCCCCATGTCGCCG 2394
Db 2281 TCAGAACTTGTCTTGCAAAAGGCCAAAGAGTGGCTGAAGTCAAGCCCCATGTCGCCG 2340
Qy 2395 GAACATCTCCATCGCCGAGGAGCAGAACTCGGCCCAAGCGCGCTCGGTGTGGAGCA 2454
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Qy 2455 GCGGGCAGGCGAGTACGGCTGCAGAACCTCGCGGGCCAGCTGCGAGCGCTGTACAGCGA 2514
Db 2401 GCGGGCAGGCGAGTACGGCTGCAGAACCTCGCGGGCCAGCTGCGAGCGCTGTACAGCGA 2460
Qy 2515 GATGGAACCCGAGAGCGGCTGCGCTTCGCCCACTACCGGCCACCTGCGGGCCCGACATGAA 2574
Db 2461 GATGGAACCCGAGAGCGGCTGCGCTTCGCCCACTACCGGCCACCTGCGGGCCCGACATGAA 2520
Qy 2575 GAGCACTCGACCGGCGCTGGTGTGGAGCTGGGCGCGGAGCGGCGCGGGGCGCGT 2634
Db 2521 GAGCACTCGACCGGCGCTGGTGTGGAGCTGGGCGCGGAGCGGCGCGGGGCGCGT 2580

Qy 2635 GGAAGCAAAGCCCGACCTGAGGCTGCGAGGCCCCCGAGGGGCTCGACCTTCGCGCAG 2694
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Qy 2695 GCACCAACCGGACCGGACCAAGACAGACCCCGCGGGGGGGAACAGACCGAGCAGA 2754
Db 2641 GCACCAACCGGACCGGACCAAGACAGACCCCGCGGGGGGACAGACCGAGCAGA 2700
Qy 2755 GGCCTCCGAAGCGGAGAGCGGGAGCCGCTGCCCGGAGAGCGCGCGCGCCACCG 2814
Db 2701 GGCCTCCGAAGCGGAGAGCGGGAGCCGCTGCCCGGAGAGCGCGCGCGCCACCG 2760
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Db 2821 AGSCCCCGAGGGCGCGCGGCGCACACCGCGCGGCTCCCGGAGGAGCGCGCGCGAGCG 2880
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Qy 2995 CAAAGGCGAGCGCGCGCGCGCACACCGCGCGGCCCCCGAGCGGGCCCCCGGAGGCGGA 3054
Db 2941 CAAAGGCGAGCGCGCGCGCGCACACCGCGCGGCCCCCGAGCGGGCCCCCGGAGGCGGA 3000
Qy 3055 GAGCGGGAGGAGCGCGCGCGCGCACACCGGCGCGGCGCAAGAGCGCGAGCTCTCTACGA 3114
Db 3001 GAGCGGGAGGAGCGCGCGCGCGCACACCGGCGCGGCGCAAGAGCGCGAGCTCTCTACGA 3060
Qy 3115 GGTGTGGAGAAGAGAGACCAACGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3174
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Qy 3175 AGCCGCAAGAGAAAAGAGCTCCGGAACCAACGAGCCCCCGGAGGCCACACTGTGACTTGA 3234
Db 3121 AGCCGCAAGAGAAAAGAGCTCCGGAACCAACGAGCCCCCGGAGGCCACACTGTGACTTGA 3180
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Db 3181 GACCACTGGGAGTGTGACTGTGGTCCCATGACACACTGCCCCAGCACCTGTCTCCAGAA 3240
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Db 3301 GCCCCAGACCCGAAACACTATTGTATATATCCAGTGTGCTGACGGGCGCTCTTGGGGA 3360
Qy 3415 AGCCACGCTGTTCCCGAGTGTAACTGGACCTGGAAGCCAGCAAGAGGGGAGGAGGA 3474
Db 3361 AGCCACGCTGTTCCCGAGTGTAACTGGACCTGGAAGCCAGCAAGAGGGGAGGAGGA 3420
Qy 3475 GGTGGAAGCGGATGACGTGATGAGAGCGGCGCCCCCGGCTTATCGTCCCATACAGCTCCAT 3534
Db 3421 GGTGGAAGCGGATGACGTGATGAGAGCGGCGCCCCCGGCTTATCGTCCCATACAGCTCCAT 3480
Qy 3535 GTTCTGTTTAAGCCCCCAACCTGTCTCGCGCGCTTCTGCACTACATCGTGACCATGAG 3594
Db 3481 GTTCTGTTTAAGCCCCCAACCTGTCTCGCGCGCTTCTGCACTACATCGTGACCATGAG 3540
Qy 3595 GTACTTCGAGGTGGTCAATTCTCGTGGTCACTCGCTTTGAGCAGCATCGCCCTGCTCTGA 3654
Db 3541 GTACTTCGAGGTGGTCAATTCTCGTGGTCACTCGCTTTGAGCAGCATCGCCCTGCTCTGA 3600
Qy 3655 GGAACCCAGTGCACAGACTCGCCAGGAACACGCTCTGAAATACCTGATTACATTTT 3714
Db 3601 GGAACCCAGTGCACAGACTCGCCAGGAACACGCTCTGAAATACCTGATTACATTTT 3660

QY 3715 CACTGGTGTCTTTACCTTTGAGATGGTGATTAAGATGATCGACTTGGGACTGTCTGCTTCA 3774
Db 3661 CACTGGTGTCTTTACCTTTGAGATGGTGATTAAGATGATCGACTTGGGACTGTCTGCTTCA 3720
QY 3775 CCCTGGAGCCTATTTCCGGGACTTGTGGACATTTCTGGACTTCATTGTGGTCACTGGGCGC 3834
Db 3721 CCCTGGAGCCTATTTCCGGGACTTGTGGACATTTCTGGACTTCATTGTGGTCACTGGGCGC 3780
QY 3835 CCTGGTGGCGTTTGGCTTTCTCGAGCTTCGTGGGAGGATCAAGAGGAAAGACATCAATAC 3894
Db 3781 CCTGGTGGCGTTTGGCTTTCTC-----AGGATCAAGAGGAAAGACATCAATAC 3828
QY 3895 CATCAAGTCTCTGAGAGTCTTGGTCTCTGGGCCCCCTCAAGACCATCAAAACGGCTGCC 3954
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QY 4015 GATTGTCTACATGCTCTTCATGTTTCATATTTTGCCTGTCATTGCGGTGCAGCTCTTCAAAGG 4074
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Db 4069 TTGTGGATTATGAGAGGAGAGTGAAGCTCAGCCAGGAGCTGGAAGATATGACTT 4128
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QY 4255 CTGGCCCATGGTGTGAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAGGCC 4314
Db 4189 CTGGCCCATGGTGTGAACACTCCGTGGATGCCACTATGAGGAGCAGGGTCCAGGCC 4248
QY 4315 TGGGTACCGCATGGAGCTGTCCATCTTCTACGTGTGTCTACTTTGTGTCTTTTCCCTTCTT 4374
Db 4249 TGGGTACCGCATGGAGCTGTCCATCTTCTACGTGTGTCTACTTTGTGTCTTTTCCCTTCTT 4308
QY 4375 CTTCGTCAACATCTTTGTGGCTTTGATCATCATCACCTTCACGAGCAGGGGGACAAGGT 4434
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QY 4555 ATTTGTGTCTCCCGCCCTTTGAATATCTTCATATGCGCCATGATAGCCCTCAACACTGT 4614
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Db 4669 GGTGTGAACTATTTTCAGAGATGCTTGAATGTCTTTGACTTGTCTACTGTGTGGGAAG 4728
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Db 4729 TATTACTGATATTTTAGTAAACAGAGATTG-----CGAACAAATTTTCATCAACCTCAGCTT 4782
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Db 4843 CATCTGCTGTGAGACCTTTGTCAGTCTTTCMAAGGCCCTGCGCTACGTGTGTCTGCTCAT 4902
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Db 5743 TGTGTCCCTGTTCCACCTCTGAAAGGCCACCTCGAGGACAGACACAGCCGGCTGTGTCCG 5802
QY 5875 AGGAGCCGGGTTTTCTTCGACAGAGATTCCACCTCCCTCAGCAATGGCGGGCCAT 5934

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Db 5963 ACAAACCAAGAGAGTGGCTCAAAAGAGTCTGTCTCTGGGGCACTCAAAAGGACCCAGGA 5922
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Qy 6175 GCGGAGACTCAGCCGCTCAGATGCGAGGCCCTCATGAAGGGCTCCATCTCCAGCTGGC 6234
Db 6103 GCGGAGACTCAGCCGCTCAGATGCGAGGCCCTCATGAAGGGCTCCATCTCCAGCTGGC 6162
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Db 6163 CCAGCGCCCGTGGGACTCATCTTTGAGCACCACCGGAGCGCCACCCCTAGCCA 6222
Qy 6295 GCGCTCGTCGACACCAACCAACCGCTGCACCGCGCGAGGACAGGAGAGGTC 6354
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Qy 6355 CTTGGAGAAGGGGCGAGCTGTCTGCGGATATGGATGGCGCACCAAGAGTGTGTGGG 6414
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Qy 6535 CTTTACTCTCGACCGCTTTGGGGCGGTGAGCGCCCGAGCCCAAGCCCTCCTCAG 6594
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Db 6763 CCGGCTCAGCGGTGGGCTTTCCGAACACAAACCGCTGTGTCAGAGAGACCCCTCAGCCA 6822
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Qy 6955 TGAGGCTCTGTCCACGCGCTGCTGAGGACACGCTCACTTTCAGAGAGGCTGTGGCCAC 7014
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RESULT 14

US-09-268-163-7
; Sequence 7, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 7177
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..6856
US-09-268-163-7

Query Match 94.3%; Score 6958; DB 4; Length 7177;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 7177; Conservative 0; Mismatches 0; Indels 199; Gaps 2;

Qy 1 GCGGCGCGGCTCGCGGCGTGGGGCGGCGAGGTCCGCTGCGGTCCGCGGCTCCGCTCGGTG 60
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Qy 61 GCTGCTCCGCTCTGAGCGCTGCGCGCCCGCGCCCTCCCTCCCGGGGCGCTGGGCGG 120
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QY	301	CGCGCGGACCATGGCGTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAA	360
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QY	361	CGCGTGTCTTTCGTCTTTCAGCGAGGACAAACGTCGTCCGCAATATCGCGAAAGCGCATCAC	420
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QY	481	GGCCCTGGAGCAGACCTCCCTGATGGGGACAAACGCCCATGTCCGAGCGCTGGACGA	540
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QY	601	GGGCTTTGTCTTCCAAAGGGCTTTTACCTGGGACAGGCTGGAAAGCTCATGAGCTTCGT	660
Db	601	GGGCTTTGTCTTCCAAAGGGCTTTTACCTGGGACAGGCTGGAAAGCTCATGAGCTTCGT	660
QY	661	GGTCGTCTCACAGGATCCTTTCACAGGCTGGAACTGATCTTCGACCTCGCAACACTGAG	720
Db	661	GGTCGTCTCACAGGATCCTTTCACAGGCTGGAACTGATCTTCGACCTCGCAACACTGAG	720
QY	721	GGCTGTGCTGTGCTGAGCGCCCTGAGCTGTGTCTGGGATTCAGATTTGAGGTGGT	780
Db	721	GGCTGTGCTGTGCTGAGCGCCCTGAGCTGTGTCTGGGATTCAGATTTGAGGTGGT	780
QY	781	GCTCAAGTCCATCATGAAGGCCATGGTTCACACTCTGCGAGATTTGGGCTCTCTCTCTT	840
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QY	841	TGCGATTCCTCATGTTTGGCCATCATTTGGCTGGAGTTCTACATGGGCAAGTTCCACAAAGC	900
Db	841	TGCGATTCCTCATGTTTGGCCATCATTTGGCTGGAGTTCTACATGGGCAAGTTCCACAAAGC	900
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Db	901	CTGTTTCCCAACAGCAGATGCGGAGCCCGTGGTGAATCCCTCTGCGAGGAGGC	960
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Db	1021	TGGCATACCAACTTTGACAAATATCCTGTTTGGCCATCTTGACGGTTCAGTGCATCAC	1080
QY	1081	CATGAGGGCTGGACTGACATCCTCTATAATACAAACGATGGCCCGGCAACACTGGAA	1140
Db	1081	CATGAGGGCTGGACTGACATCCTCTATAATACAAACGATGGCCCGGCAACACTGGAA	1140
QY	1141	CTGGCTCTACTTCACTCCCTCATCATCATCGGCTCTTCTTCATGCTCAACCTGGTGTCT	1200
Db	1141	CTGGCTCTACTTCACTCCCTCATCATCATCGGCTCTTCTTCATGCTCAACCTGGTGTCT	1200
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Db	1201	GGGCGTGTCTCGGGGAGTTTGGCAAGGAGGAGAGGGTGGAGAAACCGCCCGGCTT	1260
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Db	1261	CCTGAAGCTGCGCCGAGCAGCATCGAGCGAGCTCAACGGGTACCTGGAGTGGAT	1320
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QY	1441	GGAGGAGAGGACCGGTTTTCAGATCTCTGTGCTGTGTGGATCCCTTTCGCGCGGCGCAG	1500
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QY	1741	GATGTATGGCTGGGCGCCAGAAAGTACTTCCGCTCTCTTCAACTGTCTTCGACTTTGG	1800
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QY	1861	TGGGATCAGTGTCTCGGCGCCCTCCGCTCTGAGGATCTTCAAGATCAAGAGTACTG	1920
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QY	2041	GGGACAGTTCAACTTCAGGATGAGACTCCCAACCAACTTCGACACCTTCCCTCGCCG	2100
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RESULT 15

US-08-455-543A-8
; Sequence 8, Application US/08455543A
; Patent No. 5792846

GENERAL INFORMATION:

; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
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; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; MEDIUM OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,543A
; FILING DATE: May 31, 1995
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; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991
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; PRIOR APPLICATION DATA: US 07/482,384
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; PRIOR APPLICATION DATA: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
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; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 8:
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Query Match 94.0%; Score 6932.4; DB 1; Length 7175;

Best Local Similarity 97.3%; Pred. No. 0;
Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;

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DB 1379 TTTTGAAGCTGTGAAGAGAGCGGCCCAACAAAGAGCAGAAATGACCTGATCCACGAGA 1438
QY 1441 GGAGGAGAGGACCGGTTTGAGATCTCTGTGCTGTTGGATCCCGCTTGGCCGCGCAG 1500
DB 1439 GGAGGAGAGGACCGGTTTGAGATCTCTGTGCTGTTGGATCCCGCTTGGCCGCGCAG 1498
QY 1501 CCTCAAGAGCGGGAAGACAGAGACTCGTCAATCTTCGGAGGAGAGAGATGTTCCG 1560

DB 1499 CCTCAAGAGCGGGAAGACAGAGACTCGTCAATCTTCGGAGGAAGGAGAGATGTTCCG 1558
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DB 1559 GTTTTTTATCCGGCGCATGTGTGAAGGCTCAGAGCTTCTACTGGGTGTGTGTGCGTGGT 1618
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DB 1619 GGCCCTGAACACACTGTGTGTGGCCATGTGTCAATTAACAACAGCCGCGGCTTACCAC 1678
QY 1681 GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTCTTCTCTCACAGAGATGTCCCTGAA 1740
DB 1679 GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTCTTCTCTCACAGAGATGTCCCTGAA 1738
QY 1741 GATGTATGGCTTGGGCGCCAGAGACTACTTCCGGTCTCTTCTCTCACTGCTTGCATTTGG 1800
DB 1739 GATGTATGGCTTGGGCGCCAGAGACTACTTCCGGTCTCTTCTCTCACTGCTTGCATTTGG 1798
QY 1801 GGTTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGCCATCAAGCCGCGGAAGCTCCTT 1860
DB 1799 GGTTCATCGTGGGAGCGTCTTTGAAGTGTCTGGGCGCCATCAAGCCGCGGAAGCTCCTT 1858
QY 1861 TGGATCAGTGTGTGTGGGCCCTTCCGCTGTCTGAGGATCTTCAAAGTCAACGATCTG 1920
DB 1859 TGGATCAGTGTGTGTGGGCCCTTCCGCTGTCTGAGGATCTTCAAAGTCAACGATCTG 1918
QY 1921 GAGTCCCTCGGGAACCTGTGTGTGTCTTCCGCTGTCTGAGGATCTTCAAAGTCAACGATCTG 1980
DB 1919 GAGTCCCTCGGGAACCTGTGTGTGTCTTCCGCTGTCTGAGGATCTTCAAAGTCAACGATCTG 1978
QY 1981 GCTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2040
DB 1979 GCTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2038
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DB 2159 GATCGAATCCAAAGCGGCGTCAACAAAGCATGTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2218
QY 2221 GACACTGTTCCGAAACTACACTCTGCTGATGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2280
DB 2219 GACACTGTTCCGAAACTACACTCTGCTGATGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2278
QY 2281 GGGCAACGCCCAAGACTGACCAAGATGAAGAGGAGATGGAAGAGAGAGAGAGAGAGAGAGAG 2340
DB 2279 GGGCAACGCCCAAGACTGACCAAGATGAAGAGGAGATGGAAGAGAGAGAGAGAGAGAGAGAG 2338
QY 2341 GCTTGTCTCTGCAAAAGGCCAAAGAGTGGCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2400
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QY 2401 CTCATCTGCGCCGAGGAGGAGAACTTGGCCAAAGGCGCGCTCGGTGTGGAGGAGGAGGCGGC 2460
DB 2399 CTCATCTGCGCCGAGGAGGAGAACTTGGCCAAAGGCGCGCTCGGTGTGGAGGAGGAGGCGGC 2458
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DB 2459 CAGCAGACTACGGCTCAGAACTTGGCGGCGAGTCCGAGGCGCTCTACAGCGAGATGGA 2518
QY 2521 CCCGAGGAGCGGCTGCGTTCGCCACTACGCGCCACCTTGGCGCCGAGAGAGAGAGAGAGAGAGAG 2580
DB 2519 CCCGAGGAGCGGCTGCGTTCGCCACTACGCGCCACCTTGGCGCCGAGAGAGAGAGAGAGAGAGAG 2578
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Db 2579 CCTGGACGGGCGCTGTTGTGTGGAGTGTGGCCGCGACGCGCGCGGGGGCCCGTGGGAGG 2638
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Qy 3781 AGCCTATTTCCGGGACTTGTGGAACTTCTGGAACTTCTGGAACTTCTGGAACTTCTGGAA 3840
Db 3779 AGCCTATTTCCGGGACTTGTGGAACTTCTGGAACTTCTGGAACTTCTGGAACTTCTGGAA 3838
Qy 3841 GGCCTTTGCTTTCTCGAGCTTTCGTGGGAGGATCCAAAGGGAAAGACATCAATACCATCAA 3900
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Qy 3901 GTCTCTGAGAGTCTTCTGTCCTCGGCCCCCTCAAGACCATCAAAAGGCTGCCAAGCT 3960
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Qy 3961 CAAGGCTGTGTTGACTGTGTGGTGAACCTCCCTGAAAGAAATGTCTCAACATCTTTGATTGT 4020
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Db 4007 CTACATGCTCTTCATGTTTCATATTTGCGGTCATTTGCGGTGCAGCTCTTCAAAAGGGAAGTT 4066
Qy 4081 TTTCTACTGACACAGATGAATCCAAGGAGCTTGGAGGGGACTGACAGGGGTCAAGTTTGGGA 4140
Db 4067 TTTCTACTGACACAGATGAATCCAAGGAGCTTGGAGGGGACTGACAGGGGTCAAGTTTGGGA 4126
Qy 4141 TTATGAGAGGAGGAAGTGGAACTCAGCCAGGCGAGTGGAAAGAAATACAGCTTTCACTA 4200
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Db 4667 CGTGTTCACATCATGTTTCTCATGGAATCGGTGCTGAAGATCATCGCTTTGGGGTGTCT 4726
Qy 4741 GAACTATTTTCAGAGATGCTTGGAAATGCTTTGACTTTGTCACGTGTGTGGAAAGTATTAC 4800
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Db	4787	TGATATTTTGTAGTAAAGAGATGCGGAAACGAAATTTTCATCAACCTCAGCTTCTCTCG	4846				
QY	4861	CCTCTTTTCGAGCTCGCGGCTGATCAAGCTGCTCCGACAGGCTACACCATCGCATCTT	4920		5941	CCAAGAGATGGCATCAAAGAGTCTGTCTCTCGGGCACTCAAAAGGACCCAGGATGCACC	6000
Db	4847	CCTCTTTTCGAGCTCGCGGCTGATCAAGCTGCTCCGACAGGCTACACCATCGCATCTT	4906		5927	CCAAGAGATGGCATCAAAGAGTCTGTCTCTCGGGCACTCAAAAGGACCCAGGATGCACC	5986
QY	4921	GCTGTGAGACCTTTGTCCAGTCTTTCAAGGCGCTGCCCTAGTGTGTCTGTCTCATTTGCCAT	4980		6001	CCATGAGCCAGGCGACCCCTGAGGCTGGGCACTCCACAGAGATCCTCTGTGGGGCGGTC	6060
Db	4907	GCTGTGAGACCTTTGTCCAGTCTTTCAAGGCGCTGCCCTAGTGTGTCTGTCTCATTTGCCAT	4966		5987	CCATGAGCCAGGCGACCCCTGAGGCTGGGCACTCCACAGAGATCCTCTGTGGGGCGGTC	6046
QY	4981	GCTGTCTTCTCATCTACGCCATCATCGGCATGCAAGTGTGGGAAATTTGCCCTGGATGA	5040		6061	AGGAGCACTGTCTGTGGACGTTTCAGATGCAAGATAAACCCGAGGGGCTCTGTATGGGA	6120
Db	4967	GCTGTCTTCTCATCTACGCCATCATCGGCATGCAAGTGTGGGAAATTTGCCCTGGATGA	5026		6047	AGGAGCACTGTCTGTGGACGTTTCAGATGCAAGATAAACCCGAGGGGCTCTGTATGGGA	6106
QY	5041	TGACACGAGCATCAACCGCCACAACTTCGAGAGCTTTTTCGAGGCGCTCATGCTGTCT	5100		6121	GCCCCAGCTGGGCTGGAGAGCCAGGGTCCAGCGGCTCCATGCCCCCGCTTGGGGCGGA	6180
Db	5027	TGACACGAGCATCAACCGCCACAACTTCGAGAGCTTTTTCGAGGCGCTCATGCTGTCT	5086		6107	GCCCCAGCTGGGCTGGAGAGCCAGGGTCCAGCGGCTCCATGCCCCCGCTTGGGGCGGA	6166
QY	5101	GTTTCAGAGCGCCACCGGGGAGGCTTGGCAAGAGATCATGCTGTCTGCTTGGCAACCA	5160		6181	GACTCAGCCGCTCACAGATGCCAGCCCATGAAGCGCTCCATCTCCACGCTGGGCCAGCG	6240
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QY	5161	GGCCTGTGATGAGCAGGCCAATGCCACGAGTGTGGAAGTCTTGCCTACTCTACTTT	5220		6241	GCCCCGTGGGACTCATCTTTGCAGCACCAACCCCGGACCGCCACCCCTTAGCCAGGCGTC	6300
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QY	5221	CGTCTCCTTTCATCTCTGTGCTCTTTCTGATGTTGAACCTCTTTGTGGCTGTGATCAT	5280		6301	GTGCAACCAACCAACCCAGCTGCCACCCGCGGAGGAGCAGGAAGAGAGAGTCTCCCTGGA	6360
Db	5207	CGTCTCCTTTCATCTCTGTGCTCTTTCTGATGTTGAACCTCTTTGTGGCTGTGATCAT	5266		6287	GTGCAACCAACCAACCCAGCTGCCACCCGCGGAGGAGCAGGAAGAGAGAGTCTCCCTGGA	6346
QY	5281	GGACAAATTTGAGTACTCTACCGGGGACTCTTCCATCTTAGTCTCCACCTTGGATGA	5340		6361	GAAGGGCCCGAGCTGTCTCCGATATGATGCGGACCAAGCAGAGTCTGTGGGGCGGG	6420
Db	5267	GGACAAATTTGAGTACTCTACCGGGGACTCTTCCATCTTAGTCTCCACCTTGGATGA	5326		6347	GAAGGGCCCGAGCTGTCTCCGATATGATGCGGACCAAGCAGAGTCTGTGGGGCGGG	6406
QY	5341	GTTTCATCCGGCTCTGGGCTGAAATACGACCCGCTGTGTGGGCGCATCAGTTACAATGA	5400		6421	GCTGCCCGCGGAGAGGGGCTTACAGGCTGCCGCGGGAACGAGAGCGCTGCGAGAGCG	6480
Db	5327	GTTTCATCCGGCTCTGGGCTGAAATACGACCCGCTGTGTGGGCGCATCAGTTACAATGA	5386		6407	GCTGCCCGCGGAGAGGGGCTTACAGGCTGCCGCGGGAACGAGAGCGCTGCGAGAGCG	6466
QY	5401	CATGTTTGTAGTCTGAAACATGATGCTCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5460		6481	GGGCGGCTCCAGAGCGGAGGAGGCTTACAGGCTGCCGCGGGAACGAGAGCGCTGCGAGAGCG	6540
Db	5387	CATGTTTGTAGTCTGAAACATGATGCTCCGCTCTGGGGCTGGGGAAGAAATGCCCTGC	5446		6467	GGGCGGCTCCAGAGCGGAGGAGGAGGCTTACAGGCTGCCGCGGGAACGAGAGCGCTTCTA	6526
QY	5461	TCGAGTTGCTTACAGCGCTGGTTCGATGAACATGCGCATCTCCACGAGGAGCATGAC	5520		6541	CTCTGCGACCGCTTTTGGGGCGCTGAGCCCGCGAAGCCCAAGCCCTCCCTCAGCAGCCA	6600
Db	5447	TCGAGTTGCTTACAGCGCTGGTTCGATGAACATGCGCATCTCCACGAGGAGCATGAC	5506		6527	CTCTGCGACCGCTTTTGGGGCGCTGAGCCCGCGAAGCCCAAGCCCTCCCTCAGCAGCCA	6586
QY	5521	TGTTCACTTTCAGCTCCACGCTGATGGCCCTCATCCGACGGCACTGGAGATCAAGCTGGC	5580		6601	CCCAAGCTCGCCAAACAGCTGGCCAGGAGCGGGAGCCCAACCCACAGGGGCAATGGTTCCGT	6660
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Db	5567	CCCAGTGGGACAAAGCAGCATCAGTGTGACCGGAGTTGAGGAGGAGATTCCGTTGT	5626		6630	-----	6629
QY	5641	GTGGCCAAATCTGCCACAGAGACTTTCGATGCTGGTACCAACCCCATAGAGCTGATGA	5700		6721	GCAGTCTCCCCAGAGACGCCCTTGAATCCCGCGCCCGAGCATCACCTTACAGACGCGCAATC	6780
Db	5627	GTGGCCAAATCTGCCACAGAGACTTTCGATGCTGGTACCAACCCCATAGAGCTGATGA	5686		6630	-----	6629
QY	5701	GATGACAGTGGGGAAGGTTTATGACGCTCTGATGATATTTTGACTTCTACAGAGAGAAACAA	5760		6781	CTCACCCATCCACTTTCGCGGGGCTCAGACAGCTCCCTGCTTCTCCCTCAGGCGGGCT	6840
Db	5687	GATGACAGTGGGGAAGGTTTATGACGCTCTGATGATATTTTGACTTCTACAGAGAGAAACAA	5746		6630	-----	6629
QY	5761	AACCAACAGAGACAGATGACAGGCTTCTGGAGGCTCTCCAGATGGGTCTCTGTGC	5820		6841	CAGCCGTGGGCTTTCCGAACACAAAGCCCTGTGTGAGAGAGACCCCTCAGCCAGCCCT	6900
Db	5747	AACCAACAGAGACAGATGACAGGCTTCTGGAGGCTCTCCAGATGGGTCTCTGTGC	5806		6640	CAGCCGTGGGCTTTCCGAACACAAAGCCCTGTGTGAGAGAGACCCCTCAGCCAGCCCT	6699
QY	5821	CCTGTTCACCTCTGAAAGGCCACCTCGAGCAGACACAGCCGCTGTGCTCCGAGGAGC	5880		6901	GGCCCTTGGCTCTCGAAATTTGGCTTGAACCTTACTGGGGAGAGCTCTGGA-CAGTGAAGC	6960
Db	5807	CCTGTTCACCTCTGAAAGGCCACCTCGAGCAGACACAGCCGCTGTGCTCCGAGGAGC	5866		6700	GGCCCTTGGCTCTCGAAATTTGGCTTGAACCTTACTGGGGAGAGCTCTGGA-CAGTGAAGC	6759
QY	5881	CGGGTTTTCTTCGACAGAGAGTTTCCACTCTCTCCTCAGCAATGGCGGGGCCATACAAAA	5940		6961	CTCTGTTCACAGCCCTCGCTGAGGACACGCTCACTTTTCGAGGAGGCTGTGGCCACCACTC	7020

Db	6760	CTCTGTCCAGCCCTGTGCTGAGGACACGCTCACTTTGAGGAGGCTGTGGCCACCAACTC	6819
Qy	7021	GGGCCGCTCTCCAGGACTTTCCTACGTGTCTCCCTGACCTCCCGAGTCTCACCCCTCTCCG	7080
Db	6820	GGGCCGCTCTCTCCAGGACTTTCCTACGTGTCTCCCTGACCTCCCGAGTCTCACCCCTCTCCG	6879
Qy	7081	CCGCGTGCCCAACGGTTTACCACTGCACCTGCGGACTCAGCTCGGGTGGCCGAGCACGGCA	7140
Db	6880	CCGCGTGCCCAACGGTTTACCACTGCACCTGCGGACTCAGCTCGGGTGGCCGAGCACGGCA	6939
Qy	7141	CAGCTACCAACACCCCTGACCAAGACCACTGCTGTAGCTGCACCGTGACCGCTCAGACGC	7200
Db	6940	CAGCTACCAACACCCCTGACCAAGACCACTGCTGTAGCTGCACCGTGACCGCTCAGACGC	6999
Qy	7201	CTGCATGACGAGCGCGTGTGTTCAGTGGATGAGTTTTATCATCCACACGGGGCAGTCGG	7260
Db	7000	CTGCATGACGAGCGCGTGTGTTCAGTGGATGAGTTTTATCATCCACACGGGGCAGTCGG	7059
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Db	7060	CCCTCGGGGAGGCGCTTGCCCCACCTTGGTGAGGCTCCTGTGGCCCTCCCTCCCCCTCCT	7119
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Job time : 372 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2004, 22:19:23 ; Search time 2104 Seconds
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Perfect score: 7376

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3337386 seqs, 2532474682 residues

Total number of hits satisfying chosen parameters: 6674772

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	7342	99.5	7364	9	US-09-954-456-1179
3	7342	99.5	7364	14	US-10-033-026-5
4	7316.4	99.2	7362	16	US-10-375-253-11
5	6958	94.3	7177	14	US-10-033-026-7
6	6932.4	94.0	7175	16	US-10-375-253-13
7	6535	88.6	6792	17	US-10-627-370-1
8	5289.8	71.7	7011	14	US-10-033-026-9
9	5200.4	70.5	7023	17	US-10-627-370-3
10	2592.6	35.0	6639	9	US-09-917-800A-1586
11	2507.2	34.0	7808	16	US-10-375-253-33
12	2502.2	33.9	7791	16	US-10-375-253-35
13	2488.2	33.7	7827	15	US-10-101-510-422
14	2408.4	32.7	7291	17	US-10-322-696-83

15	2402.4	32.6	7032	16	US-10-375-253-37	Sequence 37, Appl
16	2362.2	32.0	7348	17	US-10-322-696-175	Sequence 175, App
17	2362.2	32.0	7477	17	US-10-322-696-177	Sequence 177, App
18	2356.2	31.9	7089	16	US-10-375-253-39	Sequence 39, Appl
19	2341.6	31.7	7088	15	US-10-101-510-455	Sequence 455, App
20	2299.8	31.2	9704	17	US-10-322-696-80	Sequence 80, Appl
21	1865.6	25.3	5966	16	US-10-334-143-130	Sequence 130, App
22	1225.2	16.6	3596	17	US-10-435-804-5	Sequence 5, Appll
23	1179.2	16.0	3632	17	US-10-435-804-3	Sequence 3, Appll
24	1152	15.6	3632	17	US-10-435-804-4	Sequence 4, Appll
25	725.2	9.8	5565	14	US-10-029-413A-1	Sequence 1, Appll
26	716.2	9.7	6725	16	US-10-375-253-60	Sequence 60, Appll
27	714.6	9.7	6575	16	US-10-375-253-5	Sequence 5, Appll
28	703.8	9.5	6572	17	US-10-467-491-1	Sequence 1, Appll
29	698.2	9.5	7986	12	US-10-152-319A-1695	Sequence 1695, Ap
30	682.4	9.3	9014	17	US-10-377-139-9	Sequence 9, Appll
31	676.4	9.2	6083	14	US-10-029-413A-21	Sequence 21, Appll
32	676.4	9.2	6501	14	US-10-029-413A-3	Sequence 3, Appll
33	668.2	9.1	6160	14	US-10-029-413A-11	Sequence 11, Appll
34	668.2	9.1	6160	14	US-10-029-413A-13	Sequence 13, Appll
35	633	8.6	7192	17	US-10-322-696-53	Sequence 53, Appll
36	631.4	8.6	7193	14	US-10-029-413A-17	Sequence 17, Appll
37	631.4	8.6	7193	14	US-10-029-413A-19	Sequence 19, Appll
38	631.4	8.6	7193	15	US-10-205-823-49	Sequence 49, Appll
39	631.4	8.6	7193	16	US-10-411-010-13	Sequence 13, Appll
40	629.8	8.5	7635	16	US-10-375-253-1	Sequence 1, Appll
41	623.2	8.4	7362	14	US-10-029-413A-15	Sequence 15, Appll
42	597.2	8.1	6779	17	US-10-467-491-3	Sequence 3, Appll
43	527.4	7.2	6615	14	US-10-029-413A-9	Sequence 9, Appll
44	430	5.8	7660	17	US-10-322-696-50	Sequence 50, Appll
45	259	3.5	259	13	US-10-424-599-133611	Sequence 133611,

ALIGNMENTS

RESULT 1
US-10-033-026-3
; Sequence 3, Application US/10033026
; Publication No. US20020147309A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/10/033,026
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7376
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7174
US-10-033-026-3

Query Match	100.0%;	Score 7376;	DB 14;	Length 7376;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 7376;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	GC	GC	GC
Db	1	GC	GC	GC
Qy	61	GC	GC	GC
Db	61	GC	GC	GC

QY 121 GGGATGACGCGGGGCGCGGAGGCCATGGTCCGCTTCGGGGACGAGCTGGCGGCGCGCTA 180
DB 121 GGGATGACGCGGGGCGCGGAGGCCATGGTCCGCTTCGGGGACGAGCTGGCGGCGCGCTA 180
QY 181 TGGAGGCCCCGCGGGGCGGAGCGGGCGCGGGGCGCGGGGCGCGGGGCGCGGGGCGCGG 240
DB 181 TGGAGGCCCCGCGGGGCGGAGCGGGCGCGGGGCGCGGGGCGCGGGGCGCGGGGCGCGG 240
QY 241 GGGTCCCGGGGGCTCGACGCCGCGGCGAGCGGGTCCCTACAGCAATCGATCGCGGAGCG 300
DB 241 GGGTCCCGGGGGCTCGACGCCGCGGCGAGCGGGTCCCTACAGCAATCGATCGCGGAGCG 300
QY 301 CGCGCGGACCATGCGGCTGTACAAACCCCATCCGGTCAAAGCAGAACTGCTTACACGTCAA 360
DB 301 CGCGCGGACCATGCGGCTGTACAAACCCCATCCGGTCAAAGCAGAACTGCTTACACGTCNA 360
QY 361 CGGCTCGCTCTTCTTTCAGGAGAGCAAAAGTGGTCCGCAATACGCGAAGCGCATCAC 420
DB 361 CGGCTCGCTCTTCTTTCAGGAGAGCAAAAGTGGTCCGCAATACGCGAAGCGCATCAC 420
QY 421 CGAGTGGCTCCATTGAGTATATGATCCTGGCCACCATCATCGCCAACTGATCGTGT 480
DB 421 CGAGTGGCTCCATTGAGTATATGATCCTGGCCACCATCATCGCCAACTGATCGTGT 480
QY 481 GGGCTTGGAGGACGACCTCCCTGATGGGGAACAAAGCGGCGCTGGAGCA 540
DB 481 GGGCTTGGAGGACGACCTCCCTGATGGGGAACAAAGCGGCGCTGGAGCA 540
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DB 541 CAGGAGCCCTATTTTCATCGGATCTTTTGGCTTCAGGAGGAGTCAAAATCATCGCTCT 600
QY 601 GGGCTTGTCTTCCAAAGGCTCTTACCTGGGAACGCTGGAACGCTGGAACGCTTCTG 660
DB 601 GGGCTTGTCTTCCAAAGGCTCTTACCTGGGAACGCTGGAACGCTTCTG 660
QY 661 GGTGTCTCTCAAGGATCTTTGCCACGCGTGGAACTGACTTGGACCTCGCAACACTGAG 720
DB 661 GGTGTCTCTCAAGGATCTTTGCCACGCGTGGAACTGACTTGGACCTCGCAACACTGAG 720
QY 721 GGTGTGGGTGTCTGAGGCGGCTGAGCTGGTGTCTGGGATCCAAAGTTTCAGAGTGGT 780
DB 721 GGTGTGGGTGTCTGAGGCGGCTGAGCTGGTGTCTGGGATCCAAAGTTTCAGAGTGGT 780
QY 781 GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCTCGCAGATGGGCTGCTTCTTCTT 840
DB 781 GCTCAAGTCCATCATGAAGGCCATGGTTCCACTCTCGCAGATGGGCTGCTTCTTCTT 840
QY 841 TGGCATCTCATGTTTGGCATCATTTGGCTTGGAGTTCTACATGGGCAAGTTCCAAAGGC 900
DB 841 TGGCATCTCATGTTTGGCATCATTTGGCTTGGAGTTCTACATGGGCAAGTTCCAAAGGC 900
QY 901 CTGTTTCCCAACACACAGATGCGAGCCGCTGGGTGACTTCCCTGTGGCAAGGAGGC 960
DB 901 CTGTTTCCCAACACACAGATGCGAGCCGCTGGGTGACTTCCCTGTGGCAAGGAGGC 960
QY 961 CCCAGCCGGGTGTGCGAGGCGGACACTGAGTGGCGGAGTACTGGCCAGGACCCAACTT 1020
DB 961 CCCAGCCGGGTGTGCGAGGCGGACACTGAGTGGCGGAGTACTGGCCAGGACCCAACTT 1020
QY 1021 TGGCATCAACCACTTTGACATATCCTGTTTGGCATCTTGAAGTGTTCAGTGCATCAC 1080
DB 1021 TGGCATCAACCACTTTGACATATCCTGTTTGGCATCTTGAAGTGTTCAGTGCATCAC 1080
QY 1081 CATGAGGCGCTGGACTGACATCTCTATAATAACAAACGATCGGCGGCAACACTCGAA 1140
DB 1081 CATGAGGCGCTGGACTGACATCTCTATAATAACAAACGATCGGCGGCAACACTCGAA 1140
QY 1141 CTGGCTCTACTTCTTCTCTCATCATCGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
DB 1141 CTGGCTCTACTTCTTCTCTCATCATCGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200

QY 1201 GGGCGTGTCTCTCGGGGAGTTTGCACAGGAGCAGAGAGGGTGGAGAACCCGCGGCGCTT 1260
DB 1201 GGGCGTGTCTCTCGGGGAGTTTGCACAGGAGCAGAGAGGGTGGAGAACCCGCGGCGCTT 1260
QY 1261 CCTGAAGTGTGCGCGGCGCAGCAGATCGAGCGAGAGCTCAACGGGTACCTTGGAGTGGAT 1320
DB 1261 CCTGAAGTGTGCGCGGCGCAGCAGATCGAGCGAGAGCTCAACGGGTACCTTGGAGTGGAT 1320
QY 1321 CTTCAAGCGGAGGAAGTCACTGTGGCGGAGGAGCAGGAATCGAGAGGAAGTCCCC 1380
DB 1321 CTTCAAGCGGAGGAAGTCACTGTGGCGGAGGAGCAGGAATCGAGAGGAAGTCCCC 1380
QY 1381 TTTTGAAGTGTCTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACCTGATCCACGAGCA 1440
DB 1381 TTTTGAAGTGTCTGAAGAGAGCGGCCACCAAGAGAGCAGAAATGACCTGATCCACGAGCA 1440
QY 1441 GGAGGAGAGGACCGGTTTGCAGATCTCTGTCTGTTGGATCCCGCTTCGCGCGGCGAG 1500
DB 1441 GGAGGAGAGGACCGGTTTGCAGATCTCTGTCTGTTGGATCCCGCTTCGCGCGGCGAG 1500
QY 1501 CCTCAAGAGCGGAGAGCAGAGAGCTCGTCACTACTTCCGAGGAGAGAGATGTTCCG 1560
DB 1501 CCTCAAGAGCGGAGAGCAGAGAGCTCGTCACTACTTCCGAGGAGAGAGATGTTCCG 1560
QY 1561 GTTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTTGGGTGTGCTGTGCTGGT 1620
DB 1561 GTTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTTGGGTGTGCTGTGCTGGT 1620
QY 1621 GGGCTTGAACACACTGTGTGGCCATGTGTGCATTAACACAGCGCGCGGCGTATTACAC 1680
DB 1621 GGGCTTGAACACACTGTGTGGCCATGTGTGCATTAACACAGCGCGCGGCGTATTACAC 1680
QY 1681 GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTTCTCAGAGAGATGTCCTTGA 1740
DB 1681 GACCTGTATTTTGCAGAGTTTGTTCCTGGGTCTTCTTCTCAGAGAGATGTCCTTGA 1740
QY 1741 GATGTATGGCTTGGGCGCCAGAAAGTACTTCCGGTCTCTCTTCAACTGCTTTCAGCTTTGG 1800
DB 1741 GATGTATGGCTTGGGCGCCAGAAAGTACTTCCGGTCTCTCTTCAACTGCTTTCAGCTTTGG 1800
QY 1801 GGTCTATCTGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCGCATCAAGCGGGAAGCTCTT 1860
DB 1801 GGTCTATCTGTGGGAGCGTCTTTGAAGTGTCTGGGCGGCGCATCAAGCGGGAAGCTCTT 1860
QY 1861 TGGGATCAGTGTCTCGGGCGCTTCCGCTGTGAGGATCTTCAAAGTCAAGAGTACTG 1920
DB 1861 TGGGATCAGTGTCTCGGGCGCTTCCGCTGTGAGGATCTTCAAAGTCAAGAGTACTG 1920
QY 1921 GAGTCTCTCGGAACTCGTGTGTCTCTGTGTAACTCCATGAAGTCCAATCATCAGCCT 1980
DB 1921 GAGTCTCTCGGAACTCGTGTGTCTCTGTGTAACTCCATGAAGTCCAATCATCAGCCT 1980
QY 1981 GCTCTTCTTGTCTCTCTCTTCAATGTGTCTTCCGCTGTGGGATGCTGTTTGG 2040
DB 1981 GCTCTTCTTGTCTCTCTCTTCAATGTGTCTTCCGCTGTGGGATGCTGTTTGG 2040
QY 2041 GGGACAGTTTCAACTTCCAGGATGAGACTCCCAACAACTTCGACACCTTCCCTCCCGC 2100
DB 2041 GGGACAGTTTCAACTTCCAGGATGAGACTCCCAACAACTTCGACACCTTCCCTCCCGC 2100
QY 2101 CATCTCTCATGTCTTCCAGATCTGTGAGGAGGACTGGAATGCAAGTGAJGTATCACGG 2160
DB 2101 CATCTCTCATGTCTTCCAGATCTGTGAGGAGGACTGGAATGCAAGTGAJGTATCACGG 2160
QY 2161 GATCGAATCGAAGCGGCGCTCAGCAAGGAGTGTCTGCTCTTCTTCTTCTTCTTCTTCTT 2220
DB 2161 GATCGAATCGAAGCGGCGCTCAGCAAGGAGTGTCTGCTCTTCTTCTTCTTCTTCTTCTT 2220
QY 2221 GACACTGTTTGGAACTACACTCTGTGTAATGTCTTCTTGGGCGCTGCTGTGGCAACCT 2280
DB 2221 GACACTGTTTGGAACTACACTCTGTGTAATGTCTTCTTGGGCGCTGCTGTGGCAACCT 2280
QY 2281 GGGCAAGCGCCAGAGCTGACCAAGATGAAGAGGAGTGGAAAGAGCAGCCAAATCAGAA 2340

Db	2281	GGCCAAAGCGCCCAAGAGCTGACCAAGAGATGAAGAGGATGGAAGAGCAGCCAAATCAGAA	2340
Qy	2341	GCTTGTCTCTGAAAAGGCGAAAGAGTGGCTGAAAGTCAGCGCCCATGTCTGCGCGGAACAT	2400
Db	2341	GCTTGTCTCTGAAAAGGCGAAAGAGTGGCTGAAAGTCAGCGCCCATGTCTGCGCGGAACAT	2400
Qy	2401	CTCCATCGCGCCAGGACGACGAGAACTCGCGCAAGCGCGCTCGTGTGGAGACAGCGGGC	2460
Db	2401	CTCCATCGCGCCAGGACGACGAGAACTCGCGCAAGCGCGCTCGTGTGGAGACAGCGGGC	2460
Qy	2461	CAGCAGCTAGGCTGAGACACCTGCGGCGAGCTGCGAGCGCTGTACAGCGAGATGGA	2520
Db	2461	CAGCAGCTAGGCTGAGACACCTGCGGCGAGCTGCGAGCGCTGTACAGCGAGATGGA	2520
Qy	2521	CCCCAGGAGCGGCTGCGCTTCGCGCACTACCGCGCACCTGCGGCGCCGACATGAAGACGCA	2580
Db	2521	CCCCAGGAGCGGCTGCGCTTCGCGCACTACCGCGCACCTGCGGCGCCGACATGAAGACGCA	2580
Qy	2581	CCTGGACCGGCGCTGCTGTGTGGAGCTGGGCGCGACCGGCGCGGGCGCCGTGGGAGG	2640
Db	2581	CCTGGACCGGCGCTGCTGTGTGGAGCTGGGCGCGACCGGCGCGGGCGCCGTGGGAGG	2640
Qy	2641	CAAAAGCCGACCTGAGGCTGCGAGGCGCCCGAGGGCGTCCAGCCCTCCGCGCAGGCCA	2700
Db	2641	CAAAAGCCGACCTGAGGCTGCGAGGCGCCCGAGGGCGTCCAGCCCTCCGCGCAGGCCA	2700
Qy	2701	CCGGCACCGGACAAAGCAAGACCCCGCGCGGGGACCCAGAGACCGAGCAGAGGCCCC	2760
Db	2701	CCGGCACCGGACAAAGCAAGACCCCGCGCGGGGACCCAGAGACCGAGCAGAGGCCCC	2760
Qy	2761	GAAGCGGAGAGCGGGAGCGCGGTGCGCGGAGAGCGCGCGCGCGCGCACCGCAGCCCA	2820
Db	2761	GAAGCGGAGAGCGGGAGCGCGGTGCGCGGAGAGCGCGCGCGCGCGCACCGCAGCCCA	2820
Qy	2821	CAGCAAGAGGCGCGGGGCGCGGAGGCGCGAGCGCGCGCGCGCGCGAGGCGCCAGGCCC	2880
Db	2821	CAGCAAGAGGCGCGGGGCGCGGAGGCGCGAGCGCGCGCGCGCGCGAGGCGCCAGGCCC	2880
Qy	2881	CGAGGCGCGCGCGGACCAACCGCGCGCGGTCCCGGAGAGCGCGCGCGCGGAGCGC	2940
Db	2881	CGAGGCGCGCGCGGACCAACCGCGCGCGGTCCCGGAGAGCGCGCGCGCGGAGCGC	2940
Qy	2941	CCGACGCCACCGCGCGCACCGGCAACCGAGATCCGAGCAAGAGTGCCTCGCGCGCAAGGG	3000
Db	2941	CCGACGCCACCGCGCGCACCGGCAACCGAGATCCGAGCAAGAGTGCCTCGCGCGCAAGGG	3000
Qy	3001	CGAGCGGCGCGCGGACACCGCGCGGCGCCCGAGCGGGGCGCGGAGGCGGAGCGG	3060
Db	3001	CGAGCGGCGCGCGGACACCGCGCGGCGCCCGAGCGGGGCGCGGAGGCGGAGCGG	3060
Qy	3061	GGAGGAGCGCGCGGCGCACCGGCGCCCGGCACAAAGCGCAGCGCTGCTCACGAGGCTGT	3120
Db	3061	GGAGGAGCGCGCGGCGCACCGGCGCCCGGCACAAAGCGCAGCGCTGCTCACGAGGCTGT	3120
Qy	3121	GGAGAAGGAGACCAAGAGAGGAGGCGCACGAGAGAGGAGCTGAGATAGTGAAGCCGA	3180
Db	3121	GGAGAAGGAGACCAAGAGAGGAGGCGCACGAGAGAGGAGCTGAGATAGTGAAGCCGA	3180
Qy	3181	CAAGGAAAAGAGCTCCGGAACCAAGAGCGCGGAGGCGCACCTGTGTGAGACCTGAGAC	3240
Db	3181	CAAGGAAAAGAGCTCCGGAACCAAGAGCGCGGAGGCGCACCTGTGTGAGACCTGAGAC	3240
Qy	3241	TGGGACTGTGACTGTGGGTCCATGCAACACTCCAGCACCTGCTCCAGAGAGTGA	3300
Db	3241	TGGGACTGTGACTGTGGGTCCATGCAACACTCCAGCACCTGCTCCAGAGAGTGA	3300
Qy	3301	GGAAAGCAGGAGGATGAGACAAATCAGCGGAAAGTCACTCGCATGGGCGAGTCAGCGCCC	3360
Db	3301	GGAAAGCAGGAGGATGAGACAAATCAGCGGAAAGTCACTCGCATGGGCGAGTCAGCGCCC	3360
Qy	3361	AGACCCGAAACATATGTTACATATCCAGTGTATGCTGACGCGGCGCTCTTGGGGAAGCCAC	3420
Db	3361	AGACCCGAAACATATGTTACATATCCAGTGTATGCTGACGCGGCGCTCTTGGGGAAGCCAC	3420

Db	3361	AGACCCGAAACATATGTTACATATCCAGTGTATGCTGACGCGGCGCTCTTGGGGAAGCCAC	3420
Qy	3421	GGTCGTTCCAGTGTGAAACGTTGACACCTGGAAAGCAGAGAGAGGGAAGAGGTGGA	3480
Db	3421	GGTCGTTCCAGTGTGAAACGTTGACACCTGGAAAGCAGAGAGAGGGAAGAGGTGGA	3480
Qy	3481	AGCGGATGACGTTGATGAGGAGCGGCGCCCGGCGCTATCGTCCCATACAGCTCCATGTTCTG	3540
Db	3481	AGCGGATGACGTTGATGAGGAGCGGCGCCCGGCGCTATCGTCCCATACAGCTCCATGTTCTG	3540
Qy	3541	TTTAAAGCCCAACCAACCTGCTCCGCGCTTCTGCACTACATCGTGACCATGAGGTACTT	3600
Db	3541	TTTAAAGCCCAACCAACCTGCTCCGCGCTTCTGCACTACATCGTGACCATGAGGTACTT	3600
Qy	3601	CGAGGTGGTCAATCTCGTGGTCAATCGCTTTGAGCAGCATCGCCCTGCTGCTGAGGACCC	3660
Db	3601	CGAGGTGGTCAATCTCGTGGTCAATCGCTTTGAGCAGCATCGCCCTGCTGCTGAGGACCC	3660
Qy	3661	AGTGCGGACAGACTCGCCGAGGAAACACGCTCTGAAATACCTGGATTACATTTTCACTGG	3720
Db	3661	AGTGCGGACAGACTCGCCGAGGAAACACGCTCTGAAATACCTGGATTACATTTTCACTGG	3720
Qy	3721	TGCTTTTACCTTTGAGATGCTGATGAAGATGATCGACTTGGGACTGCTGCTTCAACCTGG	3780
Db	3721	TGCTTTTACCTTTGAGATGCTGATGAAGATGATCGACTTGGGACTGCTGCTTCAACCTGG	3780
Qy	3781	AGCCTATTTCCGCGACTTGTGGAAACATTTCTGGACTTTCATTTGTGCTCAGTGGCGCCCTGGT	3840
Db	3781	AGCCTATTTCCGCGACTTGTGGAAACATTTCTGGACTTTCATTTGTGCTCAGTGGCGCCCTGGT	3840
Qy	3841	GGCGTTTCTTCTCGAGCTTCTGAGGATCCAAAGGGAAGACATCAATACCATCAA	3900
Db	3841	GGCGTTTCTTCTCGAGCTTCTGAGGATCCAAAGGGAAGACATCAATACCATCAA	3900
Qy	3901	GTCTCTGAGAGTCTTCTGCTGCTTCTGCGGCGCTTCAAGACCATCAAGCGGCTGCCAAGCT	3960
Db	3901	GTCTCTGAGAGTCTTCTGCTGCTTCTGCGGCGCTTCAAGACCATCAAGCGGCTGCCAAGCT	3960
Qy	3961	CAAGGCTGTCTTTGACTGTGTGTGAATCTCCCTGAAGAAATGCTCTCAACATCTTGATTTGT	4020
Db	3961	CAAGGCTGTCTTTGACTGTGTGTGAATCTCCCTGAAGAAATGCTCTCAACATCTTGATTTGT	4020
Qy	4021	CTACATGCTCTTCAATGTTTCAATTTGCGGTCATTTGCGGTGAGCTTCTCAACATCTTGATTTGT	4080
Db	4021	CTACATGCTCTTCAATGTTTCAATTTGCGGTCATTTGCGGTGAGCTTCTCAACATCTTGATTTGT	4080
Qy	4081	TTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGAGGAGCTGAGGAGGCTCAGTATTTGGA	4140
Db	4081	TTTCTACTGCACAGATGAATCCAAAGGAGCTGGAGAGGAGCTGAGGAGGCTCAGTATTTGGA	4140
Qy	4141	TTATGAGAAGGAGGAGTGAAGCTCAGCCAGGAGTGAAGAAATACGACTTTTCACTA	4200
Db	4141	TTATGAGAAGGAGGAGTGAAGCTCAGCCAGGAGTGAAGAAATACGACTTTTCACTA	4200
Qy	4201	CGACAAATGCTCTGGGCTCTGTGAGCTGTTTCAAGTGTCCAAGGAGAGGCTGGCC	4260
Db	4201	CGACAAATGCTCTGGGCTCTGTGAGCTGTTTCAAGTGTCCAAGGAGAGGCTGGCC	4260
Qy	4261	CATGGTCTGAAACACTCCGTTGGATGCCATATGAGGAGCGGTCCTCAAGCGCTGGGTA	4320
Db	4261	CATGGTCTGAAACACTCCGTTGGATGCCATATGAGGAGCGGTCCTCAAGCGCTGGGTA	4320
Qy	4321	CCGCATGGAGCTGTCCATCTTCTACGTTGCTTACTTTTGTGCTTTTCCCTTCTTCTTCGT	4380
Db	4321	CCGCATGGAGCTGTCCATCTTCTACGTTGCTTACTTTTGTGCTTTTCCCTTCTTCTTCGT	4380
Qy	4381	CAACATCTTTTGGCTTTGATCATCATCTTCCAGGAGCAGGGGAGCAAGGTGATGC	4440
Db	4381	CAACATCTTTTGGCTTTGATCATCATCTTCCAGGAGCAGGGGAGCAAGGTGATGC	4440
Qy	4441	TGAATGAGCCTCGAGAGAAACGAGAGGGCTTGCATTTGACTTCCGCATCAGCGCCAAACC	4500
Db	4441	TGAATGAGCCTCGAGAGAAACGAGAGGGCTTGCATTTGACTTCCGCATCAGCGCCAAACC	4500

Db 6661 GAATGGAGGCCCTTGTGTCAACATCTGGTGTAGCACCCCGCGCGGTGGCGGAG 6720
Qy 6721 GCAGCTCCCGCAGACGCCCTGACTCCCGCGCCAGCATCACTTACAAAGACGGCAACTC 6780
Db 6721 GCAGCTCCCGCAGACGCCCTGACTCCCGCGCCAGCATCACTTACAAAGACGGCAACTC 6780
Qy 6781 CTCACCATCCACTTCGCGGGGCTCAGACAGCCTCCCTGCTTCTCCCGAGCCGGCT 6840
Db 6781 CTCACCATCCACTTCGCGGGGCTCAGACAGCCTCCCTGCTTCTCCCGAGCCGGCT 6840
Qy 6841 CAGCGTGGGCTTTCGAAACACACAGCCCTGCTCAGAGAGACCCCTCAGCCAGCCCT 6900
Db 6841 CAGCGTGGGCTTTCGAAACACACAGCCCTGCTCAGAGAGACCCCTCAGCCAGCCCT 6900
Qy 6901 GGCCCTGGGCTTTCGAAATGGCTCTGACCCCTTACTTGGGGCAGCGTCTGACAGTGAAGC 6960
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Qy 6961 CTCTGTCCACGCCCTGCTGAGGACACGCTCACTTTTCGAGGAGCTGTGGCACAACCTC 7020
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Qy 7021 GGGCGGCTCTCAGGAGTCTTCTAGTGTCTCTCCCTGACCTCCAGTCTCACCTCTCCG 7080
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Qy 7081 CCGGCTGCCAAACGTTTACCACTGCACCTGGGACTCAGCTCGGGTGGCGAGCAGCGCA 7140
Db 7081 CCGGCTGCCAAACGTTTACCACTGCACCTGGGACTCAGCTCGGGTGGCGAGCAGCGCA 7140
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Db 7141 CAGTACCAACACCCCTGACCAAGACCACTGCTGTAGCTGACCGTGAACCGCTCAGACGC 7200
Qy 7201 CTGATCAGCAGCGCGTGTGTTTCAGTGTGATGATTTTATCATCCACCGGGGAGTCCG 7260
Db 7201 CTGATCAGCAGCGCGTGTGTTTCAGTGTGATGATTTTATCATCCACCGGGGAGTCCG 7260
Qy 7261 CCCTCGGGGAGGCTTGGCCACCTTGGTGAAGCTCTGTGGCCCTCCCTCCCTCCCT 7320
Db 7261 CCCTCGGGGAGGCTTGGCCACCTTGGTGAAGCTCTGTGGCCCTCCCTCCCTCCCT 7320
Qy 7321 CCCCTCTTTTACTCTAGACGACGAATAAGCCCTGTTGCTGTAGTGTACGTACCGC 7376
Db 7321 CCCCTCTTTTACTCTAGACGACGAATAAGCCCTGTTGCTGTAGTGTACGTACCGC 7376

RESULT 2
US-09-954-456-1179
; Sequence 1179, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1179
; LENGTH: 7364
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1179

Query Match 99.5%; Score 7342; DB 9; Length 7364;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Qy 1 GCGCGCGCGCTCGCGCGGTGGGGCGGGGAGGTCGGTCCGCTCCCGCGGCTCCGCG 60
Db 1 GCGCGCGCGCTCGCGCGGTGGGGCGGGGAGGTCGGTCCGCTCCCGCGGCTCCGCG 60
Qy 61 GCTGCTCCGCTCTGAGCGCTGCGCGCCCGCGCCCTCCCTCCCGGGGCGGCTGGGCG 120
Db 61 GCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCGCCCTCCCTCCCGGGGCGGCTGGGCG 120
Qy 121 GGGATGCACGCGGGGCGCGGGAGCCATGCTCCGCTTCGGGGAGCGAGCTGGGGCGGCCCTA 180
Db 121 GGGATGCACGCGGGGCGCGGGAGCCATGCTCCGCTTCGGGGAGCGAGCTGGGGCGGCCCTA 180
Qy 181 TGAAGCGCCCGCGCGGAGAGCGGGCGCGGGGCGCGGGGCGCGGGGCGGGGCGCC 240
Db 181 TGAAGCGCCCGCGCGGAGAGCGGGCGCGGGGCGCGGGGCGCGGGGCGGGGCGCC 240
Qy 241 GGTCTCCGGGGGCTGCAGCCCGCGCGAGCGGGTCTCTACAAGCAATCGATCCGCGAGCG 300
Db 241 GGTCTCCGGGGGCTGCAGCCCGCGCGAGCGGGTCTCTACAAGCAATCGATCCGCGAGCG 300
Qy 301 CCGCGGACCATGGCGCTGTACAACCCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAA 360
Db 301 CCGCGGACCATGGCGCTGTACAACCCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAA 360
Qy 361 CGCGTGGCTTCTGCTTTAGCGAGGACAAAGTGTCTCGGCAATAACGCGAAGCGCATCAC 420
Db 361 CGCGTGGCTTCTGCTTTAGCGAGGACAAAGTGTCTCGGCAATAACGCGAAGCGCATCAC 420
Qy 421 CGAGTGGCTTCAATCGAGTATATGATCTGCGGCAACCATCATCGCAACTGCACTGCT 480
Db 421 CGAGTGGCTTCAATCGAGTATATGATCTGCGGCAACCATCATCGCAACTGCACTGCT 480
Qy 481 GGCCTGGAGCAGCACCTCCCTGATGGGACAAAAGCCCATGTCCGAGCGGCTGGACGA 540
Db 481 GGCCTGGAGCAGCACCTCCCTGATGGGACAAAAGCCCATGTCCGAGCGGCTGGACGA 540
Qy 541 CAGCGAGCCCTATTTTCATCGGATCTTTTCTTCGAGGAGGAGATCAAAATCATCGCTCT 600
Db 541 CAGCGAGCCCTATTTTCATCGGATCTTTTCTTCGAGGAGGAGATCAAAATCATCGCTCT 600
Qy 601 GGGCTTGTCTTCCACAAGGGCTTTTACCTGCGGAAAGCGCTGGAACGTCAATGACTTCGT 660
Db 601 GGGCTTGTCTTCCACAAGGGCTTTTACCTGCGGAAAGCGCTGGAACGTCAATGACTTCGT 660
Qy 661 GGTGCTCTCACAGGATCTTCCACCGCTGAAACTGACTTCCAGCTCGGAACACTGAG 720
Db 661 GGTGCTCTCACAGGATCTTCCACCGCTGAAACTGACTTCCAGCTCGGAACACTGAG 720
Qy 721 GGTGCTGCTGCTGAGGCCCTTGAAGTGTGTCTGGATTCGAAGTTTCAGGTGGT 780
Db 721 GGTGCTGCTGCTGAGGCCCTTGAAGTGTGTCTGGATTCGAAGTTTCAGGTGGT 780
Qy 781 GCTCAAGTCCATCATGAGGCCATGTTCCACTCCCTGCGAGATTCCTCTCTCT 840
Db 781 GCTCAAGTCCATCATGAGGCCATGTTCCACTCCCTGCGAGATTCCTCTCTCT 840

QY	841	TGCCATCCTCATGTTTGCCATCATTTGGCCTCGAGTTCACATATGGCAAGTTTCCAAGGC	900
Db	841		
QY	841	TGCCATCCTCATGTTTGCCATCATTTGGCCTCGAGTTCACATATGGCAAGTTTCCAAGGC	900
Db	841		
QY	901	CTGTITCCCCAACAGCACAGATCGGAGCCGTCGGTGACTTCCTCTGTGCAAGGAGGC	960
Db	901		
QY	901	CTGTITCCCCAACAGCACAGATCGGAGCCGTCGGTGACTTCCTCTGTGCAAGGAGGC	960
Db	901		
QY	961	CCCAGCCGGCTGTGCGAGGCGGACATGAGTGC CGGAGTACTGGCCAGGACCAACTT	1020
Db	961		
QY	1021	TGGCATCACCAAATTGACAATACTCTGTTTTGCCATCTTGACGCTGTTCAGTGCATCAC	1080
Db	1021		
QY	1021	TGGCATCACCAAATTGACAATACTCTGTTTTGCCATCTTGACGCTGTTCAGTGCATCAC	1080
Db	1021		
QY	1081	CATGGAGGCTGGACTGACATCTCTAATAACAAACGATCGCGCCGGCAACACCTCGGAA	1140
Db	1081		
QY	1141	CTGCTCTACTTCACTCCCTCATCATCATCGGCTCCTTTCAATGCTCAACTGTTGCT	1200
Db	1141		
QY	1201	GGCGTCTCTCGGGGAGTTTGCCAAAGGACGAGAGAGGCTGAGAACCGCCGCGCTT	1260
Db	1201		
QY	1261	CCTGAAGCTGGCCGCGAGCAGCAGATCGAGCGAGACTCAAACGAGGAGGAGGAGGCTT	1320
Db	1261		
QY	1321	CTTCAAGCGGAGGAAGTCACTGTCGGCCGAGGAGCAGAAATTCAGAGAGAAGTCCCC	1380
Db	1321		
QY	1381	TTTGGACGTGCTGAAGAGAGCGGCCAACAAAGAGAGCAGAAAATGACCTGATCCACGAGA	1440
Db	1381		
QY	1441	GAGGAGAGAGACCGGTTTCAGATCTCTGTGTTGGATCCCTTCGCCCGCGCCAG	1500
Db	1441		
QY	1501	CCTCAAGAGCGGGAAGCACAGAGAGTCTCATCTTCCGAGGAAGAGAGATGTTCCG	1560
Db	1501		
QY	1561	GTITTTTATCCGCGCATGTGAGGCTCAGAGCTTCTACTGGTGGTGTGTGCTGGT	1620
Db	1561		
QY	1621	GGCCCTGAACACACTGTGTGGCCATGTGTGCATTAAACACGCGCGCGGCTTACCAC	1680
Db	1621		
QY	1681	GACCTGTATTTGACAGATTGTTTTCTTGGGTCTTCTCCTCACAAGAGATGCTCCGAA	1740
Db	1681		
QY	1741	GATGTATGGCTGGGCGCCAGAGACTTTCGGTCTCTCTCTCAAATGCTTGCATTTGG	1800
Db	1741		
QY	1801	GGTATCTGTGGGAGCGTCTTTGAATGTFCTGGGCGGCCAATCAAGCCGGAGTCTCTT	1860
Db	1801		
QY	1861	TGGGATCAGTGTCTCGGGCCCTCGGCTGCTGAGGATCTTCAAAGTCAAGGACTCTG	1920
Db	1861		

Qy	1921	GAGCTCCCTGCGGAACTGTGTGTGTCCTGTGTAATCCATGAAGTCCATCATCAGCCT	1981
Db	1921	GAGCTCCCTGCGGAACTGTGTGTGTCCTGTGTAATCCATGAAGTCCATCATCAGCCT	1980
Qy	1981	GCTCTTCTTGCTCTCTCTGTTCTATTGTGTCTTCGCGCTGCTGGGATGAGCTGTTTG	2040
Db	1981	GCTCTTCTTGCTCTCTCTGTTCTATTGTGTCTTCGCGCTGCTGGGATGAGCTGTTTG	2040
Qy	2041	GGGACAGTTCAACTTCCAGGATGAGACTCCACAACCAACTTCGACACCTTCCCTGCCGC	2100
Db	2041	GGGACAGTTCAACTTCCAGGATGAGACTCCACAACCAACTTCCTGCCGC	2100
Qy	2101	CATCCTCACTGTCTTCCAGATCTCTGACGGGAGGAGCTGGAATGCAGTGATGATCAGG	2160
Db	2101	CATCCTCACTGTCTTCCAGATCTCTGACGGGAGGAGCTGGAATGCAGTGATCAGG	2160
Qy	2161	GATCGAATTCGCAAGCGCGCTCAGCAAGACGATGTTCTCGTCTCTTTTACTTCAATGTCT	2220
Db	2161	GATCGAATTCGCAAGCGCGCTCAGCAAGACGATGTTCTCGTCTCTTTTACTTCAATGTCT	2220
Qy	2221	GACACTGTTGCGAAACTACACTCTGCTGTAATGTCTTTCTGGCCATCGCTGACAACT	2280
Db	2221	GACACTGTTGCGAAACTACACTCTGCTGTAATGTCTTTCTGGCCATCGCTGACAACT	2280
Qy	2281	GGCCAAACGCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAAGCAGCCAAATCAGAA	2340
Db	2281	GGCCAAACGCCAAGAGCTGACCAAGGATGAAGAGGAGATGGAAGAAGCAGCCAAATCAGAA	2340
Qy	2341	GCTTGTCTTGAAAAGGCCAAAGATGGCTGAAGTCAGCCCATCTCTGCCGCAACAT	2400
Db	2341	GCTTGTCTTGAAAAGGCCAAAGATGGCTGAAGTCAGCCCATCTCTGCCGCAACAT	2400
Qy	2401	CTCCATCGCGCAGGACAGCAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGC	2460
Db	2401	CTCCATCGCGCAGGACAGCAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGC	2460
Qy	2461	CAGCCAGTACGGCTGCAGAACCTCGCGGCCAGCTGCGAGGGCGCTGACAACGAGATGGA	2520
Db	2461	CAGCCAGTACGGCTGCAGAACCTCGCGGCCAGCTGCGAGGGCGCTGACAACGAGATGGA	2520
Qy	2521	CCCGAGGAGCGCTGCGCTTCGCCACTACGCCCACTCGCGGCCACCTGCGGCCGCGA	2580
Db	2521	CCCGAGGAGCGCTGCGCTTCGCCACTACGCCCACTCGCGGCCACCTGCGGCCGCGA	2580
Qy	2581	CCTGGAACCGCCCTGCTGTGTGAGCTGGCGCCGACCGCGCGGGCGCTGTGGAGG	2640
Db	2581	CCTGGAACCGCCCTGCTGTGTGAGCTGGCGCCGACCGCGCGGGCGCTGTGGAGG	2640
Qy	2641	CMAAGCCCGACCTGAGGCTGCGGAGCGCCCGAGGGCGTTCGACCTTCGCGCAGGCA	2700
Db	2641	CMAAGCCCGACCTGAGGCTGCGGAGCGCCCGAGGGCGTTCGACCTTCGCGCAGGCA	2700
Qy	2701	CCGSCACCGCGACAAGACAAGACCCCGCGCGGGGACCAAGACCGAGCAGAGCCCC	2760
Db	2701	CCGSCACCGCGACAAGACAAGACCCCGCGCGGGGACCAAGACCGAGCAGAGCCCC	2760
Qy	2761	GAAGCGGAGAGCGGGAGCCCGGTGCTCCGAGGAGCGCGCGCGCGCAGCAGCA	2820
Db	2761	GAAGCGGAGAGCGGGAGCCCGGTGCTCCGAGGAGCGCGCGCGCGCAGCAGCA	2820
Qy	2821	CAGCAAGGAGCGCGGGGCCCCCGAGGCGCGGACGAGCGCGCGCGAGTCCAGGCC	2880
Db	2821	CAGCAAGGAGCGCGGGGCCCCCGAGGCGCGGACGAGCGCGCGCGAGTCCAGGCC	2880
Qy	2881	CGAGGCGCGCGCGGACCAACCGCGCGGCTCCCGAGGAGCGCGCGCGCGGAGCC	2940
Db	2881	CGAGGCGCGCGCGGACCAACCGCGCGGCTCCCGAGGAGCGCGCGCGCGGAGCC	2940
Qy	2941	CCGACGCCACCGCGCGCAACCGGATCCGAGCAAGGATGCGCGCGCGCGCAAGGG	3000
Db	2941	CCGACGCCACCGCGCGCAACCGGATCCGAGCAAGGATGCGCGCGCGCGCAAGGG	3000
Qy	3001	CGAGCGCGCGCGCGCAACCGCGCGGCCCCCGAGCGGGGCCCCCGGAGGTCGAGAGCGG	3060

Db 3001 CGAGCGGCGCGCGGACACCGCGGCGCCCCCGAGCGGGCCCCGGGAGCGGAGCGG 3060
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Db 3061 GGAGGAGCGCGCGCGGCGCACCGGGGCCCGGCAACAGCGCGAGCCTGCTCACAGAGCTGT 3120
Qy |||||||
Db 3061 GGAGGAGCGCGCGCGCGGCGCACCGGGGCCCGGCAACAGCGCGAGCCTGCTCACAGAGCTGT 3120
Qy |||||||
Db 3121 GGAGAGGAGACCAACGAGAGAGAGGCGCACGAGAGAGGCGCTGAGATAGTGGAAAGCCGA 3180
Qy |||||||
Db 3121 GGAGAGGAGAGACCAACGAGAGAGAGGCGCACGAGAGAGGCGCTGAGATAGTGGAAAGCCGA 3180
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Qy |||||||
Db 3181 CAAGGAAAGAGACTCCGGACCAACAGCCAGCCCGGAGGCCACACTGTGACCTGGAGACCAG 3240
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Db 3241 TGGGACTGTGACTGTGGGTCCCATGACACACACTCCCGAGCACCTGTCTCAGAAAGGTGGA 3300
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Db 3889 GTCTCTGAGAGTCTTGTGTTGCTGCGGCCCTCAAGACCATCAAAAGGCTGCCAAGCT 3948
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Db 4249 CATGGTGTGAAACACTCCGTTGATGCCACTATGAGGAGCAGGGTCCAAAGCCCTGGGTA 4308
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Db 4549 GGTCTCCCGCCCTTTGAATACCTTTCATCATGCGCATGATAGCCCTCAACACTGTGTGCT 4608
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Db 4621 GATGATGAAGTCTTATGATGACACCTTATGATGACGAGCTGATGCTGCTGCTGCTGCTGCT 4680
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Db 4609 GATGATGAAGTCTTATGATGACACCTTATGATGACGAGCTGATGCTGCTGCTGCTGCTGCT 4668
Qy |||||||
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Db 4669 CGTGTTCACATCCATGTTCTCCATGGAAATGCGTGTGCTGAAAGATCATCGCCCTTTGGGGTGT 4728
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Db 5149 GGCCTGTGATGAGCAGGCCAAATGCCACCGAGTGTGGAAGTACTTTTGCCTTCTTACTTT 5208
Qy |||||||

QY	5221	CGTCTCCTTCATCTTCTGTGCTCCTTTCTGATGTTGAACCTCTTTGTGCTGTGATCAT	5280
Db	5209	CGTCTCCTTCATCTTCTGTGCTCCTTTCTGATGTTGAACCTCTTTGTGCTGTGATCAT	5268
QY	5281	GGACAATTTTGAAGTACCTCACGCGGAGCTTCCATCCTTAGTTCCTCACCACTTGGATGA	5340
Db	5269	GGACAATTTTGAAGTACCTCACGCGGAGCTTCCATCCTTAGTTCCTCACCACTTGGATGA	5328
QY	5341	GTTCATCCGGTCTGGGCTGAATACCAACCGGCTGCTGTGGGCGCATCAGTTACAATGA	5400
Db	5329	GTTCATCCGGTCTGGGCTGAATACCAACCGGCTGCTGTGGGCGCATCAGTTACAATGA	5388
QY	5401	CATGTTTGAAGATCTGAACACATGTCCTCCGCTCTGGGCTGGGGAAGAAATGCCCTGC	5460
Db	5389	CATGTTTGAAGATCTGAACACATGTCCTCCGCTCTGGGCTGGGGAAGAAATGCCCTGC	5448
QY	5461	TCAGTGTGTTACAAGGCTGTTGCGATGAACATGCCCATCTCCACGAGGACATGAC	5520
Db	5449	TCAGTGTGTTACAAGGCTGTTGCGATGAACATGCCCATCTCCACGAGGACATGAC	5508
QY	5521	TGTTCACTTCACGCTCCACGCTGATGCCCTCATCCGAGCGCACTGGAGATCAAGCTGGC	5580
Db	5509	TGTTCACTTCACGCTCCACGCTGATGCCCTCATCCGAGCGCACTGGAGATCAAGCTGGC	5568
QY	5581	CCAGCTGGGACAAAGCAGATCAGTGTGAACGCGAGTTGAGGAAGGAGATTCCGTTGT	5640
Db	5569	CCAGCTGGGACAAAGCAGATCAGTGTGAACGCGAGTTGAGGAAGGAGATTCCGTTGT	5628
QY	5641	GTGGGCCAATCTGCCCCAGAACATTTGCACTTGTGTTGATGATATTTGACTTCTCAAGACGAAACA	5700
Db	5629	GTGGGCCAATCTGCCCCAGAACATTTGCACTTGTGTTGATGATATTTGACTTCTCAAGACGATGA	5688
QY	5701	GATGACAGTGGGAGAGTTTATGACGCTCTGATGATATTTGACTTCTCAAGACGAAACA	5760
Db	5689	GATGACAGTGGGAGAGTTTATGACGCTCTGATGATATTTGACTTCTCAAGACGAAACA	5748
QY	5761	AACCAAGAGACCAAGATGCAAGGCTCTCGAGGCTCTCCAGATGGGTCTGTGTGC	5820
Db	5749	AACCAAGAGACCAAGATGCAAGGCTCTCGAGGCTCTCCAGATGGGTCTGTGTGC	5808
QY	5821	CTGTTTCCACCTCTGTAAGGCCACCTGGAGCAGACACAGCCGCTGTGCTCCGAGGAGC	5880
Db	5809	CTGTTTCCACCTCTGTAAGGCCACCTGGAGCAGACACAGCCGCTGTGCTCCGAGGAGC	5868
QY	5881	CCGGTCTTTCGACAGAGAGTTCCACCTCCTCAGCAATGGCGGGGCCATACAAAA	5940
Db	5869	CCGGTCTTTCGACAGAGAGTTCCACCTCCTCAGCAATGGCGGGGCCATACAAAA	5928
QY	5941	CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAGGACCCAGGATGCACC	6000
Db	5929	CCAAGAGATGGCATCAAGAGTCTGTCTCTGGGGCACTCAAGGACCCAGGATGCACC	5988
QY	6001	CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCTGTGGGCGGTC	6060
Db	5989	CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTCCACAGAGATCCTGTGGGCGGTC	6048
QY	6061	AGGACACTGGCTGTGAGCGTTTCAATCAGACAGCATAAACCCGAGGGGCTCTGATGGGGA	6120
Db	6049	AGGACACTGGCTGTGAGCGTTTCAATCAGACAGCATAAACCCGAGGGGCTCTGATGGGGA	6108
QY	6121	GCCCCAGGCTGGGCTGGAGAGCCAGGCTCGAGCGGCTCCATGCGCGCTTGGCGCGGA	6180
Db	6109	GCCCCAGGCTGGGCTGGAGAGCCAGGCTCGAGCGGCTCCATGCGCGCTTGGCGCGGA	6168
QY	6181	GACTCAGCCGCTCAGATGCCAGCCCCCATGAAGCGTTTCAATCTCCACGCTGGCCCCAGCG	6240
Db	6169	GACTCAGCCGCTCAGATGCCAGCCCCCATGAAGCGTTTCAATCTCCACGCTGGCCCCAGCG	6228
QY	6241	GCCCCGTGGGACTCATCTTTCAGACCAACCCCGGACCGGCCCTTAGCCAGGCGTC	6300
Db	6229	GCCCCGTGGGACTCATCTTTCAGACCAACCCCGGACCGGCCCTTAGCCAGGCGTC	6288

QY	6301	GTCCGACCAACCAACCAACCGCTGCCACCGCGCAGGGAAGCAAGAGTCCCTTGA	6360
Db	6289	GTCCGACCAACCAACCAACCGCTGCCACCGCGCAGGGAAGCAAGAGTCCCTTGA	6348
QY	6361	GAAGGGGCCCAACGCTGTCTGCCGATATGGAATGGCGCAACCAAGCAGTGTCTGTGGGCGCGG	6420
Db	6349	GAAGGGGCCCAACGCTGTCTGCCGATATGGAATGGCGCAACCAAGCAGTGTCTGTGGGCGCGG	6408
QY	6421	GCTGCCCTCCGGAAGAGGGGCTTACAGGCTGCCGCGGGAACGAGAGCGCCGGCAGGAGCG	6480
Db	6409	GCTGCCCTCCGGAAGAGGGGCTTACAGGCTGCCGCGGGAACGAGAGCGCCGGCAGGAGCG	6468
QY	6481	GGGCCGCTTCCAGAGCGGAGGAGCCCTCATCTCTCTCTCGGAGAGCAGCGCTTCTA	6540
Db	6469	GGGCCGCTTCCAGAGCGGAGGAGCCCTCATCTCTCTCTCGGAGAGCAGCGCTTCTA	6528
QY	6541	CTCTCTCGACCGCTTTTGGGGCCGTGAGCCCCCGGAAGCCCAAGCCCTCTCAGCAGCCCA	6600
Db	6529	CTCTCTCGACCGCTTTTGGGGCCGTGAGCCCCCGGAAGCCCAAGCCCTCTCAGCAGCCCA	6588
QY	6601	CCCAACCTTCCGACACAGCTGGCCAGGAGCCGGACCCCAACCCACAGGGCA3TGGTTCCGT	6660
Db	6589	CCCAACCTTCCGACACAGCTGGCCAGGAGCCGGACCCCAACCCACAGGGCA3TGGTTCCGT	6648
QY	6661	GAATGGGAGCCCTTGTCTCAACATCTGTGTAGCACCCCGCGCGCTGGGGGAG	6720
Db	6649	GAATGGGAGCCCTTGTCTCAACATCTGTGTAGCACCCCGCGCGCTGGGGGAG	6708
QY	6721	GCAGCTCCCCCAGACGCCCCCTGACTCCCCGCCCAAGCATCACTACAAGA3GCCCAACTC	6780
Db	6709	GCAGCTCCCCCAGACGCCCCCTGACTCCCCGCCCAAGCATCACTACAAGA3GCCCAACTC	6768
QY	6781	CTACCCATCACTCTCGCGGGCTCAGACCGCTCTCCCTGCTCTCC3AGCGCGCT	6840
Db	6769	CTACCCATCACTCTCGCGGGCTCAGACCGCTCTCCCTGCTCTCC3AGCGCGCT	6828
QY	6841	CAGCGTGGGCTTTCCGAAACAACACGCTTACCTTGGGCGAGCCCTCA3CCAGGCCCT	6900
Db	6829	CAGCGTGGGCTTTCCGAAACAACACGCTTACCTTGGGCGAGCCCTCA3CCAGGCCCT	6888
QY	6901	GGCCCTTGGCTCTCGAATTTGGCTCTGACCTTACCTTGGGCGAGCGTCTGGA3AGTGAAGC	6960
Db	6889	GGCCCTTGGCTCTCGAATTTGGCTCTGACCTTACCTTGGGCGAGCGTCTGGA3AGTGAAGC	6948
QY	6961	CTCTGTCCAGCGCTCTGAGGACACGCTCACTTTTCGAGGAGGCTGTG3CACCAACTC	7020
Db	6949	CTCTGTCCAGCGCTCTGAGGACACGCTCACTTTTCGAGGAGGCTGTG3CACCAACTC	7008
QY	7021	GGCCGCTCTCCAGGACTTCTTAAGCTCTGCTCTCTCTGACCTCCAGTCTCA3CCCTCTCG	7080
Db	7009	GGCCGCTCTCCAGGACTTCTTAAGCTCTGCTCTCTCTGACCTCCAGTCTCA3CCCTCTCG	7068
QY	7081	CCGCGTCCCAAGGTTACCACTGACACCTGGGACTCAGCTGGGTTGGCGAGCAGGCA	7140
Db	7069	CCGCGTCCCAAGGTTACCACTGACACCTGGGACTCAGCTGGGTTGGCGAGCAGGCA	7128
QY	7141	CAGCTACCAACCTTGAACCAAGACCACTGTGTAGCTGCAACCGTCA3CCAGCG	7200
Db	7129	CAGCTACCAACCTTGAACCAAGACCACTGTGTAGCTGCAACCGTCA3CCAGCG	7188
QY	7201	CTGCATGACAGGCGGTGTGTTCAGTGTGATGATTTTATCATCAACGCGGCGAGTCGG	7260
Db	7189	CTGCATGACAGGCGGTGTGTTCAGTGTGATGATTTTATCATCAACGCGGCGAGTCGG	7248
QY	7261	CCCTCGGGGAGGCTTGGCCACCTTGTGTAGGCTCTGTGGCCCTCCCTCCCGCTCT	7320
Db	7249	CCCTCGGGGAGGCTTGGCCACCTTGTGTAGGCTCTGTGGCCCTCCCTCCCGCTCT	7308
QY	7321	CCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTGTGCTTGAGTGTAGTACCGC	7376
Db	7309	CCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTGTGCTTGAGTGTAGTACCGC	7364

RESULT 3

US-10-033-026-5
; Sequence 5, Application US/10033026
; Publication No. US20020147309A1
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/10/033,026
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/268,163
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 60/077,901
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 7364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7162
US-10-033-026-5

Query Match 99.5%; Score 7342; DB 14; Length 7364;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7364; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

Qy 1 GCGCGCGGGTGTGGGGTGGGGCGGGCGAGTCCGCTGCGGTCCCGGGCGGTCCGTG 60
Db |||||

Qy 1 GCGCGCGGGTGTGGGGTGGGGCGGGCGAGTCCGCTGCGGTCCCGGGCGGTCCGTG 60
Db |||||

Qy 61 GCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCGCCCTCCCTGCGGGCGGTGGGCGG 120
Db |||||

Qy 61 GCTGCTCCGCTCTGAGCGCTTGGCGCGCCCGCGCCCTCCCTGCGGGCGGTGGGCGG 120
Db |||||

Qy 121 GGGATGACGCGGGGCGGGAGGCAATGCTCGGTTCGGGAGCAGCTGGGCGGCGCTA 180
Db |||||

Qy 121 GGGATGACGCGGGGCGGGAGGCAATGCTCGGTTCGGGAGCAGCTGGGCGGCGCTA 180
Db |||||

Qy 181 TGGAGGCGCGGCGGAGAGCGGGCGGGGGCGGGCGGGCGGGCGGGGGCGG 240
Db |||||

Qy 181 TGGAGGCGCGGCGGAGAGCGGGCGGGGGCGGGCGGGCGGGCGGGGGCGG 240
Db |||||

Qy 241 GGGTCCCGGGGGTGTGAGCCCGGCGAGCGGTCTCTACAAGCAATCGATCGGCGAGCG 300
Db |||||

Qy 241 GGGTCCCGGGGGTGTGAGCCCGGCGAGCGGTCTCTACAAGCAATCGATCGGCGAGCG 300
Db |||||

Qy 301 CGCGCGACCATGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 360
Db |||||

Qy 301 CGCGCGACCATGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 360
Db |||||

Qy 361 CCGCTCGCTCTTCTTACGAGGAGCAACGTCGTCGCGMAATACGCGAAGCGCATCAC 420
Db |||||

Qy 361 CCGCTCGCTCTTCTTACGAGGAGCAACGTCGTCGCGMAATACGCGAAGCGCATCAC 420
Db |||||

Qy 421 CGAGTGGCTCCATTCGAGTATATGATCTGGCCACCATCATCGCCAACTGCACTCGT 480
Db |||||

Qy 421 CGAGTGGCTCCATTCGAGTATATGATCTGGCCACCATCATCGCCAACTGCACTCGT 480
Db |||||

Qy 481 GGCCCTGGAGCAGCACTCCCTGATGGGAGCAAAACGCCATGTCGAGCGGCTGGACGA 540
Db |||||

Qy 481 GGCCCTGGAGCAGCACTCCCTGATGGGAGCAAAACGCCATGTCGAGCGGCTGGACGA 540
Db |||||

Qy 541 CACGAGCCCTATTTCTATTCGGGATCTTTTGTTCGAGCGGGATCAAAATCATCGCTCT 600
Db |||||

Qy 541 CACGAGCCCTATTTCTATTCGGGATCTTTTGTTCGAGCGGGATCAAAATCATCGCTCT 600
Db |||||

Qy 601 GGGCTTTGCTTCCACAAGGCTCTTACCTCGGAAAGCGCTGGAACTCATGGATTCGT 660
Db |||||

Qy 601 GGGCTTTGCTTCCACAAGGCTCTTACCTCGGAAAGCGCTGGAACTCATGGATTCGT 660
Db |||||

Qy 661 GGTGCTCTCACAGGGATCCTTGCACGGCTGGAACTGACTTGCACCTGCGAACACTGAG 720
Db |||||

Qy 661 GGTGCTCTCACAGGGATCCTTGCACGGCTGGAACTGACTTGCACCTGCGAACACTGAG 720
Db |||||

Qy 721 GGTGCTGCGTGTCTGAGGCGGCTGAGCTGCTGAGCTGCTGAGGATCCAAAGTTTGCAGGTGGT 780
Db |||||

Qy 721 GGTGCTGCGTGTCTGAGGCGGCTGAGCTGCTGAGCTGCTGAGGATCCAAAGTTTGCAGGTGGT 780
Db |||||

Qy 781 GCTCAAGTCCATCATGAAAGGCCATGGTTCCACCTCTGCAGATTGGGCTGCTTCTTCTT 840
Db |||||

Qy 781 GCTCAAGTCCATCATGAAAGGCCATGGTTCCACCTCTGCAGATTGGGCTGCTTCTTCTT 840
Db |||||

Qy 841 TGGCATCTCATGTTTGGCATCATTTGGCTCTGAGTTCTAATGGGCAAGTTCCAAAGGC 900
Db |||||

Qy 841 TGGCATCTCATGTTTGGCATCATTTGGCTCTGAGTTCTAATGGGCAAGTTCCAAAGGC 900
Db |||||

Qy 901 CTGTTTTCCCAACAGACAGATCGGAGCCCTGGGTGACTTCCCTGTGCGAAGGAGGC 960
Db |||||

Qy 901 CTGTTTTCCCAACAGACAGATCGGAGCCCTGGGTGACTTCCCTGTGCGAAGGAGGC 960
Db |||||

Qy 961 CCCAGCCCGGCTGTGCGAGGCGGACACTGAGTGC CGGGAGTACTTGGCCAGGACCCAACTT 1020
Db |||||

Qy 961 CCCAGCCCGGCTGTGCGAGGCGGACACTGAGTGC CGGGAGTACTTGGCCAGGACCCAACTT 1020
Db |||||

Qy 1021 TGGCATCACCACTTTGACAAATCTCTGTTTGGCATCTTGCAGGTGTTCCAGTGCATCAC 1080
Db |||||

Qy 1021 TGGCATCACCACTTTGACAAATCTCTGTTTGGCATCTTGCAGGTGTTCCAGTGCATCAC 1080
Db |||||

Qy 1081 CATGGAGGCTGACACTGACATCTCTATATAAAGAGTGGCGGCGGCAACCTTGGAA 1140
Db |||||

Qy 1081 CATGGAGGCTGACACTGACATCTCTATATAAAGAGTGGCGGCGGCAACCTTGGAA 1140
Db |||||

Qy 1141 CTGGCTTACTTCTCATCTCTCATCATCGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
Db |||||

Qy 1141 CTGGCTTACTTCTCATCTCTCATCATCGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1200
Db |||||

Qy 1201 GGGCGTGTCTCTCGGGGAGTTTCCAAAGGAGCGAGAGGCTGAGAAACCGCGCGCTT 1260
Db |||||

Qy 1201 GGGCGTGTCTCTCGGGGAGTTTCCAAAGGAGCGAGAGGCTGAGAAACCGCGCGCTT 1260
Db |||||

Qy 1261 CCTGAGAGTGGCGCGGAGCAGAGTCCGAGCGAGAGGCTCAAGGGTACCTGAGTGGAT 1320
Db |||||

Qy 1261 CCTGAGAGTGGCGCGGAGCAGAGTCCGAGCGAGAGGCTCAAGGGTACCTGAGTGGAT 1320
Db |||||

Qy 1321 CTTCAAGGCGGAGGAACTCATGTGCGCGAGGAGGACAGGAATGCAGAGAGAGTCCCC 1380
Db |||||

Qy 1321 CTTCAAGGCGGAGGAACTCATGTGCGCGAGGAGGACAGGAATGCAGAGAGAGTCCCC 1380
Db |||||

Qy 1381 TTTGGACGTCTGAAAGAGCGGCGCACCAAGAGAGCAGAAATGACCTGATCCACGAG 1440
Db |||||

Qy 1381 TTTGGACGTCTGAAAGAGCGGCGCACCAAGAGAGCAGAAATGACCTGATCCACGAG 1440
Db |||||

Qy 1441 GGAGGAGAGGACCGGTTTGCAGATCTCTGCTGTGTTGATCCCTTCCCGCGCGCAG 1500
Db |||||

Qy 1441 GGAGGAGAGGACCGGTTTGCAGATCTCTGCTGTGTTGATCCCTTCCCGCGCGCAG 1500
Db |||||

Qy 1501 CCTCAAGAGCGGAGAGCAGAGAGCTCGTATATCTTCCGAGGAGAGAGAGATGTTCCG 1560
Db |||||

Qy 1501 CCTCAAGAGCGGAGAGCAGAGAGCTCGTATATCTTCCGAGGAGAGAGAGATGTTCCG 1560
Db |||||

Qy 1561 GTTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTTGGGTGGTGTGCTGCGTGGT 1620
Db |||||

Qy 1561 GTTTTTTATCCGGCGCATGGTGAAGGCTCAGAGCTTCTACTTGGGTGGTGTGCTGCGTGGT 1620
Db |||||

Qy 1621 GGCCCTGAAACACTGTGTGTCGTCATGTCATTAACACAGCCGCGCGGCTTACCAC 1680
Db |||||

Qy 1621 GGCCCTGAAACACTGTGTGTCGTCATGTCATTAACACAGCCGCGCGGCTTACCAC 1680
Db |||||

Qy 1681 GACCTGTATTTTTCAGAGTTTCTTTTCTTGGGTCTTCTTCTCAGAGAGATGTTCCCTGAA 1740
Db |||||

Qy 1681 GACCTGTATTTTTCAGAGTTTCTTTTCTTGGGTCTTCTTCTCAGAGAGATGTTCCCTGAA 1740
Db |||||

QY 6121 GCCCCAGCCTGGGCTCGAGAGCAGCGGTGAGCGGCTCCATGCCCCCGCTTTCGCGCGGA 6180
Db 6109 GCCCCAGCCTGGGCTCGAGAGCAGCGGTGAGCGGCTCCATGCCCCCGCTTTCGCGCGGA 6168
QY 6181 GACTCAGCCGTCACAGATGCCAGCCCCATGAGCGCTCCATCTCCACGCTGGCCCGAGG 6240
Db 6169 GACTCAGCCGTCACAGATGCCAGCCCCATGAGCGCTCCATCTCCACGCTGGCCCGAGG 6228
QY 6241 GCCCCGCTGGGACTCATCTTTTGAGCACCACCCCGGACCCGCCACCCCTTAGCAGCGCTC 6300
Db 6229 GCCCCGCTGGGACTCATCTTTTGAGCACCACCCCGGACCCGCCACCCCTTAGCAGCGCTC 6288
QY 6301 GTGCGACACACACACACACCGCTGCCACCCCGCGCAGGAGCAGAGATCCCTCGA 6360
Db 6289 GTGCGACACACACACACCGCTGCCACCCCGCGCAGGAGCAGAGATCCCTCGA 6348
QY 6361 GAAGGGCCCCAGCTGCTGCCGATATGATGGCGCCACCAAGCAGTGTGTGGGCGCGG 6420
Db 6349 GAAGGGCCCCAGCTGCTGCCGATATGATGGCGCCACCAAGCAGTGTGTGGGCGCGG 6408
QY 6421 GCTGCCCGCGGAGAGGGCCTACAGGCTGCCGGCGGGAACGAGAGCGCGCGCAGAGCG 6480
Db 6409 GCTGCCCGCGGAGAGGGCCTACAGGCTGCCGGCGGGAACGAGAGCGCGCGCAGAGCG 6468
QY 6481 GGGCGGCTCCAGGAGCGGAGGAGCCCTCATCTCTCTCGAGAGAGCAGCGTTCTTA 6540
Db 6469 GGGCGGCTCCAGGAGCGGAGGAGCCCTCATCTCTCTCGAGAGAGCAGCGTTCTTA 6528
QY 6541 CTCCTGCGACCGCTTTGGGGCGGCTGAGCCCGGAGCCCAAGCCCTCCCTCAGCAGCA 6600
Db 6529 CTCCTGCGACCGCTTTGGGGCGGCTGAGCCCGGAGCCCAAGCCCTCCCTCAGCAGCA 6588
QY 6601 CCCAAGCTCGCCCAACAGCTGGCAGGAGCGGGACCCCAACCCACAGGGCAGTGTTCGT 6660
Db 6589 CCCAAGCTCGCCCAACAGCTGGCAGGAGCGGGACCCCAACCCACAGGGCAGTGTTCGT 6648
QY 6661 GAATGGAGCCCTTGTGTGAACATCTGTGTCTAGACACCCCGCGCGGCTGGGCGGAG 6720
Db 6649 GAATGGAGCCCTTGTGTGAACATCTGTGTCTAGACACCCCGCGCGGCTGGGCGGAG 6708
QY 6721 GCAGCTCCCGCAGAGCGCCCTGACTCCCGCGCCAGCATCACTACAGAGCGCCCACTC 6780
Db 6709 GCAGCTCCCGCAGAGCGCCCTGACTCCCGCGCCAGCATCACTACAGAGCGCCCACTC 6768
QY 6781 CTCACCCATCCACTTCGCGGGGCTCAGACAGCCCTCCCTGCTTCTCCCGAGGCGGCT 6840
Db 6769 CTCACCCATCCACTTCGCGGGGCTCAGACAGCCCTCCCTGCTTCTCCCGAGGCGGCT 6828
QY 6841 CAGCGCTGGCTTTCGGAACACACCGCCCTGTCAGAGAGACCCCTCAGCGAGCCCT 6900
Db 6829 CAGCGCTGGCTTTCGGAACACACCGCCCTGTCAGAGAGACCCCTCAGCGAGCCCT 6888
QY 6901 GGGCCCTGGCTCTCGAATTGGCTCTGACCCCTTACTCGGGGAGCGTCTGGACAGTGGC 6960
Db 6889 GGGCCCTGGCTCTCGAATTGGCTCTGACCCCTTACTCGGGGAGCGTCTGGACAGTGGC 6948
QY 6961 CTCCTGCAAGCCCTGCTGAGGACACGCTCACTTCGAGGAGGCTGTGGCCACCACTC 7020
Db 6949 CTCCTGCAAGCCCTGCTGAGGACACGCTCACTTCGAGGAGGCTGTGGCCACCACTC 7008
QY 7021 GGGCGCTCCCTCAGGACTCTTAGCTGCTCTCCCTGACCTCCAGCTCCACCTCTCCG 7080
Db 7009 GGGCGCTCCCTCAGGACTCTTAGCTGCTCTCCCTGACCTCCAGCTCCACCTCTCCG 7068
QY 7081 CCGCTGCCCCAACGGTTACCACTGACCCCTGGGACTCAGCTCGGCTGGCGAGCAGCGCA 7140
Db 7069 CCGCTGCCCCAACGGTTACCACTGACCCCTGGGACTCAGCTCGGCTGGCGAGCAGCGCA 7128
QY 7141 CAGCTACCAACCCCTGACCAAGACCACTGTGTGTAGCTGACCGCTCAGACGC 7200
Db 7129 CAGCTACCAACCCCTGACCAAGACCACTGTGTGTAGCTGACCGCTCAGACGC 7188
QY 7201 CTGCATGCAGAGGCGTGTGTTCCAGTGATGATTTTATCATCCACACGCGGCGAGTCGG 7260

Db 7189 CTGCATGCAGAGGCGTGTGTTCCAGTGATGATTTTATCATCCACACGCGGAGTCGG 7248
QY 7261 CCCTCGGGGAGGCGCTTGCACACCTTGGTGAAGGCTCCTGTGGCCCTCCCTCCCTCCT 7320
Db 7249 CCCTCGGGGAGGCGCTTGCACACCTTGGTGAAGGCTCCTGTGGCCCTCCCTCCCTCCT 7308
QY 7321 CCCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTGCTTGAAGTGTACGTPACGCG 7376
Db 7309 CCCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTGCTTGAAGTGTACGTPACGCG 7364

RESULT 4

US-10-375-253-11
; Sequence 11, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10/375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or: PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 7362
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (144)...(7163)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(143)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (7161)...(7362)
US-10-375-253-11

Query Match 99.2%; Score 7316.4; DB 16; Length 7362;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 7361; Conservative 0; Mismatches 1; Indels 14; Gaps 3;

QY 1 GCGGCGCGGCTCGCGGCTGGGCGCGGAGGTCCGCTCGGCTCCCGGCGGCTCCG 60
Db 1 GCGGCGCGGCTCGCGGCTGGGCGCGGAGGTCCG-TGCGGTCCCGGCGGCTCCG 59
QY 61 GCTGCTCCGCTCTGAGCGCTTGGCGGCGCGCGGCTCCCTGCGGCGGCGGCT 120
Db 60 GCTGCTCCGCTCTGAGCGCT-GCGGCGCGCGGCTCCCTGCGGCGGCGGCT 118

[illegible][illegible]

Db 2279 GGCACAGCCGCAAGAGCTGACCAAGATGAAGAGGAGATGGAAGAAGCAGCCAAATCAGAA 2338
QY 2341 GCTTGTCTGCGAAAGCGCCAAAGAGTGTGCTGAAGTTCAGCCCATGCTGCGCGCAACAT 2400
Db 2339 GCTTGTCTGCGAAAGCGCCAAAGAGTGTGCTGAAGTTCAGCCCATGCTGCGCGCAACAT 2398
QY 2401 CTCATCGCGCCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGCG 2460
Db 2399 CTCATCGCGCCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCGGCG 2458
QY 2461 CAGCAGCTACGGCTGTCAGAACTCGGGGCCAGCTGCGAGGCGCTGTACAGCGAATGGA 2520
Db 2459 CAGCAGCTACGGCTGTCAGAACTCGGGGCCAGCTGCGAGGCGCTGTACAGCGAATGGA 2518
QY 2521 CCCGAGGAGCGCTGCGCTTCGCCACTACGCGCCACCTGCGGGCCCGACATGAAGACCA 2580
Db 2519 CCCGAGGAGCGCTGCGCTTCGCCACTACGCGCCACCTGCGGGCCCGACATGAAGACCA 2578
QY 2581 CTTGACCGCGCCGCTGCTGCTGAGCTGGGCGCGACCGCGCGCGGGGCCCGTGGGAGG 2640
Db 2579 CTTGACCGCGCCGCTGCTGCTGAGCTGGGCGCGACCGCGCGCGGGGCCCGTGGGAGG 2638
QY 2641 CAAAGCCGACCTGAGGCTGCGAGGCCCGCCAGGGCGTGCACCTCGCGCAGGACCA 2700
Db 2639 CAAAGCCGACCTGAGGCTGCGAGGCCCGCCAGGGCGTGCACCTCGCGCAGGACCA 2698
QY 2701 CCGGCACCGCGCAAGGACAAAGCACCCTCGCGCGGGGACAGGACCGAGCAGAGGCCCC 2760
Db 2699 CCGGCACCGCGCAAGGACAAAGCACCCTCGCGCGGGGACAGGACCGAGCAGAGGCCCC 2758
QY 2761 GAAAGCGGAGAGCGGGGAGCCCGGTGCCGGGAGAGCGCGCGCGGCCGACCCGAGCCA 2820
Db 2759 GAAAGCGGAGAGCGGGGAGCCCGGTGCCGGGAGAGCGCGCGCGGCCGACCCGAGCCA 2818
QY 2821 CAGCAAGAGGCGCGGGGCCCGCGAGCGCGGAGCGAGCGCGCCGAGGCCAGGCC 2880
Db 2819 CAGCAAGAGGCGCGGGGCCCGCGAGCGCGGAGCGAGCGCGGCCGAGGCCAGGCC 2878
QY 2881 CGAGGCGCGCGCGCGCACACCGCGCGGGCTCCCGCGAGGAGCGCGCGCGGAGGCC 2940
Db 2879 CGAGGCGCGCGCGCGCACACCGCGCGGGCTCCCGCGAGGAGCGCGCGCGGAGGCC 2938
QY 2941 CCGAGCGCACCGCGCGCACCGGCAACAGGATCCGAGCAAGAGTGCCTCGCGCGCCAAAGG 3000
Db 2939 CCGAGCGCACCGCGCGCACCGGCAACAGGATCCGAGCAAGAGTGCCTCGCGCGCCAAAGG 2998
QY 3001 CGAGCGCGCGCGCGCACCGCGCGGCCCGCGAGCGGGGCCCGGGAGCGGAGCGG 3060
Db 2999 CGAGCGCGCGCGCGCACCGCGCGGCCCGCGAGCGGGGCCCGGGAGCGGAGCGG 3058
QY 3061 GGAGAGCGCGCGCGCGCACCGGGCCCGGCACAAGCGCGAGCTGTCTACAGAGGCTGT 3120
Db 3059 GGAGAGCGCGCGCGCGCACCGGGCCCGGCACAAGCGCGAGCTGTCTACAGAGGCTGT 3118
QY 3121 GGAGAGGAGACCAAGGAGAGGAGGCCACCGAGAGGAGGCTGAGATGTGGAAGCCGA 3180
Db 3119 GGAGAGGAGAGACCAAGGAGAGGAGGCCACCGAGAGGAGGCTGAGATGTGGAAGCCGA 3178
QY 3181 CAAAGAAAAGAGCTCCCGAAACACAGCCCGCGGAGCCACACTGTGACCTGGAGAGCCAG 3240
Db 3179 CAAAGAAAAGAGCTCCCGAACCACAGCCCGGAGGCCACACTGTGACCTGGAGAGCAAG 3238
QY 3241 TGGGACTGTGACTGTGGTCCCATGCAACACTGCCCCAGCACACTGTCTCCAGAAAGGTGGA 3300
Db 3239 TGGGACTGTGACTGTGGTCCCATGCAACACTGCCCCAGCACACTGTCTCCAGAAAGGTGGA 3298
QY 3301 GGAACAGCAGAGGATGAGACATCAGCGAAAGTCACTCGCATGGGCGAGTCAGCCCC 3360
Db 3299 GGAACAGCAGAGGATGAGACATCAGCGAAAGTCACTCGCATGGGCGAGTCAGCCCC 3358
QY 3361 AGACCCGAACACTATTGTACATATCCCAAGTATGCTGACGGGCCCTCTTGGGGAGGCCAC 3420
Db 3359 AGACCCGAACACTATTGTACATATCCCAAGTATGCTGACGGGCCCTCTTGGGGAGGCCAC 3418

QY 3421 GGTGTTCCAGTGGTAACGTGGACCTGGAAAGCCAAAGCAGCAGAGGGGAAGAGGAGGTGGA 3480
Db 3419 GGTGTTCCAGTGGTAACGTGGACCTGGAAAGCCAAAGCAGCAGAGGGGAAGAGGAGGTGGA 3478
QY 3481 AGCGGATGACGTGATGAGGAGCGGCCCGCGCTATCGTCCATACAGCTCATGTTCTG 3540
Db 3479 AGCGGATGACGTGATGAGGAGCGGCCCGCGCTATCGTCCATACAGCTCATGTTCTG 3538
QY 3541 TTTAAGCCCAACAACTGCTCCGCCCTTCTGCGCATACATCGTGACCATGAGGTACTT 3600
Db 3539 TTTAAGCCCAACAACTGCTCCGCCCTTCTGCGCATACATCGTGACCATGAGGTACTT 3598
QY 3601 CGAGTGGTCAATCTCTGCTGCTGATCGGCTTGAGCAGCATCGCCCTGCTGAGGACCC 3660
Db 3599 CGAGTGGTCAATCTCTGCTGCTGATCGGCTTGAGCAGCATCGCCCTGCTGAGGACCC 3658
QY 3661 AGTCGCACAGACTCGCCCAAGAACAAAGCTCTGAAATACCTGGATTACATTTTCACTGG 3720
Db 3659 AGTCGCACAGACTCGCCCAAGAACAAAGCTCTGAAATACCTGGATTACATTTTCACTGG 3718
QY 3721 TGTCTTTACCTTTGAGATGATGATAAAGATGATCGACTTGGGACTGCTGCTTCAACCTGG 3780
Db 3719 TGTCTTTACCTTTGAGATGATGATAAAGATGATCGACTTGGGACTGCTGCTTCAACCTGG 3778
QY 3781 AGCCTATTTCCGGGACTTGTGGAACTTCTGGACTTCAATGTGTGCTGAGTGCGCCCTGGT 3840
Db 3779 AGCCTATTTCCGGGACTTGTGGAACTTCTGGACTTCAATGTGTGCTGAGTGCGCCCTGGT 3838
QY 3841 GGCCTTTGCTTTCTCGAGCTTCGTGGGAGATCCAAAGGGAAAGACATCAATACCATCAA 3900
Db 3839 GGCCTTTGCTTTCTC-----AGGATCCAAAGGGAAAGACATCAATACCATCAA 3886
QY 3901 GTCTCTGAGAGTCTTCTGCTGCTGCGGCCCTCAAGACCATCAACCGGCTGCCCAAGCT 3960
Db 3887 GTCTCTGAGAGTCTTCTGCTGCTGCGGCCCTCAAGACCATCAACCGGCTGCCCAAGCT 3946
QY 3961 CAAAGCTGTGTTGACTGTGTGTGAACCTCCCTGAAAGAAATGCTCAACATCTTGATTGT 4020
Db 3947 CAAAGCTGTGTTGACTGTGTGTGAACCTCCCTGAAAGAAATGCTCAACATCTTGATTGT 4006
QY 4021 CTACATGCTCTTCAATGTTCAATTTGCGGTCAATGCGGTGAGCTCTTCAAGAGGAATTT 4080
Db 4007 CTACATGCTCTTCAATGTTCAATTTGCGGTCAATGCGGTGAGCTCTTCAAGAGGAATTT 4066
QY 4081 TTTCTACTGCACAGATGAATCCAAAGAGCTTGGAGAGGAGCTGCGGGGTCAAGTTTGGGA 4140
Db 4067 TTTCTACTGCACAGATGAATCCAAAGAGCTTGGAGAGGAGCTGCGAGGGGTCAAGTTTGGGA 4126
QY 4141 TTATGAGAAAGAGGAAGTGAAGCTCAGCCAGCGCAGTGAAGAAATACGACTTTTCACTA 4200
Db 4127 TTATGAGAAAGAGGAAGTGAAGCTCAGCCAGCGCAGTGAAGAAATACGACTTTTCACTA 4186
QY 4201 CGAACATGTGCTCTGGGCTCTGCTGACGCTGTTCACAGTGTCCACGGGAGAGGCTGGCC 4260
Db 4187 CGAACATGTGCTCTGGGCTCTGCTGACGCTGTTCACAGTGTCCACGGGAGAGGCTGGCC 4246
QY 4261 CATGCTGTGAACACTCCGTTGGATGCCACTATAGGAGCAGGGTCCAAAGCCCTGGGTA 4320
Db 4247 CATGCTGTGAACACTCCGTTGGATGCCACTATAGGAGCAGGGTCCAAAGCCCTGGGTA 4306
QY 4321 CCGCATGGAGCTGTCCATCTTCTACGTGGTCTACTTTGTGGTCTTTCCCTTCTTCTCGT 4380
Db 4307 CCGCATGGAGCTGTCCATCTTCTACGTGGTCTACTTTGTGGTCTTTCCCTTCTTCTCGT 4366
QY 4381 CAACATCTTTGTGGCTTGTATCATCATCACTTCCAGGAGCAGGGGACAGGTGATGTC 4440
Db 4367 CAACATCTTTGTGGCTTGTATCATCATCACTTCCAGGAGCAGGGGACAGGTGATGTC 4426
QY 4441 TGAATCGAGCTGGAGAAAGAACGAGAGGGCTTGCAATTGACTTGCCTCATCAGCGCCAAACC 4500
Db 4427 TGAATCGAGCTGGAGAAAGAACGAGAGGGCTTGCAATTGACTTGCCTCATCAGCGCCAAACC 4486

Qy	4501	CCTGACACGGTACATGATGCCCCAAAACCGGCGAGTGGTTCCAGTATTAAGACGTGGACATTTTGT	4561
Db	4487	CCTGACACGGTACATGATGCCCCAAAACCGGCGAGTGGTTCCAGTATTAAGACGTGGACATTTTGT	4546
Qy	4561	GGTCTCCCGGCCCTTTGAATACTTTCATCATGCGCCATGATAGCCCTCAACACTGTGGTGCT	4620
Db	4547	GGTCTCCCGGCCCTTTGAATACTTTCATCATGCGCCATGATAGCCCTCAACACTGTGGTGCT	4606
Qy	4621	GATGATGAAGTTCTPATGATGCACCCCTATGAGTACGAGCTGATGTGAAATGSCCTGAAACAT	4680
Db	4607	GATGATGAAGTTCTPATGATGCACCCCTATGAGTACGAGCTGATGTGAAATGSCCTGAAACAT	4666
Qy	4681	CGTGTTACATTCATGTTCTCCATGGAATGGGTGCTGAAGATCATGCCCTTTGGGGTGCT	4740
Db	4667	CGTGTTACATTCATGTTCTCCATGGAATGGGTGCTGAAGATCATGCCCTTTGGGGTGCT	4726
Qy	4741	GAACATATTTACAGAGATGCCGTGGAATGCTTTGACTTTGTCACTGTGTTGGGAAGTATTAC	4800
Db	4727	GAACATATTTACAGAGATGCCGTGGAATGCTTTGACTTTGTCACTGTGTTGGGAAGTATTAC	4786
Qy	4801	TGATATTTTATGTAACAGAGATTTGGGAAAACGAACAATTTTCATCAACCTCAGCTTTCCTCCG	4860
Db	4787	TGATATTTTATGTAACAGAGATTTGGGAAAACGAACAATTTTCATCAACCTCAGCTTTCCTCCG	4846
Qy	4861	CCTCTTTGAGCTGCGCGGTGATCAAGCTGCTCCGCCAGGGCTACACATCCGCATCCT	4920
Db	4847	CCTCTTTGAGCTGCGCGGTGATCAAGCTGCTCCGCCAGGGCTACACATCCGCATCCT	4906
Qy	4921	GCCTGACACTTTGTCCAGTCCCTCAAGGCCCTGCCCTAGCTGTGCTGCTCATTCGCAT	4980
Db	4907	GCCTGACACTTTGTCCAGTCCCTCAAGGCCCTGCCCTAGCTGTGCTGCTCATTCGCAT	4966
Qy	4981	GCCTGTTCTTCATCTACGCCATCATCGGCATGCGAGTGTTTTGGGAATATGCCCTGATGA	5040
Db	4967	GCCTGTTCTTCATCTACGCCATCATCGGCATGCGAGTGTTTTGGGAATATGCCCTGATGA	5026
Qy	5041	TGACACAGCATCAACCGCCACAACACTCCCGAGCTTTTGGAGCAATATGCCCTGATGCT	5100
Db	5027	TGACACAGCATCAACCGCCACAACACTCCCGAGCTTTTGGAGCAATATGCCCTGATGCT	5086
Qy	5101	GTTTCAGAGCGCCACGGGGAGGCTCGCACGAGATCATGCTGCTCCGCTGAGCAACCA	5160
Db	5087	GTTTCAGAGCGCCACGGGGAGGCTCGCACGAGATCATGCTGCTCCGCTGAGCAACCA	5146
Qy	5161	GGCCTGTGATGAGCAGCGCCAAATGCACCGAGTGTGGAAGTGACTTTGCCCTACTTCTACTT	5220
Db	5147	GGCCTGTGATGAGCAGCGCCAAATGCACCGAGTGTGGAAGTGACTTTGCCCTACTTCTACTT	5206
Qy	5221	CGTCTCCTTCATCTTCCTGTGCTCTTTCTGATGTTGAACTCTTTGTGGCTGTGATCAT	5280
Db	5207	CGTCTCCTTCATCTTCCTGTGCTCTTTCTGATGTTGAACTCTTTGTGGCTGTGATCAT	5266
Qy	5281	GGACAAATTTTGAGTACCTTCACGGGGACTCTTCATCCTTAGTCTCTCACCACTTGGATGA	5340
Db	5267	GGACAAATTTTTGAGTACCTTCACGGGGACTCTTCATCCTTAGTCTCTCACCACTTGGATGA	5326
Qy	5341	GTTTCATCCGGGTCTGGGTGAATACGACCGCGCTGCGGTGGCGCATCAGTTTACAAATGA	5400
Db	5327	GTTTCATCCGGGTCTGGGTGAATACGACCGCGCTGCGGTGGCGCATCAGTTTACAAATGA	5386
Qy	5401	CATGTTTGGATGCTGAAACACATGTCCTCCGCTCTCGGGCTGGGGAGAGAAATGCCCTGC	5460
Db	5387	CATGTTTGGATGCTGAAACACATGTCCTCCGCTCTCGGGCTGGGGAGAGAAATGCCCTGC	5446
Qy	5461	TCGAGTTGCTTAAAGCGCCTGGTTTCGATGAACATGCCCATCTCCAAACGAGGACATGAC	5520
Db	5447	TCGAGTTGCTTAAAGCGCCTGGTTTCGATGAACATGCCCATCTCCAAACGAGGACATGAC	5506
Qy	5521	TGTTTCATCTCACGCTCAGCTGATGGGCCCTCATCCGGACCGCATCTGAGATCAAGCTGGC	5580
Db	5507	TGTTTCATCTCACGCTCAGCTGATGGGCCCTCATCCGGACCGCATCTGAGATCAAGCTGGC	5566
Qy	5581	CCCAGCTGGGACAAAGCAGCATCAGTGTGACGGCGAGTTGAGGAGAGAGATTTTCCGTTGT	5640

Db	5567	 CCCAGCTGGGCAAAAGCAGCATCAGTGTGACCGGAGTTTGAGAAAGGAGATTTCCGTTGT	5626
Qy	5641	GTGGGCCAATCTGCCCCAGAAAGACTTTGGACTTGTCTGTGTACCAACCCTCAAGCCTGATGA	5700
Db	5627	GTGGGCCAATCTGCCCCAGAGACTTTGGACTTGTCTGTGTACCAACCCTCAAGCCTGATGA	5686
Qy	5701	GATGACAGTGGGGAAGTTTATGCAAGCTCTGATGATATTTGACTTCTCAAGCAGAACAA	5760
Db	5687	GATGACAGTGGGGAAGTTTATGCAAGCTCTGATGATATTTGACTTCTCAAGCAGAACAA	5746
Qy	5761	AACACACAGAGACCAAGATGCAGCAGGCTCTGGAGGCCTCTCCAGATGGTCTCTGTGTC	5820
Db	5747	AACACACAGAGACCAAGATGCAGCAGGCTCTGGAGGCCTCTCCAGATGGTCTCTGTGTC	5806
Qy	5821	CCTGTTCCACCTCTGAAAGGCCACCTCGAGCAGACACAGCCGGCTGTGCTCCGAGGAGC	5880
Db	5807	CCTGTTCCACCTCTGAAAGGCCACCTCGAGCAGACACAGCCGGCTGTGCTCCGAGGAGC	5866
Qy	5881	CCGGGTTTTCTTTCGACAGAAAGTTTCACTCTCTCAGCAATATGGCGGGCCATACAAAA	5940
Db	5867	CCGGGTTTTCTTTCGACAGAAAGTTTCACTCTCTCAGCAATATGGCGGGCCATACAAAA	5926
Qy	5941	CCAAGAGAGTGGCATCAAAAGAGTCTGTCTCTGGGGCACTCAAAGAGCCACCGATGCACC	6000
Db	5927	CCAAGAGAGTGGCATCAAAAGAGTCTGTCTCTGGGGCACTCAAAGAGCCACCGATGCACC	5986
Qy	6001	CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTTCCACAGAGATCCCTGTGGGGCGGTC	6060
Db	5987	CCATGAGGCCAGGCCACCCCTGGAGCGTGGCCACTTCCACAGAGATCCCTGTGGGGCGGTC	6046
Qy	6061	AGGAGCACTGGCTGTGGACGTTTCTGATGCAGAGCATTAACCCGAGAGGGGCCCTGATGGGGA	6120
Db	6047	AGGAGCACTGGCTGTGGACGTTTCTGATGCAGAGCATTAACCCGAGAGGGGCCCTGATGGGGA	6106
Qy	6121	GCCCCAGCCTGGGCTGGAGAGCCAGGCTCGAGCGGCTCCATGCCCGGCTTGGCGCCGA	6180
Db	6107	GCCCCAGCCTGGGCTGGAGAGCCAGGCTCGAGCGGCTCCATGCCCGGCTTGGCGCCGA	6166
Qy	6181	GACTCAGCCCGTTCACAGATGCCAGCCCAATGAAGCGCTCCATCTCCAAGCTGGGCCAGCG	6240
Db	6167	GACTCAGCCCGTTCACAGATGCCAGCCCAATGAAGCGCTCCATCTCCAAGCTGGGCCAGCG	6226
Qy	6241	GCCCCGTGGGACTCATTTTGCAGACCAACCCCGGACCGGCCCAACCCCTAGCCAGGCGTC	6300
Db	6227	GCCCCGTGGGACTCATTTTGCAGACCAACCCCGGACCGGCCCAACCCCTAGCCAGGCGTC	6286
Qy	6301	GTGCGACCAACCAACCAACCGCTGCCACCGCCGCGAGGACAGGAAGCAGAGTCCCTGGA	6360
Db	6287	GTGCGACCAACCAACCAACCGCTGCCACCGCCGCGAGGACAGGAAGCAGAGTCCCTGGA	6346
Qy	6361	GAAGGGGCCAGCGTGTCTGCCGATATGATGCGCGCACCAAGCAGTGTGTGGGGCCGG	6420
Db	6347	GAAGGGGCCAGCGTGTCTGCCGATATGATGCGCGCACCAAGCAGTGTGTGGGGCCGG	6406
Qy	6421	GCTGCCCCGGGAGAGGGGCTTACAGGCTGCCGGGGGAAACAGAGCGCGGAGGAGCG	6480
Db	6407	GCTGCCCCGGGAGAGGGGCTTACAGGCTGCCGGGGGAAACAGAGCGCGGAGGAGCG	6466
Qy	6481	GGGCGCGTCCAGAGAGCGGAGCGCCCTCATCTCTCTCTCGAGAAAGCAGCGCTTCTA	6540
Db	6467	GGGCGCGTCCAGAGAGCGGAGCGCCCTCATCTCTCTCTCGAGAAAGCAGCGCTTCTA	6526
Qy	6541	CTCCTGCGACCGCTTTGGGGCGGTGAGCCCCCGAAGCCCAAGCCCTCCTCAGAGGCCA	6600
Db	6527	CTCCTGCGACCGCTTTGGGGCGGTGAGCCCCCGAAGCCCAAGCCCTCCTCAGAGGCCA	6586
Qy	6601	CCCAAAGCTGCGCAACAGCTGGCCAGGAGCGGGACCCCAACCAAGAGGAGTGGTTCGT	6660
Db	6587	CCCAAAGCTGCGCAACAGCTGGCCAGGAGCGGGACCCCAACCAAGAGGAGTGGTTCGT	6646
Qy	6661	GAATGGGAGCCCTTGTCTCAACATCTGTGTAGCACCCCGGCGCGGTGGGCGGAG	6720

Db 1021 TGGCATCACCACTTGAATAATCCCTGTTTGCCATCTTGACGGTGTCCAGTGATCAC 1080
Qy 1081 CATGGAGGCTGGACTGACATCTCTATAATAACAAACGATCGCGCCGGCAACACTGGAA 1140
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Db 1141 CTGGCTCTACTTCAATCCCTCTCATCATCATCGGCTCTCTTCTTCAATGCTCAACCTGGTGCT 1200
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Qy 1441 GGAGGAGAGACCGGTTTGAGATCTCTGTGCTGTTGGATCCCGCTTGGCGCGCGAG 1500
Db 1441 GGAGGAGAGACCGGTTTGAGATCTCTGTGCTGTTGGATCCCGCTTGGCGCGCGAG 1500
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Db 1621 GGCCCTGAACACACTGTGTGGCCATGCTGTCATTACAACAGCGCGCGCGCTTACAC 1680
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Db 1741 GATGATGGCTGGGCCCAAGACTACTTCCGCTCCTTCAACTGCTTCGACTTTGG 1800
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Db 1801 GGTCAATCGTGGGAGCGCTCTTTGAAGTGGTCTGGCGCGCCATCAAGCGGGAAGCTCCTT 1860
Qy 1861 TGGATCAGTGTGTCGGGCGCTTCCGCTCTGAGGATCTTCAAGGTACAGAACTG 1920
Db 1861 TGGATCAGTGTGTCGGGCGCTTCCGCTCTGAGGATCTTCAAGGTACAGAACTG 1920
Qy 1921 GAGCTCCCTGGGAACCTGGTGGTCTCCCTGCTGAACTCCATGAAGTCCATCAGCCT 1980
Db 1921 GAGCTCCCTGGGAACCTGGTGGTCTCCCTGCTGAACTCCATGAAGTCCATCAGCCT 1980
Qy 1981 GCTCTTCTGCTCTTCTGTTTCAATGTTGGTCTTCGCTGCTGGGATGACAGCTGTTTG 2040
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5281 GGAACATTTTGTAGTACTCAAGGGGACTTTCATCTCTAGGCTCTCACCTTTGATGA 5340
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Db 5809 CCTGTTCCACCTCTGAAGGCCACCTGGAGCAGACAGCCGCTCTGCTCCGAGGAGC 5868
Qy 5881 CCGGGTTTTCTTCGACAGAAAGTTTCCACTCTCCCTCAGCAATGGCGGGCCATACAAAA 5940
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Qy 5941 CCAAGAGTGGCATCAAGAGTCTGTCTCTGGGGCACTCAAGAGACCCAGAGTGCACC 6000
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Qy 6181 GACTCAGCCCGTCAAGATGCCAGCCCATGAAGCGTCTCATCTCCACGCTGGGCCAGCG 6240
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Db 6229 GCCCCGTGGGACTCATCTTTGACAGCACACCCCGGACCGGCCCTTACCCAGGCGTC 6288
Qy 6301 GTCCACCAACCAACCAACCGCTGCCACCGCGCAGGACAGGAAGCAGAGTCCCTGGA 6360
Db 6289 GTCCACCAACCAACCAACCGCTGCCACCGCGCAGGACAGGAAGCAGAGTCCCTGGA 6348
Qy 6361 GAAGGGGCCAGCTGTCTGCCGATATGATGGCGCACCAAGCAGTGTCTGTGGGGCCGG 6420
Db 6349 GAAGGGGCCAGCTGTCTGCCGATATGATGGCGCACCAAGCAGTGTCTGTGGGGCCGG 6408
Qy 6421 GCTGCCCGGGAGAGGGGCTTACAGGCTGCGCGGGAAACGAGAGCGCGCGGAGGAGCG 6480
Db 6409 GCTGCCCGGGAGAGGGGCTTACAGGCTGCGCGGGAAACGAGAGCGCGCGGAGGAGCG 6468
Qy 6481 GGGCGGCTCCAGAGCGGAGGAGCGCTCATCTCTCTCGAGAGAGCAGCGCTTCTA 6540

Db 6469 GGGCGGCTCCAGAGCGGAGGAGCGCCTCATCTCTCTCGGAGAGCAGCGCTTCTA 6528
Qy 6541 CTCTCGACACCGCTTTTGGGGCGCTGAGCCCCCGAAGCCCAAGCCCTCTCCCTCAGACGCCA 6600
Db 6529 CTCTCGACACCGCTTTTGGGGCGCTGAGCCCCCGAAGCCCAAGCCCTCTCCCTCAGACGCCA 6588
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Db 6589 CCNAAAGTTCGCCAAACAGCTGGCCAGGAGCGGAGACCCCAACCCCA 6631
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Db 6632 6631
Qy 6721 GCAGCTCCCCAGACGCCCTCTGACTCCCGCCCCAGCATCACCTACAAGACGGCCAACTC 6780
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Qy 6841 CAGCGGTGGGCTTTCCGAAACACAAACGCCCTGTGTCAGAGAGACCCCTCAGCCAGCGCCCT 6900
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Db 7002 CTGATGCGACGCGGTGTCTCCAGTGGATGATTTTATCATCCACACGGGCGAGTCCG 7061
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RESULT 6
US-10-375-253-13
; Sequence 13, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10/375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354

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/ PRIOR FILING DATE: 1995-02-15
/ PRIOR APPLICATION NUMBER: 07/914,231
/ PRIOR FILING DATE: 1992-07-13
/ PRIOR APPLICATION NUMBER: 08/314,083
/ PRIOR FILING DATE: 1994-09-28
/ PRIOR APPLICATION NUMBER: 07/914,231
/ PRIOR FILING DATE: 1992-07-13
/ PRIOR APPLICATION NUMBER: 07/603,751
/ PRIOR FILING DATE: 1990-11-09
/ PRIOR APPLICATION NUMBER: 08/290,012
/ PRIOR FILING DATE: 1994-08-11
/ PRIOR APPLICATION NUMBER: 08/149,097
/ PRIOR FILING DATE: 1993-11-05
/ PRIOR APPLICATION NUMBER: 08/105,536
/ PRIOR FILING DATE: 1993-08-11
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/ PRIOR FILING DATE: 1993-11-05
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 7175
/ TYPE: DNA
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/ FEATURE:
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/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: (1)... (143)
/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: (6855)... (7175)
US-10-375-253-13

Query Match          94.0%; Score 6932.4; DB 16; Length 7175;
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Matches 7174; Conservative 0; Mismatches 1; Indels 201; Gaps 4;

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QY 61 GCTGCTCGGCTCTGAGCGGCTGGCGGCGCGCGCCCTCCCTGCGGGGCGGCTGGGCG 120
DB 60 GCTGCTCGGCTCTGAGCGCT -GCGCGCGCGCGCGCCCTCCCTGCGGGGCGGCTGGGCG 118

QY 121 GGGATGCA CGCGGCGCGGAGCCATGCTCGGCTTCGGGAGAGAGCTGGGCGGCGGCTA 180
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QY 181 TGGAGGCGCGCGCGGAGAGCGGCGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCG 240
DB 179 TGGAGGCGCGCGCGGAGAGCGGCGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCG 238

QY 241 GGGTCCGCGGCGGCTGAGCGCGCGCGCGCGCGGCTCTCTACAGCAATGATCGCGGAGCG 300
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QY 301 CGCGGAGACCAATGGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTCACCGTCAA 360
DB 299 CGCGGAGACCAATGGCGCTGTACAAACCCATCCCGGTCAAGCAGAACTGCTTCACCGTCAA 358

QY 361 CGGCTCGCTCTGCTTTCAGCGAGGACAACTGCTCGCGAAATACGCGAAGCGCATCAC 420
DB 359 CGGCTCGCTCTGCTTTCAGCGAGGACAACTGCTCGCGAAATACGCGAAGCGCATCAC 418

QY 421 CGAGTGGCGCTCCATTCGAGTATATGATCTCGGCCACCATCATCGGCAACTGCTGCTGCT 480
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QY 481 GGGCTTGAGCAGCAGCTCCCTGATGGGACAAACGCCCATGCTCCGAGCGGCTGGACGA 540
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QY 541 CACGAGCGCTATTTTCATCGGGATCTTTGCTTCGAGGCGAGGATCAAAATCATCGCTCT 600
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QY 1141 CTGGCTCTACTTCTCATCCCTCTCATCATATCGGCTCTTCTTCTCATGCTCAACTGGTGT 1200
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QY 1201 GGGCGTCTCTCGGGGAGTTTGCACAGGAGCGAGAGGCTGGAGAACCGCGCGGCTT 1260
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QY 1261 CTTGAAGCTGCGCGGCGGAGCAGCAGATCGAGCAGAGCTCAACGGGTACTTGGAGTGGAT 1320
DB 1259 CTTGAAGCTGCGCGGCGGAGCAGCAGATCGAGCAGAGCTCAACGGGTACTTGGAGTGGAT 1318

QY 1321 CTTCAAGCGGAGAGAGTCACTGCTGCGCGAGGAGCAGAGAAATGCAAGAGAGAGTCCCC 1380
DB 1319 CTTCAAGCGGAGAGAGTCACTGCTGCGCGAGGAGCAGAGAAATGCAAGAGAGAGTCCCC 1378

QY 1381 TTTTGAAGCTGCTGAAGAGAGCGGCGGACCAAGAGAGAGAGAGAGAGTCACTGATCCACG 1440
DB 1379 TTTTGAAGCTGCTGAAGAGAGCGGCGGACCAAGAGAGAGAGAGAGAGTCACTGATCCACG 1438

QY 1441 GAGAGGAGAGGAGCGGTTTTCAGATCTCTGCTGCTGTTGGATCCCCCTTCCGCGGCGCAG 1500
DB 1439 GAGAGGAGAGGAGCGGTTTTCAGATCTCTGCTGCTGTTGGATCCCCCTTCCGCGGCGCAG 1498

QY 1501 CTTCAAGCGGAGAGAGAGAGAGCTGCTCATATCTTCCGAGAGAGAGAGAGATGTTCCG 1560
DB 1499 CTTCAAGCGGAGAGAGAGAGAGAGCTGCTCATATCTTCCGAGAGAGAGAGAGATGTTCCG 1558

QY 1561 GTTTTTTATCCGCGCATGCTGAAGGCTCAGAGCTTCTACTGGGTGGTCTGCTGGGTGCT 1620
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Qy	1621	GGCCCTGAAACACACTGTGTGTGGCCATGTGTGCAATTA	CAACAGCGCGCGGGGCTTACAC	1680
Db	1619	GGCCCTGAAACACACTGTGTGTGGCCATGTGTGCAATTA	CAACAGCGCGGGGCTTACAC	1678
Qy	1681	GACCCCTGATTTTGCAGAGTTTGTTCCTGGGTCTCTTCT	CACAGAGATGTCCTGAA	1740
Db	1679	GACCCCTGATTTTGCAGAGTTTGTTCCTGGGTCTCTTCT	CACAGAGATGTCCTGAA	1738
Qy	1741	GATGTATGGCTGGGGCCGAAAGCTACTTCCGGTCTCTT	CAACTGCTTCCGACTTTGG	1800
Db	1739	GATGTATGGCTGGGGCCGAAAGCTACTTCCGGTCTCTT	CAACTGCTTCCGACTTTGG	1798
Qy	1801	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGCGGCC	CAATCAAGCCGGGAAGCTCCTT	1860
Db	1799	GGTCATCGTGGGAGCGTCTTTGAAGTGTCTGGCGGCC	CAATCAAGCCGGGAAGCTCCTT	1858
Qy	1861	TGGGATCAGTGTGTGGGGCCCTCCGCTGCTGAGGATCT	CAAGTCAAGTACTG	1920
Db	1859	TGGGATCAGTGTGTGGGGCCCTCCGCTGCTGAGGATCT	CAAGTCAAGTACTG	1918
Qy	1921	GAGCTCCTCGGAACTGTGTGTGCTCCTGCTGAACT	CCATGAAGTCCATCAGCCT	1980
Db	1919	GAGCTCCTCGGAACTGTGTGTGCTCCTGCTGAACT	CCATGAAGTCCATCAGCCT	1978
Qy	1981	GCTCTTCTGCTCTTCTGCTTCAATTGTGTCTTCCGCT	TGCTGGGATGAGCTGTTGG	2040
Db	1979	GCTCTTCTGCTCTTCTGCTTCAATTGTGTCTTCCGCT	TGCTGGGATGAGCTGTTGG	2038
Qy	2041	GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCA	CACTTCCGACACTTCCCTGCCG	2100
Db	2039	GGGACAGTTCAACTTCCAGGATGAGACTCCCAACCA	CACTTCCGACACTTCCCTGCCG	2098
Qy	2101	CATCCTCACTGTCTTCCAGATCTCGAGGAGAGGAT	GTGAATGCAGTGTATCAGG	2160
Db	2099	CATCCTCACTGTCTTCCAGATCTCGAGGAGAGGAT	GTGAATGCAGTGTATCAGG	2158
Qy	2161	GATCGAATCGCAAGCGCGTCAACAAAGGCATGTTCT	CGTCTTTTACTTCAATGTCCCT	2220
Db	2159	GATCGAATCGCAAGCGCGTCAACAAAGGCATGTTCT	CGTCTTTTACTTCAATGTCCCT	2218
Qy	2221	GACACTGTTGGAAACTACACTCTGCTGAATGTCTTT	CTGGCCATCGCTGTGGACACCT	2280
Db	2219	GACACTGTTGGAAACTACACTCTGCTGAATGTCTTT	CTGGCCATCGCTGTGGACACCT	2278
Qy	2281	GGCCAAAGCCCAAGAGCTGACCAAGGATGAAGAG	GAGATGAAGAGCAGCAATCAGAA	2340
Db	2279	GGCCAAAGCCCAAGAGCTGACCAAGGATGAAGAG	GAGATGAAGAGCAGCAATCAGAA	2338
Qy	2341	GCTTGTCTCTGCAAAAGGCCCAAGAGTGGCTGAA	AGTCAGCCCCCATGTCTGCGCGAAACAT	2400
Db	2339	GCTTGTCTCTGCAAAAGGCCCAAGAGTGGCTGAA	AGTCAGCCCCCATGTCTGCGCGAAACAT	2398
Qy	2401	CTCATCGCGCCAGGAGCAGAGAACTCGGCCCA	AGGCGGCTCGGTGTGGAGCAGCGGGC	2460
Db	2399	CTCATCGCGCCAGGAGCAGAGAACTCGGCCCA	AGGCGGCTCGGTGTGGAGCAGCGGGC	2458
Qy	2461	CAGCCAGCTACGGCTGCAGAACCTCGGGCCAGCT	GTGAGAGCGCTGTACAGCGAGATGGA	2520
Db	2459	CAGCCAGCTACGGCTGCAGAACCTCGGGCCAGCT	GTGAGAGCGCTGTACAGCGAGATGGA	2518
Qy	2521	CCCCGAGGAGCGGTGGCGTCTGCGCACTACGCG	CACCTGCGGCCCGACATGAAGACGCA	2580
Db	2519	CCCCGAGGAGCGGTGGCGTCTGCGCACTACGCG	CACCTGCGGCCCGACATGAAGACGCA	2578
Qy	2581	CCTGGACCGGCGCTGTGTGTGAGACTGGGCGG	CGAGCGGCGGGGCGGCTGGGAGG	2640
Db	2579	CCTGGACCGGCGCTGTGTGTGAGACTGGGCGG	CGAGCGGCGGGGCGGCTGGGAGG	2638
Qy	2641	CAAAAGCCGACCTCAGGCTGGGAGGCCCCCG	AGGGCGTGCACCTCCGCGCAGGACCA	2700
Db	2639	CAAAAGCCGACCTCAGGCTGGGAGGCCCCCG	AGGGCGTGCACCTCCGCGCAGGACCA	2698

Qy	2701	CCGGCACCGCGCAACAGGACAAAGACCCCGCG	CGGGGACACGACCGAGCAGAGGCCCC	2760
Db	2699	CCGGCACCGCGCAACAGGACAAAGACCCCGCG	CGGGGACACGACCGAGCAGAGGCCCC	2758
Qy	2761	GAAGGCGGAGAGCGGAGCCCGGTCTCCCGG	AGGAGCGGCCCGCCGACCGCAGCCA	2820
Db	2759	GAAGGCGGAGAGCGGAGCCCGGTCTCCCGG	AGGAGCGGCCCGCCGACCGCAGCCA	2818
Qy	2821	CAGCAAGGAGCCCGCGGGCCCGGAGCGCG	AGCGCGCGGCGCCAGGCCCCAGGCC	2880
Db	2819	CAGCAAGGAGCCCGCGGGCCCGGAGCGCG	AGCGCGCGGCGCCAGGCCCCAGGCC	2878
Qy	2881	CAGAGGCGGCGCGCGGACCAACCGCGCG	CGCTCCCGGAGGAGCGCGCGGAGGCC	2940
Db	2879	CAGAGGCGGCGCGCGGACCAACCGCGCG	CGCTCCCGGAGGAGCGCGCGGAGGCC	2938
Qy	2941	CCGACGCCACCGCGCGCACCGGCACACAG	GATCCGAGCAAGAGTGTGCCGCGCCAAAGGG	3000
Db	2939	CCGACGCCACCGCGCGCACCGGCACACAG	GATCCGAGCAAGAGTGTGCCGCGCCAAAGGG	2998
Qy	3001	CAGAGCGCGCGCGCGGACCAACCGCGCG	CGCCCGGAGGCGCGGAGCGGAGCGG	3060
Db	2999	CAGAGCGCGCGCGCGGACCAACCGCGCG	CGCCCGGAGGCGCGGAGCGGAGCGG	3058
Qy	3061	GGAGGAGCGCGCGCGGGGACCCCGGCG	CGGCAAAAGCGCGACCTGCTCACAGGCTGT	3120
Db	3059	GGAGGAGCGCGCGCGGGGACCCCGGCG	CGGCAAAAGCGCGACCTGCTCACAGGCTGT	3118
Qy	3121	GGAGAGGAGACCAACCGAGAGGAGGAG	CGCCAGGAGGAGGCTGAGATAGTGAAGCCGA	3180
Db	3119	GGAGAGGAGACCAACCGAGAGGAGGAG	CGCCAGGAGGAGGCTGAGATAGTGAAGCCGA	3178
Qy	3181	CAAGGAAAAGGAGCTCCGGAAACCAAC	CAGCCCGCGGAGCCACACTGTGTGACCTG	3240
Db	3179	CAAGGAAAAGGAGCTCCGGAAACCAAC	CAGCCCGCGGAGCCACACTGTGTGACCTG	3238
Qy	3241	TGGGACTGTGACTGTGGGTCCATGACAC	ACTGCGCCAGCACCTGTCTCCAGAAAGTGGA	3300
Db	3239	TGGGACTGTGACTGTGGGTCCATGACAC	ACTGCGCCAGCACCTGTCTCCAGAAAGTGGA	3298
Qy	3301	GGAAACGACAGAGATGACAGCAATCAG	GGGAACGTCACCTCGCATGGGAGTCAGGCCCC	3360
Db	3299	GGAAACGACAGAGATGACAGCAATCAG	GGGAACGTCACCTCGCATGGGAGTCAGGCCCC	3358
Qy	3361	AGACCCGAAACACTATTTGTATCATAT	CCAGTGTCTGCTCGGGCCCTCTTGGGAAAGCCAC	3420
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Qy	3421	GGTCTGTTCCAGTGTGTAAACGTGGA	ACCTGGAAAGCCAGAGAGGGAAGAGAGTGGA	3480
Db	3419	GGTCTGTTCCAGTGTGTAAACGTGGA	ACCTGGAAAGCCAGAGAGGGAAGAGAGTGGA	3478
Qy	3481	AGCGGATGAGTGTATGAGGAGCGGCG	CGCCCTATGCTCCCATACAGCTCCATGTTCTG	3540
Db	3479	AGCGGATGAGTGTATGAGGAGCGGCG	CGCCCTATGCTCCCATACAGCTCCATGTTCTG	3538
Qy	3541	TTTAAAGCCCAACCAACCTGCTCCG	CGCTTCTGCCACTACATCGTACCATGAGGTACTT	3600
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Qy	3601	CGAGGTGGTCATTCTCGTGGTCAAT	CGCCTGTAGCAGCATGCGCCTGGCTGTGAGGACCC	3660
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Qy	3661	AGTGCCGACAGACTCCCGCAGGAA	CAACGCTCTGAAATACCTGGATTACATTTTCACTGG	3720
Db	3659	AGTGCCGACAGACTCCCGCAGGAA	CAACGCTCTGAAATACCTGGATTACATTTTCACTGG	3718
Qy	3721	TGCTTTTACCTTTGAGATGGTGA	TAAAGATGATCGGACTTGGGACTGCTGCTCACCTCTGG	3780
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Qy	3781	AGCCTATTTCCGGGACTTGTGTG	GAAATTTCTGGAATTCATTTGTGTGTCAGTGGCGCCCTGGT	3840

Db	3779		AGCCTATTTCCGGGACTTGTGGAACATTTCTGACATTCATTGTGGTCAGTGGCGCCCTGGT	3838
QY	3841	GGCGTTTGCTTCTCGAGCTTCGTGGGAGATCCAAAGGGAAGACATCAATACCATCAA	3900	
Db	3839	GGCGTTTGCTTCTC-----AGATCCAAAGGGAAGACATCAATACCATCAA	3886	
QY	3901	GTCTCTGAGAGTCCTTCTGTCTCTCGGCCCTCTCAAGACCATCAAACGGCTGCCCAAGCT	3960	
Db	3887	GTCTCTGAGAGTCCTTCTGTCTCTCGGCCCTCTCAAGACCATCAAACGGCTGCCCAAGCT	3946	
QY	3961	CAAGGCTGTGTTGACTGTGTGGTGAATCTCCCTGAAGAAATGTCCTCAACATCTTGATTTGT	4020	
Db	3947	CAAGGCTGTGTTGACTGTGTGGTGAATCTCCCTGAAGAAATGTCCTCAACATCTTGATTTGT	4006	
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Db	4007	CTACATGCTCTTTCATGTTTCATATTTTGGCGTCAATTCGGTGCAGCTCTTCAAAGGGAAGTT	4066	
QY	4081	TTTCTACTGCA CAGATGAATCCAAAGAGCTGGAGAGGACTGCAAGGGTTCAGTATTTGGA	4140	
Db	4067	TTTCTACTGCA CAGATGAATCCAAAGAGCTGGAGAGGACTGCAAGGGTTCAGTATTTGGA	4126	
QY	4141	TTATGAGAGGAGGAAGTGGAGCTCAGCCAGGCAAGTGGAGAAATACGACTTTCACTA	4200	
Db	4127	TTATGAGAGGAGGAAGTGGAGCTCAGCCAGGCAAGTGGAGAAATACGACTTTCACTA	4186	
QY	4201	CGACAAATGTGCTCTGGGCTCTGCTCAGCGTGTTCACAGTGTCCACGGGAGAGGCTGGCC	4260	
Db	4187	CGACAAATGTGCTCTGGGCTCTGCTCAGCGTGTTCACAGTGTCCACGGGAGAGGCTGGCC	4246	
QY	4261	CATGTGCTGAAACACTCCGCTGGATGCGCACTTATGAGGAGAGGCTCAAGCCCTGGGTA	4320	
Db	4247	CATGTGCTGAAACACTCCGCTGGATGCGCACTTATGAGGAGAGGCTCAAGCCCTGGGTA	4306	
QY	4321	CCGCATGAGCTGCCATCTCTACGTGTCTACTTTTGTGTCCTTCTCCCTTCTCTTCTG	4380	
Db	4307	CCGCATGAGCTGCCATCTCTACGTGTCTACTTTTGTGTCCTTCTCCCTTCTCTTCTG	4366	
QY	4381	CAACATCTTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGGAACAAGTGATGTC	4440	
Db	4367	CAACATCTTTTGTGGCTTTGATCATCATCACTTCCAGGAGCAGGGGGAACAAGTGATGTC	4426	
QY	4441	TGAATGCACTGGAGAGAGACAGAGGGCTTGCATTCATTCGCATCAGCGGCAAAACC	4500	
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QY	4501	CCTGACCGGTACATGCCCCCAAAACCGGCAGTCGTTCCAGTATAGAGCTGAGCATTTGT	4560	
Db	4487	CCTGACCGGTACATGCCCCCAAAACCGGCAGTCGTTCCAGTATAGAGCTGAGCATTTGT	4546	
QY	4561	GGTCTCCCCGCCCTTTGAATACTTCATCATGGCCAATGATGCCCTCAACACTGTGGTGCT	4620	
Db	4547	GGTCTCCCCGCCCTTTGAATACTTCATCATGGCCAATGATGCCCTCAACACTGTGGTGCT	4606	
QY	4621	GATGATGAAGTCTATGATGCAACCTATAGATACAGAGCTGATGTGAATGCCCTGAACAT	4680	
Db	4607	GATGATGAAGTCTATGATGCAACCTATAGATACAGAGCTGATGTGAATGCCCTGAACAT	4666	
QY	4681	CGTGTTCACATCCATGTTCTCCATGGAATGGTGTGCTGAAGATCATCGCTTTGGGGTCT	4740	
Db	4667	CGTGTTCACATCCATGTTCTCCATGGAATGGTGTGCTGAAGATCATCGCTTTGGGGTCT	4726	
QY	4741	GAACCTATTTCAGAGATGCTTGAATGTCTTTGACTTTGTCACTGTGTTGGGAAGTATTAC	4800	
Db	4727	GAACCTATTTCAGAGATGCTTGAATGTCTTTGACTTTGTCACTGTGTTGGGAAGTATTAC	4786	
QY	4801	TGATATTTTAGTAAACAGAGATTGGGAAACGAACTTATCACTCAACCTCAGCTTCTCCG	4860	
Db	4787	TGATATTTTAGTAAACAGAGATTGGGAAACGAACTTATCACTCAACCTCAGCTTCTCCG	4846	
QY	4861	CCTCTTTTCAGCTGCGGGCTGATCAAGCTGCTCGGCCAGGGCTACACCATCCGCACTCT	4920	

Db	4847	CCTCTTTTCAGCTGCGGGCTGATCAAGCTGCTCCGCCAGGGCTACACCATCCGCACTCT	4906	
QY	4921	GCTGTGACCTTTTCTCCAGTCTCTTCAAGGCCCTGSCCTAGTGTGTCTGTCTATTGGCAT	4980	
Db	4907	GCTGTGACCTTTTCTCCAGTCTCTTCAAGGCCCTGSCCTAGTGTGTCTGTCTATTGGCAT	4966	
QY	4981	GCTGTCTTTCATCTACGCCATCATCGGCATGCGAGTGTGTTGGGAATATTGSCCTGGATGA	5040	
Db	4967	GCTGTCTTTCATCTACGCCATCATCGGCATGCGAGTGTGTTGGGAATATTGSCCTGGATGA	5026	
QY	5041	TGACACAGCATCAACCGCCACACAACCTTCCGGACGTTTTTGGCAAGCCCTGATGCTGCT	5100	
Db	5027	TGACACAGCATCAACCGCCACACAACCTTCCGGACGTTTTTGGCAAGCCCTGATGCTGCT	5086	
QY	5101	GTTTCAGAGCGCCACCGGGGAGGCTCGCACAGATCATGCTGCTCCTGCTGAGCAACCA	5160	
Db	5087	GTTTCAGAGCGCCACCGGGGAGGCTCGCACAGATCATGCTGCTCCTGCTGAGCAACCA	5146	
QY	5161	GGCCTGTGATGAGCAGGCCCAATGCCACCGAGTGTGGAAGTGACTTTTGCTCTACTT	5220	
Db	5147	GGCCTGTGATGAGCAGGCCCAATGCCACCGAGTGTGGAAGTGACTTTTGCTCTACTT	5206	
QY	5221	CGTCTCCTTTCATCTTCTGCTGCTCTTCTGATGTTGAACTCTTCTGTGCTGTGATCAT	5280	
Db	5207	CGTCTCCTTTCATCTTCTGCTGCTCTTCTGATGTTGAACTCTTCTGTGCTGTGATCAT	5266	
QY	5281	GGACAAATTTTGAATACCTCACCGGGGACTCTTCCATCCTAGGTCCTCACCACTTGGATGA	5340	
Db	5267	GGACAAATTTTGAATACCTCACCGGGGACTCTTCCATCCTAGGTCCTCACCACTTGGATGA	5326	
QY	5341	GTTTCATCCGGGCTGTGGCTGAATACGACCCGGCTGGTGTGGGGCGCATCAATCAATGA	5400	
Db	5327	GTTTCATCCGGGCTGTGGCTGAATACGACCCGGCTGGTGTGGGGCGCATCAATCAATGA	5386	
QY	5401	CATGTTTGAATGCTGAAACACACATGTCCTGCGCTCTGGGGCTGGGGAGAAATGCCCTGC	5460	
Db	5387	CATGTTTGAATGCTGAAACACACATGTCCTGCGCTCTGGGGCTGGGGAGAAATGCCCTGC	5446	
QY	5461	TCGAGTTGCTTTACAAGCGCCTGGTTGCGCATGAACATGCCCATCTCCAACGAGACATGAC	5520	
Db	5447	TCGAGTTGCTTTACAAGCGCCTGGTTGCGCATGAACATGCCCATCTCCAACGAGACATGAC	5506	
QY	5521	TGTTTCATCTTCACTGTCACGCTGATGCGCTCATCCGGAACGCACTGGAGATCAAGCTGGC	5580	
Db	5507	TGTTTCATCTTCACTGTCACGCTGATGCGCTCATCCGGAACGCACTGGAGATCAAGCTGGC	5566	
QY	5581	CCAGCTTGGGACAAAGCAGCATCAAGTGTGACGGGAGTTTTCAGGAAGGAGATTTCCGTTGT	5640	
Db	5567	CCAGCTTGGGACAAAGCAGCATCAAGTGTGACGGGAGTTTTCAGGAAGGAGATTTCCGTTGT	5626	
QY	5641	GTGGGCCAATCTGCCCCAGAAGAATTTTGGACTTTGCTGGTACCAACCCCATTAAGCCTGATGA	5700	
Db	5627	GTGGGCCAATCTGCCCCAGAAGAATTTTGGACTTTGCTGGTACCAACCCCATTAAGCCTGATGA	5686	
QY	5701	GATGACAGTGGGGAAGTTTATGCACTCTGATGATATTTGACTTCTAAGCAGAACAA	5760	
Db	5687	GATGACAGTGGGGAAGTTTATGCACTCTGATGATATTTGACTTCTAAGCAGAACAA	5746	
QY	5761	AACCCACAGAGACCATGACAGCAGCTCTCTGAGGCTCTCCACAGATGGTCTCTGTGTC	5820	
Db	5747	AACCCACAGAGACCATGACAGCAGCTCTCTGAGGCTCTCCACAGATGGTCTCTGTGTC	5806	
QY	5821	CCTGTTTCCACCTCTGAAAGGCCACCTTGGAGCAGACACAGCCGGCTGTGCTCCGAGGAGC	5880	
Db	5807	CCTGTTTCCACCTCTGAAAGGCCACCTTGGAGCAGACACAGCCGGCTGTGCTCCGAGGAGC	5866	
QY	5881	CCGGGTTTCTTCGACAGAGATTCACCTCCCTCAGCAATGGCGGGGCTATACAA	5940	
Db	5867	CCGGGTTTCTTCGACAGAGATTCACCTCCCTCAGCAATGGCGGGGCTATACAA	5926	
QY	5941	CCAAGAGATGGCATCAAGAGTCTGCTCTCTGGGCACTCAAGAGCCTCAGGATGACCC	6000	
Db	5927	CCAAGAGATGGCATCAAGAGTCTGCTCTCTGGGCACTCAAGAGCCTCAGGATGACCC	5986	

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QY 6001 CCATGAGGCCAGGCCACCCCTGGAGCGTGCCCACTCCACAGAGATCCCTGTGGGGCGGTC 6060
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QY 6061 AGGAGCACTGGCTGTGAGACGTTCAAGATGCAGAGCATAAACCGGAGGGCCCTGATGGGA 6120
Db 6047 AGGAGCACTGGCTGTGAGACGTTCAAGATGCAGAGCATAAACCGGAGGGCCCTGATGGGA 6106
QY 6121 GCCCCAGCCTGGGCTGAGAGCACCAGGCTCGAGCGGCCCTCCATGCCCGCCCTTGCGGCCGA 6180
Db 6107 GCCCCAGCCTGGGCTGAGAGCACCAGGCTCGAGCGGCCCTCCATGCCCGCCCTTGCGGCCGA 6166
QY 6181 GACTCAGCCGCTCAGATGCAGATGCCAGCCCATGAAGCGTCTCATCTCCACGTCGTGCGCCAGCG 6240
Db 6167 GACTCAGCCGCTCAGATGCAGATGCCAGCCCATGAAGCGTCTCATCTCCACGTCGTGCGCCAGCG 6226
QY 6241 GCCCGGTGGACATCTTTTGACGACACACCCCGGACCGGCCACCCCTAGCCAGGGGTC 6300
Db 6227 GCCCGGTGGACATCTTTTGACGACACACCCCGGACCGGCCACCCCTAGCCAGGGGTC 6286
QY 6301 GTCCACACACACACACCGCTGCCACCGCGCAGGACAGGAGTCCCTTGA 6360
Db 6287 GTCCACACACACACACCGCTGCCACCGCGCAGGACAGGAGTCCCTTGA 6346
QY 6361 GAAGGGCCCAAGCCTGTCTGCCGATATGGATGCGCACCAAGCAGTCTGTGGGGCCGG 6420
Db 6347 GAAGGGCCCAAGCCTGTCTGCCGATATGGATGCGCACCAAGCAGTCTGTGGGGCCGG 6406
QY 6421 GCTGCCCGCGGAGAGGGCTTACAGCTCGCGCGGGAAGAGAGCGCGGACAGAGCG 6480
Db 6407 GCTGCCCGCGGAGAGGGCTTACAGCTCGCGCGGGAAGAGAGCGCGGACAGAGCG 6466
QY 6481 GGGCGGCTGCCAGGAGCGGAGCGCCTCATCTCTCTCGAGAGAGCAGCGCTTCTA 6540
Db 6467 GGGCGGCTGCCAGGAGCGGAGCGCCTCATCTCTCTCGAGAGAGCAGCGCTTCTA 6526
QY 6541 CTCCTGCGACCGCTTTGGGGCCGTGAGCCCCCGAAGCCCAAGCCCTTCCCTCAGCAGCCA 6600
Db 6527 CTCCTGCGACCGCTTTGGGGCCGTGAGCCCCCGAAGCCCAAGCCCTTCCCTCAGCAGCCA 6586
QY 6601 CCNAACGTGCCACACGTGGCAGGAGCGGGACCCACCCACAGGGCAGTGGTTCGT 6660
Db 6587 CCCAACGTGCCACACGTGGCAGGAGCGGGACCCACCCACAGGGCAGTGGTTCGT 6629
QY 6661 GAATGGAGGCCCTTGTGTCAACATCTGGTGCTAGCACCCCCCGCGCGTGGGCGGAG 6720
Db 6630 ----- 6629
QY 6721 GCAGCTCCCCAGAGCGCCCTGACTCCCCCGCCCCAGCATCACCTACAAGACGGCCAACTC 6780
Db 6630 ----- 6629
QY 6781 CTCACCCATCCACTTCCGCGGGGCTCAGACCAGGCTCCCTGCCCTTCTCCCCAGGCGGGCT 6840
Db 6630 -----CAGCGCGGCT 6639
QY 6841 CAGCGGTGGGCTTTCCGAACACAAACGCGCTGCTCAGAGAGACCCCTCAGCGAGCCCT 6900
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QY 6901 GGCCCTTGGCTCTCGAATTTGGCTCTGACCCCTTACTTGGGGCAGCGTCTGGACAGTGAAGC 6960
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QY 6961 CTCTGTCAAGCCCTGTGAGGACAGCTCAGCTCATTTTCAGAGAGCTGTGGCACCACATC 7020
Db 6760 CTCTGTCAAGCCCTGTGAGGACAGCTCAGCTCATTTTCAGAGAGCTGTGGCACCACATC 6819
QY 7021 GGGCGGCTCTCCAGGACTTCTTACGTTGCTCTCCCTGACCTCCAGCTCACCCTCTCCG 7080
Db 6820 GGGCGGCTCTCTCCAGGACTTCTTACGTTGCTCTCCCTGACCTCCAGCTCACCCTCTCCG 6879
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QY 7081 CCGCGTCCCAACGGTTTACCACTGCAACCTTGGGACTCAGCTCGGGTGGCCGAGCAGCGCA 7140
Db 6880 CCGCGTCCCAACGGTTTACCACTGCAACCTTGGGACTCAGCTCGGGTGGCCGAGCAGCGCA 6939
QY 7141 CAGCTACCAACCCCTGACCAAGACCACTGGTCTAGCTGACCGTACCGCTCAGACGC 7200
Db 6940 CAGCTACCAACCCCTGACCAAGACCACTGGTCTAGCTGACCGTACCGCTCAGACGC 6999
QY 7201 CTCGATCGACGAGCGGTGTTCAGTGGATGATTTTATCATCCACACGCGGCGAGTCGG 7260
Db 7000 CTCGATCGACGAGCGGTGTTCAGTGGATGATTTTATCATCCACACGCGGCGAGTCGG 7059
QY 7261 CCCTCGGGGAGGCGCTTGCCACCTTGGTGGAGCTCCTGTGGCCCTTCCCTCCCTCCT 7320
Db 7060 CCCTCGGGGAGGCGCTTGCCACCTTGGTGGAGCTCCTGTGGCCCTTCCCTCCCTCCT 7119
QY 7321 CCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTTGCTTGTAGTGTAGTACCGC 7376
Db 7120 CCCTCTTTTACTCTAGACGACGAATAAAGCCCTGTTGCTTGTAGTGTAGTACCGC 7175

RESULT 7
US-10-627-370-1
; Sequence 1, Application US/10627370
; Publication No. US20040081988A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jason M.
; APPLICANT: Castle, John C.
; APPLICANT: Armour, Christopher D.
; TITLE OF INVENTION: SPLICE VARIANT ISOFORMS OF HUMAN CALCIUM CHANNEL CACNA1B
; FILE REFERENCE: RS0202Y
; CURRENT APPLICATION NUMBER: US/10/627,370
; CURRENT FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 6792
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-370-1

Query Match 88.6%; Score 6535; DB 17; Length 6792;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 6792; Conservative 0; Mismatches 0; Indels 237; Gaps 2;

QY 146 ATGGTCCGCTTCGGGACGAGCTGGGCGCGCGCTATGAGGCGCCCGCGCGCGGAGAGCGG 205
Db 1 ATGGTCCGCTTCGGGACGAGCTGGGCGCGCGCTATGAGGCGCCCGCGCGCGGAGAGCGG 60

QY 206 GCCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 265
Db 61 GCCCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 120

QY 266 CAGCGGGTCTCTACAAGCAATCGATCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 325
Db 121 CAGCGGGTCTCTACAAGCAATCGATCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

QY 326 CCCATCCCGGTCAAGCAGAACTGCTTCCACGTCACACCGCTCGCTCTTCGTCCTTCAGCGAG 385
Db 181 CCCATCCCGGTCAAGCAGAACTGCTTCCACGTCACACCGCTCGCTCTTCGTCCTTCAGCGAG 240

QY 386 GACAAGCTGTCTCGCAAAATACGCAAGCGCATCACCGAGTGGCTTCCATTCGAGTATATG 445
Db 241 GACAAGCTGTCTCGCAAAATACGCAAGCGCATCACCGAGTGGCTTCCATTCGAGTATATG 300

QY 446 ATCTTGGCCACCATCATCGGCAACTGCTCATCTGCTGCGCTTGGAGCAGACACCTCCCTGAT 505
Db 301 ATCTTGGCCACCATCATCGGCAACTGCTCATCTGCTGCGCTTGGAGCAGACACCTCCCTGAT 360

QY 506 GGGGACAAAACGCCCATGTCCGAGCGGCTGGACGACACGAGCGCTATTTCATCGGGATC 565
Db 361 GGGGACAAAACGCCCATGTCCGAGCGGCTGGACGACACGAGCGCTATTTCATCGGGATC 420
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QY	566	TTTTGCTTCGAGCGAGGATCAAAATCATCGCTCTGGGCTTTGTCTTCCACAAGGGCTCT	625
Db	421	TTTTGCTTCGAGCGAGGATCAAAATCATCGCTCTGGGCTTTGTCTTCCACAAGGGCTCT	480
QY	626	TACCTGCGAAACGGCTGGAAACGTCATGGAATTCGTGTGCTCCTCACAGGATCCTTGCC	685
Db	481	TACCTGCGAAACGGCTGGAAACGTCATGGAATTCGTGTGCTCCTCACAGGATCCTTGCC	540
QY	686	ACGGCTGGAACGACTTCGACCTGGGAAACATCGAGGGCTGTGCTGAGGCGCCCTG	745
Db	541	ACGGCTGGAACGACTTCGACCTGGGAAACATCGAGGGCTGTGCTGAGGCGCCCTG	600
QY	746	AAGCTGGTGTCTGGGATTCGAAATTTGCAAGTGTGCTCAAGTCATCATGAAGGCCATG	805
Db	601	AAGCTGGTGTCTGGGATTCGAAATTTGCAAGTGTGCTCAAGTCATCATGAAGGCCATG	660
QY	806	GTTTCACTCCTGCAGATTCGGGCTGCTCTCTTTTGGCATCCTCATGTTTGGCATCAT	865
Db	661	GTTTCACTCCTGCAGATTCGGGCTGCTCTCTTTTGGCATCCTCATGTTTGGCATCAT	720
QY	866	GGCTTGGAGTTCTACATGGGCAAGTTCCAAAGGCGCTGTTTCCCAACAGCACAGATGCG	925
Db	721	GGCTTGGAGTTCTACATGGGCAAGTTCCAAAGGCGCTGTTTCCCAACAGCACAGATGCG	780
QY	926	GAGCCGTGGGTGACTTCCCTGTGGCAAGAGGCGCCAGCCCGGCTGTGGAGGGCGAC	985
Db	781	GAGCCGTGGGTGACTTCCCTGTGGCAAGAGGCGCCAGCCCGGCTGTGGAGGGCGAC	840
QY	986	ACTGAGTCGGGGAGTACTGGCCAGGACCAACTTTGGCATCACCACCACTTTGACAAATC	1045
Db	841	ACTGAGTCGGGGAGTACTGGCCAGGACCAACTTTGGCATCACCACCACTTTGACAAATC	900
QY	1046	CTGTTTGGCATCTTGACGGTGTTCAGTGTCATCACCATGGAGGGCTGGACTGACATCCTC	1105
Db	901	CTGTTTGGCATCTTGACGGTGTTCAGTGTCATCACCATGGAGGGCTGGACTGACATCCTC	960
QY	1106	TATATACAAACGATCGCGCGGCAACACCTGGAACTGGCTCTACTTCACTCCTCTCATC	1165
Db	961	TATATACAAACGATCGCGCGGCAACACCTGGAACTGGCTCTACTTCACTCCTCTCATC	1020
QY	1166	ATCATCGGCTCTTCTTCACTGCTCAACCTGGTGTGGGCTGCTCTCGGGGGAGTTTGCC	1225
Db	1021	ATCATCGGCTCTTCTTCACTGCTCAACCTGGTGTGGGCTGCTCTCGGGGGAGTTTGCC	1080
QY	1226	AAGGACGAGAGAGGTGGAGAACCGCCGCGCTTTCCTGAAGCTGCGCGGACAGCAG	1285
Db	1081	AAGGACGAGAGAGGTGGAGAACCGCCGCGCTTTCCTGAAGCTGCGCGGACAGCAG	1140
QY	1286	ATCGAGCGAGACTCAACGGGTACCTGGAGTGGATCTTCAAGGCGGAGGAAGTCATGCTG	1345
Db	1141	ATCGAGCGAGACTCAACGGGTACCTGGAGTGGATCTTCAAGGCGGAGGAAGTCATGCTG	1200
QY	1346	GCCGAGGAGGACAGGAATGCAGAGGAGAAGTCCCTTTGGACGTGCTGAAGAGAGCGGCC	1405
Db	1201	GCCGAGGAGGACAGGAATGCAGAGGAGAAGTCCCTTTGGACGTGCTGAAGAGAGCGGCC	1260
QY	1406	ACCAAGAGAGCAGAAATGAACCTGATCCAGCAGAGGAGGAGGACCGGTTTGCAGAT	1465
Db	1261	ACCAAGAGAGCAGAAATGAACCTGATCCAGCAGAGGAGGAGGACCGGTTTGCAGAT	1320
QY	1466	CTCTGTGCTGTGGATCCCTTCCCGCGCCAGCCTCAAGAGGGGAGACAGAGAGC	1525
Db	1321	CTCTGTGCTGTGGATCCCTTCCCGCGCCAGCCTCAAGAGGGGAGACAGAGAGC	1380
QY	1526	TCGTCAATCTTCGGAGGAAGAGATGTTTCCGGTTTTTTTATCCGGCGCATGCTGAAG	1585
Db	1381	TCGTCAATCTTCGGAGGAAGAGATGTTTCCGGTTTTTTTATCCGGCGCATGCTGAAG	1440
QY	1586	GCTCAGAGCTTCTACTGGGTGGTGTGTGCTGTGTGGCCCTGAAACACATGTGTGTGCC	1645
Db	1441	GCTCAGAGCTTCTACTGTGGTGGTGTGTGCTGTGTGGCCCTGAAACACATGTGTGTGCC	1500
QY	1646	ATGGTGCAATTACACCGCCGGCGGCTTACCAGCACCTTGATTTTTCAGAGATTTTGT	1705

Db	1501	ATGGTGCAATTACAAACGAGCGCGGCTTACCACGACCCCTGTATTTTGCAGAGTTTGT	1560
QY	1706	TTCCCTGGGTCTCTTCCCTCACAGAGATCTCCCTGGAAGATGTATGCTGGGCGGCCAGAGC	1765
Db	1561	TTCCCTGGGTCTCTTCCCTCACAGAGATGTCCCTGAAGATGTATGCTGGGCGGCCAGAGC	1620
QY	1766	TACTTCCGGTCTCTCTTCAACTGCTTCGACTTTTGGGTCATCGTGGGAGCGTCTTTGAA	1825
Db	1621	TACTTCCGGTCTCTCTTCAACTGCTTCGACTTTTGGGTCATCGTGGGAGCGTCTTTGAA	1680
QY	1826	GTGTCCTGGGCGGCATCAAGCGGGGAAGCTCTTTTGGGTCAGTGTGCTGCGGGCCCTC	1885
Db	1681	GTGTCCTGGGCGGCATCAAGCGGGGAAGCTCTTTTGGGTCAGTGTGCTGCGGGCCCTC	1740
QY	1886	CGCTGCTGAGGATCTTCAAGTACCAAGTACTGGAAGCTCCCTGCGGAACCTGCTGGT	1945
Db	1741	CGCTGCTGAGGATCTTCAAGTACCAAGTACTGGAAGCTCCCTGCGGAACCTGCTGGT	1800
QY	1946	TCCCTGCTGAATCCATGAAGTCCATCATCAGGCTGCTCTTCTTGTCTCTTCTGTTCAAT	2005
Db	1801	TCCCTGCTGAATCCATGAAGTCCATCATCAGGCTGCTCTTCTTGTCTCTTCTGTTCAAT	1860
QY	2006	GTGTCCTTCCGCTGTGGGATGAGCTGTTTGGGGGAACAGTTCAACTTCCAGGATGAG	2065
Db	1861	GTGTCCTTCCGCTGTGGGATGAGCTGTTTGGGGGAACAGTTCAACTTCCAGGATGAG	1920
QY	2066	ACTCCCAACAACTTTCGACACCTTCCCTGCGCCCATCTCTCACTGTCTTCCAGATCCTG	2125
Db	1921	ACTCCCAACAACTTTCGACACCTTCCCTGCGCCCATCTCTCACTGTCTTCCAGATCCTG	1980
QY	2126	ACGGGAGAGACTGGAAATGCAATGATATCAGGGATCGAATCGCAAGCGGCGTCAGC	2185
Db	1981	ACGGGAGAGACTGGAAATGCAATGATATCAGGGATCGAATCGCAAGCGGCGTCAGC	2040
QY	2186	AAAGGCATGTTCTGCTCTTTTACTTCTGACACTGTTCGGAACCTACACTCTG	2245
Db	2041	AAAGGCATGTTCTGCTCTTTTACTTCTGACACTGTTCGGAACCTACACTCTG	2100
QY	2246	CTGAATGCTCTTCTGGCCATCGTGTGGCAACCTTGSCCAACGCCCAAGAACTACAC	2305
Db	2101	CTGAATGCTCTTCTGGCCATCGTGTGGCAACCTTGSCCAACGCCCAAGAACTACAC	2160
QY	2306	GATGAAGAGAGATGGAAGAGCAGCAATCAGAAGCTTGTCTGCAAAAAGCCAAAGAA	2365
Db	2161	GATGAAGAGAGATGGAAGAGCAGCAATCAGAAGCTTGTCTGCAAAAAGCCAAAGAA	2220
QY	2366	GTGGCTGAAGTCAAGCCCATGCTGCGCGGAACATCTCCATCGCGCGCAGGACAGAAC	2425
Db	2221	GTGGCTGAAGTCAAGCCCATGCTGCGCGGAACATCTCCATCGCGCGCAGGACAGAAC	2280
QY	2426	TCGGCCAAAGCGCGCTCGGTGTGGGAGCAGCGGGCCAGCAGCTAGCGGTGACAGAACCTG	2485
Db	2281	TCGGCCAAAGCGCGCTCGGTGTGGGAGCAGCGGGCCAGCAGCTAGCGGTGACAGAACCTG	2340
QY	2486	CGGGCAGCTGCGAGCGCTGTACAGCAGATGGAACCCGAGAGCGGCTGCGCTTCGCC	2545
Db	2341	CGGGCAGCTGCGAGCGCTGTACAGCAGATGGAACCCGAGAGCGGCTGCGCTTCGCC	2400
QY	2546	ACTACGGCCACTGCGGGCCCGACATGAAGCCACTTGGACCGGCGCTGTGTGTGGAG	2605
Db	2401	ACTACGGCCACTGCGGGCCCGACATGAAGCCACTTGGACCGGCGCTGTGTGTGGAG	2460
QY	2606	CTGGGCGCGGACCGGCGGGGGGGCGGTGGGAGGCAAGACCCGACCTGAAGCTGCGGGAG	2665
Db	2461	CTGGGCGCGGACCGGCGGGGGGGCGGTGGGAGGCAAGACCCGACCTGAAGCTGCGGGAG	2520
QY	2666	GCCCCGAGGGGCTGCAACCTTCCGCGCAGCGACACCCGCGACCGCGCAAGGACAGACC	2725
Db	2521	GCCCCGAGGGGCTGCAACCTTCCGCGCAGCGACACCCGCGACCGCGCAAGGACAGACC	2580
QY	2726	CCCGCGCGGGGACCGAGGACCGAGCAGAGGCCCCGGAAGCGGAGAGCGGAGCCCGGT	2785

Db 2581 CCCCGGGGGGACCGAGCAGAGAGGCCCCCGGAGGCGGAGAGCGGGGAGCCCGGT 2640
Qy 2786 GCCCGGAGAGCGCGCGCCGACCGCAGCCACAGCAAGGAGGCGCGGGGCCCCCG 2845
Db 2641 GCCCGGAGAGCGCGCGCCGACCGCAGCCACAGCAAGGAGGCGCGGGGCCCCCG 2700
Qy 2846 GAGCGCGGAGCGAGCGCGCGCGAGCGCCAGGCGCCCGAGGCGCGCGCGCGGACACACGG 2905
Db 2701 GAGCGCGGAGCGAGCGCGCGCGAGCGCCAGGCGCCCGAGGCGCGCGCGGACACCGG 2760
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Qy 3206 CAGCCCCGAGGAGCCACACTGTGACCTGGAGACCAAGTGGAGCTGTGAGCTGTGGGTCCCATG 3265
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Qy 3266 CACACACTGCCAGCACTGTCTCCAGAGGTGGAGGAACAGCCAGAGGATGCGAGACAAT 3325
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Qy 3386 CCAAGTATGTGACGGGCGCTTTGGGGAAGCCACGGTCTGTTCCAGTGGTAAGCTGGAC 3445
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Qy 3446 CTGGAAGCCAAAGCAGAGGGGAAGAGAGGTGGAAGCGGATGACGTGATGAGGAGCGGC 3505
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Qy 3506 CCCCGGCTATGCTCCCATACAGCTCCATGTTCTGTTTAAAGCCCGACCAACCTGCTCCGC 3565
Db 3361 CCCCGGCTATGCTCCCATACAGCTCCATGTTCTGTTTAAAGCCCGACCAACCTGCTCCGC 3420
Qy 3566 CGCTTCTGCCATACATCGTGACCAATGAGGTACTTTCGAGGTGCTATTCGTGGTCAATC 3625
Db 3421 CGCTTCTGCCATACATCGTGACCAATGAGGTACTTTCGAGGTGCTATTCGTGGTCAATC 3480
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Qy 3686 AACGCTCTGAAATACCTGGATTACATTTTCACTGGTGTCTTTACTTTGAGATGGTGATA 3745
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Qy 3746 AAGATGATGCACTTGGAGCTGCTGCTTCAACCTGGAGCCTATTTCCGGGACTTGTGGAAC 3805
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Qy 3806 ATTCTGACATTCATTTGTTGTCAGTGGCGGCTGCTGGTGGCTTTGCTTCTCGAGCTTCGTG 3865
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Qy 3866 GGAGGATCCAAAGGGAAGAAGACATCAATACCATCAAGTCTCTGAGAGTCTTCTGTTGCTCTG 3925
Db 3711 --AGGATCCAAAGGGAAGAAGACATCAATACCATCAAGTCTCTGAGAGTCTTCTGTTGCTCTG 3768
Qy 3926 CGGCCCCCTCAAGACCATCAAAACGGCTGCCCAAGCTCAAGGCTGTGTTGAGCTGTGTTGCTG 3985
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Qy 3986 AACTCCCTGAAGAAATGTCTCTCAACATCTTGATTTGTCTACATGTCTTCTCATGTTTCATATTT 4045
Db 3829 AACTCCCTGAAGAAATGTCTCTCAACATCTTGATTTGTCTACATGTCTTCTCATGTTTCATATTT 3888
Qy 4046 GCGCTCATTCGCTGAGCTCTTCAAAGGAAAGTTTCTTACTGCAAGATGAATCAAG 4105
Db 3889 GCGCTCATTCGCTGAGCTCTTCAAAGGAAAGTTTCTTACTGCAAGATGAATCAAG 3948
Qy 4106 GAGCTGGAGGAGGACTGTCAGGGGTCAAGTATTTGATTTATGAGGAGGAGTGGAGCT 4165
Db 3949 GAGCTGGAGGAGGACTGTCAGGGGTCAAGTATTTGATTTATGAGGAGGAGTGGAGCT 4008
Qy 4166 CAGCCCCAGGAGTGGAGAAATACGACTTTTCACTACGACAATGTGCTCTGGGCTCTGCTG 4225
Db 4009 CAGCCCCAGGAGTGGAGAAATACGACTTTTCACTACGACAATGTGCTCTGGGCTCTGCTG 4068
Qy 4226 ACCTCTGTTCAAGTGTCCACGGGAGAGGCTGCCCATGGTGTCTGAAACAACACTCCGTGGAT 4285
Db 4069 ACCTCTGTTCAAGTGTCCACGGGAGAGGCTGCCCATGGTGTCTGAAACAACACTCCGTGGAT 4128
Qy 4286 GCCACCTATGAGAGAGAGGCTCCAGCCCTGGGTACCGCATGGAGCTGTCTCATCTTCTAC 4345
Db 4129 GCCACCTATGAGAGAGAGGCTCCAGCCCTGGGTACCGCATGGAGCTGTCTCATCTTCTAC 4188
Qy 4346 GTGCTTACTTTGTGCTTTTCCCTTCTTCTCGTCAACATCTTTGTGGCTTTGATCATC 4405
Db 4189 GTGCTTACTTTGTGCTTTTCCCTTCTTCTTGTCTCAACATCTTTGTGGCTTTGATCATC 4248
Qy 4406 ATCACTTTCAGAGCAGGGGGAACAAGTGATGTCTGAAATGCAAGCTTGGAGAGAACGAG 4465
Db 4249 ATCACTTTCAGAGCAGGGGGAACAAGTGATGTCTGAAATGCAAGCTTGGAGAGAACGAG 4308
Qy 4466 AGGCTTGTGATTTGACTTTCGCATCAGGGCCAAACCCCTGACAGGTCATATGCCCCAAAC 4525
Db 4309 AGGCTTGTGATTTGACTTTCGCATCAGGGCCAAACCCCTGACAGGTCATATGCCCCAAAC 4368
Qy 4526 CGCAGTCTGTTCCAGTATAGAGCTGGACATTTTGTGTCTCCCGCCCTTTGAAATCTTC 4585
Db 4369 CGCAGTCTGTTCCAGTATAGAGCTGGACATTTTGTGTCTCCCGCCCTTTGAAATCTTC 4428
Qy 4586 ATCATGGCCATGATAGCCCTCAAACACTGTGGTGTCTGATGATGAAGTTCTATGATGACCC 4645
Db 4429 ATCATGGCCATGATAGCCCTCAAACACTGTGGTGTCTGATGATGAAGTTCTATGATGACCC 4488
Qy 4646 TATGAGTACAGAGCTGATGTAATGCTGAAACATGTGTGTTACATCCATGTTCTCCATG 4705
Db 4489 TATGAGTACAGAGCTGATGTAATGCTGAAATGCTGTAACATCGTGTTCACATGTTCTCCATG 4548
Qy 4706 GAATGGTGTGAAGATCATCGCTTTGGGGTGTCTGAACTATTTTCAGAGATGCTGGAAT 4765
Db 4549 GAATGGTGTGAAGATCATCGCTTTGGGGTGTCTGAACTATTTTCAGAGATGCTGGAAT 4608
Qy 4766 GTCTTTGACTTTGCTCACTGTGTTGGGAAGTATTTACTGATATTTTAGTAACAGAGATTTGG 4825
Db 4609 GTCTTTGACTTTGCTCACTGTGTTGGGAAGTATTTACTGATATTTTAGTAACAGAGATTTGG 4668
Qy 4826 GAAACGAACATTTCACTCAACCTCAGCTTCTCCGCTCTTTTCAGAGTGGCGGCTGATC 4885
Db 4669 GAAACGAACATTTCACTCAACCTCAGCTTCTCCGCTCTTTTCAGAGTGGCGGCTGATC 4728
Qy 4886 AAGCTGCTCGGAGGCTACACCATCGCATCTCTGCTGGGACCTTTTGTCCAGTCTCTC 4945
Db 4729 AAGCTGCTCGGAGGCTACACCATCGCATCTCTGCTGGGACCTTTTGTCCAGTCTCTC 4788

QY	4946	AAGCCCTGCCCCACCTGCTGCTGCTCATGTCATGTCCTTCTTCTATCTACGCCATCATC	5005
Db	4789	AAGCCCTGCCCCACCTGCTGCTGCTCATGTCATGTCCTTCTTCTATCTACGCCATCATC	4848
QY	5006	GGCATCGAGGTGTTGGGAATATGCCCCCTGGATGATGACACGACGATCAACCGCCACAAC	5065
Db	4849	GGCATCGAGGTGTTGGGAATATGCCCCCTGGATGATGACACGAGCATCAACCGCCACAAC	4908
QY	5066	AACCTCCGAGCGTTTGTGAAGCCCTGATGCTGCTGCTTCCAGGAGGCCACGCGGGAGGCC	5125
Db	4909	AACCTCCGAGCGTTTGTGAAGCCCTGATGCTGCTGCTTCCAGGAGGCCACGCGGGAGGCC	4968
QY	5126	TGGCAGAGATCATGCTGCTGCTGCTGAGCAACCGACCTGTGATGAGCAGCCCAATGCC	5185
Db	4969	TGGCAGAGATCATGCTGCTGCTGCTGAGCAACCGACCTGTGATGAGCAGCCCAATGCC	5028
QY	5186	ACCGAGTGGAGTACATTTGCTTCTGCTGAGCAACCGACCTGTGATGAGCAGCCCAATGCC	5245
Db	5029	ACCGAGTGGAGTACATTTGCTTCTGCTGAGCAACCGACCTGTGATGAGCAGCCCAATGCC	5088
QY	5246	TTTCTGATGTTGAACCTCTTTGTGGGCTGTGATGATCGAGCAATTTTGTGATCTCACGGG	5305
Db	5089	TTTCT-----	5093
QY	5306	GACTCTTCATCCTAGGTCTCACCACTTGGAGTATGATCCCGGCTGCGGCTGAATAC	5365
Db	5094	-----	5093
QY	5366	GACCCGGCTGCTGTGGGCGCATCAGTTACATGATGATGTTGAGATGCTGAAACACATG	5425
Db	5094	-----	5093
QY	5426	TCCCCGCTCTGGGCTGGGGAAGAAATGCCCTGCTCGAGTTGCTTACAAGCGCCTGGTT	5485
Db	5094	-----GGGCTGGTT	5103
QY	5486	CGCATGAATGCCATCTCCAAACGAGGACATGACTGTTGACTTCAGTCCACGCTGATG	5545
Db	5104	CGCATGAATGCCATCTCCAAACGAGGACATGACTGTTGACTTCAGTCCACGCTGATG	5163
QY	5546	GCCCTCATCCGACCGGCACTGGAGATCAAGCTGGCCCCAGCTGGGCAAAAGCAGCATCAG	5605
Db	5164	GCCCTCATCCGACCGGCACTGGAGATCAAGCTGGCCCCAGCTGGGCAAAAGCAGCATCAG	5223
QY	5606	TGTGACGGGAGTTGAGGAAGGAGATTCGGTTGTTGGGCCAATCTGCCCCAGAAAGCT	5665
Db	5224	TGTGACGGGAGTTGAGGAAGGAGATTCGGTTGTTGGGCCAATCTGCCCCAGAAAGCT	5283
QY	5666	TTGGACTTGTGTTACCAACCCCATAGCCTGATGAGATGACAGTGGGGAGGTTTATGCA	5725
Db	5284	TTGGACTTGTGTTACCAACCCCATAGCCTGATGAGATGACAGTGGGGAGGTTTATGCA	5343
QY	5726	GCTCTGATGATATTTGACTTCTTACAAGCAGAAACAAACACAGAGACAGATGACAGAG	5785
Db	5344	GCTCTGATGATATTTGACTTCTTACAAGCAGAAACAAACACAGAGACAGATGACAGAG	5403
QY	5786	GCTCTGAGGCTCTCCAGATGGGTCTGTGTCCTGTTTCCACCTCTGAAGGCCAACC	5845
Db	5404	GCTCTGAGGCTCTCCAGATGGGTCTGTGTCCTGTTTCCACCTCTGAAGGCCAACC	5463
QY	5846	CTGGAGACACACGCGGCTGTCTCCGAGAGCCCGGTTTCTTCGACAGAAAGT	5905
Db	5464	CTGGAGACACACGCGGCTGTCTCCGAGAGCCCGGTTTCTTCGACAGAAAGT	5523
QY	5906	TCCACCTCCCTCAGCAATGGGGGGCCATACAAACCAAGAGAGTGGCATCAAAAGTCT	5965
Db	5524	TCCACCTCCCTCAGCAATGGGGGGCCATACAAACCAAGAGAGTGGCATCAAAAGTCT	5583
QY	5966	GTCCTCTGGGCACTCAAGACCCAGGATGCCACCCATGAGGCCAGGCCACCCCTGGAG	6025
Db	5584	GTCCTCTGGGCACTCAAGACCCAGGATGCCACCCATGAGGCCAGGCCACCCCTGGAG	5643
QY	6026	CGTGGCCACTCCACAGAGATCCCTGTGGGGGGTTCAGGAGCACTGGCTGTGGAGCTTCAG	6085

Db	5644	CGTGGCCACTCCACAGAGATCCCTGTGGGGGGTTCAGGAGCACTGGCTGTGGAGCTTCAG	5703
QY	6086	ATGCAGAGCATAAACCGGAGGGGCCCTGATGGGAGGCCACAGCCTGGCTGGAGAGCCAG	6145
Db	5704	ATGCAGAGCATAAACCGGAGGGGCCCTGATGGGAGGCCACAGCCTGGCTGGAGAGCCAG	5763
QY	6146	GGTCAGGGGCTCCATGCCCCCGCTTGGGGCCAGACTCAGCCGTCACAGATGCCAGC	6205
Db	5764	GGTCAGGGGCTCCATGCCCCCGCTTGGGGCCAGACTCAGCCGTCACAGATGCCAGC	5823
QY	6206	CCCATGAAGCGCTCCATCTCCACGCTGGCCAGCGGCCCGCTGGGAGCTCATCTTTGGAGC	6265
Db	5824	CCCATGAAGCGCTCCATCTCCACGCTGGCCAGCGGCCCGCTGGGAGCTCATCTTTGGAGC	5883
QY	6266	ACCAACCCGAGACCGCCACACCCCTAGCCAGGCTGTGTGCAACACACACACCGCTGC	6325
Db	5884	ACCAACCCGAGACCGCCACACCCCTAGCCAGGCTGTGTGCAACACACACACCGCTGC	5943
QY	6326	CACCGCCGAGGAGACAGAAAGAGGTCCCTGGAGAGGGGCCACAGCCTCTCTGCCGAT	6385
Db	5944	CACCGCCGAGGAGACAGAAAGAGGTCCCTGGAGAGGGGCCACAGCCTCTCTGCCGAT	6003
QY	6386	ATGATGCGCAACCAAGCACTGTGTGGGCTCGGGGCTGCCCGGGGAGAAGGGCTTACA	6445
Db	6004	ATGATGCGCAACCAAGCACTGTGTGGGCTCGGGGCTGCCCGGGGAGAAGGGCTTACA	6063
QY	6446	GGCTGCGCGGGGAAACGAGAGCGCCGAGAGGGGGCCGCTCCAGAGAGCGGAGGAGCAG	6505
Db	6064	GGCTGCGCGGGGAAACGAGAGCGCCGAGAGGGGGCCGCTCCAGAGAGCGGAGGAGCAG	6123
QY	6506	CCCTCATCTCTCTCGGAGAACAGCGCTTCTACTCTGCGACCGCTTGGGGGCGGT	6565
Db	6124	CCCTCATCTCTCTCGGAGAACAGCGCTTCTACTCTGCGACCGCTTGGGGGCGGT	6183
QY	6566	GAGCCCCGAGGCCCAAGCCCTCCTCAGCAGCCACCCAAAGCTCGCCAAACAGCTGGCCAG	6625
Db	6184	GAGCCCCGAGGCCCAAGCCCTCCTCAGCAGCCACCCAAAGCTCGCCAAACAGCTGGCCAG	6243
QY	6626	GAGCGGGACCCCAACAGAGGAGTGGTTCGTAATGGGAGCCCTTCTGTCAACA	6685
Db	6244	GAGCGGGACCCCAACAGAGGAGTGGTTCGTAATGGGAGCCCTTCTGTCAACA	6303
QY	6686	TCTGCTAGTACACCCCGGCTGGGCGGAGGAGCAGCTCCCGCCAGAGCCCTCTGACT	6745
Db	6304	TCTGCTAGTACACCCCGGCTGGGCGGAGGAGCAGCTCCCGCCAGAGCCCTCTGACT	6363
QY	6746	CCCGCCCGAGCATCCTTACAAGACGGCCAACTCCTCAGCCATCCCATCTTCGCGGGGCT	6805
Db	6364	CCCGCCCGAGCATCCTTACAAGACGGCCAACTCCTCAGCCATCCCATCTTCGCGGGGCT	6423
QY	6806	CAGACAGCCTCCTGCTTCTCCAGCGCGCTCAGCGTGGGCTTTCGGAACACAAC	6865
Db	6424	CAGACAGCCTCCTGCTTCTCCAGCGCGCTCAGCGTGGGCTTTCGGAACACAAC	6483
QY	6866	GCCTCTGTCAGAGACCCCTCAGCCAGCCCTCGGCCCCCTGGCTCTCGAATGGCTCT	6925
Db	6484	GCCTCTGTCAGAGACCCCTCAGCCAGCCCTCGGCCCCCTGGCTCTCGAATGGCTCT	6543
QY	6926	GACCTTACCTGGGCGAGGCTGTGGACAGTGGGCTCTGTCCACGCCCTTCCTGAGGAC	6985
Db	6544	GACCTTACCTGGGCGAGGCTGTGGACAGTGGGCTCTGTCCACGCCCTTCCTGAGGAC	6603
QY	6986	ACGCTCACTTTCAGAGAGGCTGTGGCCACAACTGGGCGGCTTCTCCGAAACAAAC	7045
Db	6604	ACGCTCACTTTCAGAGAGGCTGTGGCCACAACTGGGCGGCTTCTCCGAAACAAAC	6663
QY	7046	GTGCTCTCCCTGACCTCCAGTCTACCTCTCCGCGGCTGCCAAACGGTTACCACTGC	7105
Db	6664	GTGCTCTCCCTGACCTCCAGTCTACCTCTCCGCGGCTGCCAAACGGTTACCACTGC	6723
QY	7106	ACCCTGGGACTCAGCTCGGCTGGCGAGCAGCTACCAACCCCTGACCAAGAC	7165

Db 6724 ACCCTGGAGTCACTCGGTGGCCGAGCAGCGCACAGCTTACCACCACTTGCACCAAGAC 6783

Qy 7166 CACTGGTGC 7174

Db 6784 CACTGGTGC 6792

RESULT 8

US-10-033-026-9

; Sequence 9, Application US/10033026

; Publication No. US20020147309A1

; GENERAL INFORMATION:

; APPLICANT: Lipscombe, Diane

; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF

; FILE REFERENCE: B1055/7000

; CURRENT APPLICATION NUMBER: US/10/033,026

; CURRENT FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: US 09/268,163

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: US 60/077,901

; PRIOR FILING DATE: 1998-03-13

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 9

; LENGTH: 7011

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..7008

US-10-033-026-9

Query Match 71.7%; Score 5289.8; DB 14; Length 7011;

Best Local Similarity 85.5%; Pred. No. 0;

Matches 6045; Conservative 0; Mismatches 927; Indels 99; Gaps 10;

Qy 146 ATGTCCTCGTTCGGGGACGAGCTCGGCGCGCGTATGAGGCCCGCGCGGAGCGG 205

Db 1 ATGTCCTCGTTCGGGGACGAGCTAGGCGCGCTATGGGGCACCGCGCGGGAGCGG 60

Qy 206 GCCCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 265

Db 61 GTCGCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGG 120

Qy 266 CAGCGGTCTCTACAAGCAATCGATCGCGAGCGCGCGGACCATGGCGCTGTACAAC 325

Db 121 CAGCGGTCTCTACAAGCAATCGATCGCGAGCGCGCGGACCATGGCGCTGTACAAC 180

Qy 326 CCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAACCGCTCGCTCTTTCGTCAGCGAG 385

Db 181 CCCATCCCGTCAAGCAGAACTGCTTCAACCGTCAACCGCTCGCTCTTTCGTCAGCGAG 240

Qy 386 GACAACTGTCGCCAAATACGGAAGGCGATCAACGAGTGGCTCCATTCGAGTATATG 445

Db 241 GACAACTGTCGCCAAATATGCTAAGCGCATCAACGAAATGGCGCGCTTCGAAATATG 300

Qy 446 ATCTGCGCCACCATCATCGCAACTGCATCGTGTGGCGCTTGGAGCAGCACCTCCCTGAT 505

Db 301 ATCTGCGCCACCATCATCGCAACTGCATCGTGTGGCGCTTGGAGCAGCACCTCCCTGAT 360

Qy 506 GGGGACAAAACGCCCATGTCCGAGCGGTGGAGCACCGAGCGGCTATTTTCATCGGGATC 565

Db 361 GGGGACAAAGACTCCCATGTCTGAACGATGGATGACACGGAACCTTACTTCATCGGCATC 420

Qy 566 TTTTGTCTCGAGGAGGAGTCAAAATCATCGCTCTGGGCTTTGCTTCCACAAGGGCTCT 625

Db 421 TTTTGTCTCGAGGAGGAGTCAAAATCATAGCTCTGGGCTTTGCTTCCACAAGGGCTCC 480

Qy 626 TACCTGCGGAACGGCTGGAAGCTCATGCACTTCGTTGCTCGTCTCAGAGGATCTTGGC 685

Db 481 TACCTGCGGAATGGCTGGAAGCTCATGCACTTCGTTGCTCGTCTCAGAGATTCCTTGGC 540

686 ACGGCTGGAACTGACCTTGACCTTGCAGAACTAGGGGCTGTGCTGTGCTGAGGCCCCCTG 745

Db 541 ACAGCTGGAACTGACCTTGTGATCTCGCACCTTGAAGGCTGTGCTGTGCTTAGGCCCCCTG 600

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Db 601 AAGTGTGTGTCTGGAATTCAGCTTGCAGGTGCTCAAGTCCATCAATCAAGAGGCCATG 660

Qy 806 GTTCCCACTCTCTGAGATTTGGGCTGCTTCTTCTTTGGCAATCTCTCATGTTTGGCATCAT 865

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Qy 866 GGCTGTGAGTTTACATGGGCAAGTTCCACAAGGCTGTTTCCCAACAGCAGATGCG 925

Db 721 GGCTGTGAGTTTATATGGGCAATTCATAAGGCTGCTTCCCAACAGCAGATGCA 780

Qy 926 GAGCGCTGGGTGACCTTCCCTGTGCGAAGGAGGCCCGCGGCTGTGCGAGGGCGAC 985

Db 781 GAGCGCTGGGTGACCTTCCCTGTGCGAAGGAGGCCCGCTGTGCTGTGTGACAGTGAC 840

Qy 986 ACTGAGTGCAGGAGTACTGCGCCAGGACCCAACTTTGGCATCACCAACTTTGACAATATC 1045

Db 841 ACCGAATGCGGAGTACTGCGCCAGGACCCAACTTTGGCATCACCAACTTTGACACATC 900

Qy 1046 CTGTTTGCCATCTGACGGTTCAGGTGTCATCACATGAGGGCTGGAATGACATCCTC 1105

Db 901 CTGTTTGCCATCTGACGGTTCAGGTGTCATCACATGAGGGCTGGAATGACATCCTC 960

Qy 1106 TATAATACAAACGATCGCGCGGCAACACTGGAACCTGGCTTACTTCACTCCCTCATC 1165

Db 961 TACAATACAAATGATCGCGCGGCAACACTGGAACCTGGTGTGTTACTTCACTCCCTCATC 1020

Qy 1166 ATCATCGGCTCTTCTTTCATGCTCAACCTGGTCTGCGGCTGCTCTCGGGGAGTTTGGC 1225

Db 1021 ATCATTTGGCTCTTCTTTCATGCTCAACCTGGTCTGCGTGTGCTTTCAGGAGTTTGGC 1080

Qy 1226 AAGGAGGAGAGAGGTGGAGAACCGCGCGGCTTCTTGAAGCTGCGCCCGGAGCAG 1285

Db 1081 AAGAGCGGAGCGAGTCGAGAACCGCGGCTTCTTGAAGCTTCCGAGCGGAGCAG 1140

Qy 1286 ATGAGGAGAGCTCAACGGTACTGAGTGTGATCTTCAAGCGGAGGAGTCACTGCTG 1345

Db 1141 ATTGAGCGAGAACTGAATGGGTACTTGGAGTGTGATCTTCAAGCGGAGGAGTCACTG 1200

Qy 1346 GCCGAGGAGACAGGAATGACAGAGGAAGTCCCTCTTTTGA---CGTGTGAAAGAGAGCG 1402

Db 1201 GCAGAGGAGACAGGAACGACAGAGAGTCCCTTTTGAATGCACTGTTTGAAGAGACT 1260

Qy 1403 GCCACCAAGAGAGCAAAATGACCTGATCCACGAGAGGAGGAGAGGACCGGTTTGA 1462

Db 1261 GCTACCAAGAGAGCGGAATGACCTCATCATGCAAGAGAGGAGGAGGACCGGTTTGA 1320

Qy 1463 GATCTGTGCTGTGGATCCCTTTCGCGCGGCGGAGCTTCAAGCGGAGGAGACAGAG 1522

Db 1321 GACCTGTGCTGTGGTCTTCTTTCGCTGCTGCGAGCTTCAAGAGTGGGAAGACAGAG 1380

Qy 1523 AGCTGTGCTATCTTCGAGGAGAGGAGATGTTCCGGTTTATTTATCCCGGCGCATGGT 1582

Db 1381 AGCTCATGCTTTCGAGGAGAGGAGATGTTCCGGTTTCTTATCCGCTGTATGTTG 1440

Qy 1583 AAGGCTCAGAGCTTCTTCTGAGGTGCTGTGCTGTGGCTTGAACACATCTGTGTG 1642

Db 1441 AAGGCAAGAGCTTCTTCTGAGGTGCTGTGCTGTGGCTTGAACACATCTGTGTG 1500

Qy 1643 GCCATGGTTCATTAACACGCGCGGCTTACCAAGCCCTGTATTTTGCAGAGTTT 1702

Db 1501 GCCATGGTTCATTAATCAGCCTCAGCGCTTACCACTGCACTGTACTTTGCAGAGTTT 1560

Qy 1703 GTTTTCTGCTGCTTCTTCTCAGAGATGTCCTTGAAGATGATGCGCTTGGGCGCCAGA 1762

Db 1561 GTTTTCTGCTGCTTCTTCTCAGAGATGTCCTTGAAGATGATGCGTCTAGGCGCCAGA 1620

Qy 1763 AGCTACTTCCGCTCTCTTCTTCAACTGCTTTCGACTTTTGGGCTCATCTGTGGGAGCGCTTT 1822

Db 1621 AGCTACTTCGGGTCTTCTTCAACTCTCTTGAATTTGGGGTGTATTTGGGAGTATCTTT 1680
Qy 1823 GAAGTGGTCTGGCGGCGCATCAAGCCGGAAGTCTCTTTGGGATCATGTGTCTGGGGCC 1882
Db 1681 GAAGTAGTCTGGGCTGCCATCAAGCCAGGAACCTCTTCGGAATCAGTGTCTGGGGCT 1740
Qy 1883 CTCGGCTCTGAGGATCTTCAAAGTCACGAAGTACTGAGTCTCCCTGGGAACCTGGTG 1942
Db 1741 CTCGGACTCTGAGGATTTCAAAGTCACGAAGTATTTGGAATCTCTGAGGAACCTGGTT 1800
Qy 1943 GTGTCCCTCTGAACCTCCATGAAGTCCATCATCAGCTCTCTTTCTGTCTTCTCTGTTTC 2002
Db 1801 GTTTCCTCTCAACTCCATGAAGTCCATCATCAGCTCTCTCTCTGCTTTCTCTTTTC 1860
Qy 2003 ATTGTGGTCTTCCGCTCTGGGATGTCAGTCTTTCGCGGATGTCAGTCTCAACTTTCAAGT 2062
Db 1861 ATTGTGGTCTTCCGCTCTGGGATGTCAGTCTTTCGCGGATGTCAGTCTCAACTTTCAAGT 1920
Qy 2063 GAGACTCCCAACCAACTTTCGACACTTTCCTGCGCCATCTCTCACTGTCTTCCAGATC 2122
Db 1921 GAGACTCCCAACCAACTTTCGACACTTTCCTGCGCCATCTCTCACTGTCTTCCAGATC 1980
Qy 2123 CTGACGGGAGAGACTGGAATGAGTATGATATCAGGGATCGAATCGGAAGGCGCTC 2182
Db 1981 CTGACAGGAGAGACTGGAATGAGTATGATATCAGGGATGAGTCAAGAGGAGTCTC 2040
Qy 2183 AGCAAGGAGTCTCTCGTCTTTCCTTACTTCTGATGTCAGTCTTTCGGAATCTCACT 2242
Db 2041 AGCAAGGAGTCTCTCGTCTTTCCTTACTTCTGATGTCAGTCTTTCGGAATCTCACT 2100
Qy 2243 CTGCTGAATGTCTTTCGCGCATCTGCTGTGGAACAACCTGGCCAGCCCAAGAGCTGACC 2302
Db 2101 CTGTTGAACGTTTCTTGGCCATTTGCTGTGGACAACCTTGCCAAATGCCAGAGTTGACC 2160
Qy 2303 AAGGATGAAGAGAGATGGAAGAGAGAGCAATCAGAGCTTGCTCTGCAAAAGGCCAAA 2362
Db 2161 AAGGATGAAGAGAGATGGAAGAGAGAGCAATCAGAGCTTGCTCTTTCAGAAAGGCCAAA 2220
Qy 2363 GAAGTGGCTGAAGTCAAGCCCACTGCTGCGGGAACATCTCCATCGCCAGGAGGAGCAG 2422
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Qy 2423 AACTCGGCAAGGCGCTCGTGTGGAGCAGCGGGCCAGCAGCTACGCTGAGAGCAGAAC 2482
Db 2281 AACTCGGCAAGGCGCTCGTGTGGAGCAGCGGGCCAGCAGCTACGCTGAGAGCAGAAC 2340
Qy 2483 CTGCGGGCAGCTGCGAGGCGCTGTACAGGAGATGGAACCCGAGGAGGCGCTGCGCTTC 2542
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Qy 2543 GCCACTAGCGCCACTTGGCGCCGACATGAAGAGCAGCACCCTGGACCGGCGCTGTTGGTG 2602
Db 2401 GCCAGCAGCGCCACTTGGCGCCGACATGAAGAGCAGCACCCTGGACCGGCGCTGTTGGTG 2460
Qy 2603 GAGCTGGCGCGGAGCGGCGGGGGCGGTGGAGAGCAAGCCCGAGCCTGAGGCTGCG 2662
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Qy 2663 GAGGCCCCGAGGGCGGTGCAACCTCCGCGCAGGACACACCGGCACCGGCAAGAGCAAG 2722
Db 2521 GAGGCCACCGAAGGTGCGGATCCACCGCGACACCCAGGCGATCTGTGATAGGGAACAG 2580
Qy 2723 -----ACCCCGCGCGGGGACCAAGGACCGAGCAGAGGCGCCCGAAGCGCGAG 2770
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Qy 2771 AGCGGGAGCGCGTGTCCCGGAGAGGCGCGCGCGCGACCGAGCCACAGCAAGAGAG 2830
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Db 2701 GCTCCAGGGCT-----GACACACAAGTGGTGTGTGAGGCGAGT 2739
Qy 2891 CGGCGGACACACCGCGGGGCTCCCCGGAGAGAGCGGCGCGGAGCCCCCGAGCGCCAC 2950
Db 2740 AGAGCTCACCACCGCGCGGATCCCGGAGGAGGCCACTGAACGGGAACCTTCGCGCGCCAC 2799
Qy 2951 CGCGCGCACCGGCAC---CAGGATCCGAGCAAGGAGTGGCGCGCG--- 2993
Db 2800 CGTCCACACCGGACCGCACAGGACTCAAGCAAGGAAGCAAGGAGGCGACTGCAACCGGTG 2859
Qy 2994 -----CAGGCGGAGCGCGCGCGGCGCACCGCGCGCGCGCGCGCGCGCGCGCGG 3046
Db 2860 CTTGTATCCCAAGGCGGAGCGTTCGCGCAAGACATC---GAGCGCGCGGTACGGGCCCCGT 2916
Qy 3047 GAGCGGAGAGCGGGGAGGAGCGCGCGCGGGGCGGACCGGGGCGCGGACACAA3GCGCAGCCT 3106
Db 2917 GAGACAGAGAACAGTGTGAGGAGCCACACCGCAGGCGCGGTGCAAGAGCATAA3GTGCCACCA 2976
Qy 3107 GCTCACGAGGCTGTGGAGAAGGAGCACCGAGAGAAGGAGGCCAGCGAGAA3GAGGCTGAG 3166
Db 2977 ACATTTGAGCCCCCAGAGAGGAGGTTTGACAGAGAGGAGACACGTGTGTGAAAG----- 3031
Qy 3167 ATAGTGAAGCGCAGAAAGGAGGACTCCGGAACCAACAGCGCGCGCGGAG3CCACACTGT 3226
Db 3032 -----GGGATTAAGMAACTCGAAATCACCAGGCCAAGGAACCTCGCTGT 3075
Qy 3227 GACCTGAGACCACTGGGACTGTGACTGTGGGTCCCATGACACACATGCCCAGGACCTGT 3286
Db 3076 GACCTGAGGCGCAATTTGCGGTTACAGGCGTGGGCTCTCTGCACATGTGTGCCAGCACCTGT 3135
Qy 3287 CTCAGAAAGTGGAGGAACAGCCAGAGGATGCAGACAATCAGCGGGAACGTCATCTCGCATG 3346
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Qy 3347 GGCAGTCAGCCCCCAGACCCGAAACATATTGTATCATATCCAGTGTATGTT3AGCGGCGCT 3406
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Db 3256 CCGGGGAGGCGCACTGTAGTTCCAGTGTAAACAGGACCTGGAAGGCCAAGCGGAGGGC 3315
Qy 3467 AAGAAGAGGTGAAGCGGATGACGTGATGAGAGAGGCGCGCGCGCTATTTGCCATAC 3526
Db 3316 AAGAAGAGGACAGAGGCTGACGATGTGTCGAGAAGAGGCGCGCGCGCTATTTGCCATAC 3375
Qy 3527 AGCTCATGTTCTTTAAGCCCCCAACAGCTGCTCGCGCTTCTGCCATACATCGTG 3586
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Qy 3587 ACCATGAGGTACTTCGAGGTGGTCAATTTCTGCTGCTCATTCGCTTTGAGCAGCATCGCGCCTG 3646
Db 3436 ACCATGCGGTACTTTGAGATGGTATTTCTGTGCTCATCGCTTTGAGCAGCATTTGCCCTG 3495
Qy 3647 GTTGTGAGGAACCGAGTGGGCAAGCTGCCAGGAACAAACGCTCTGAATACCTGGAT 3706
Db 3496 GCTGCTGAGGATCCCGTGGGACCGGACTCATTCGGGAACAAATGCTCTGAATACATGGAC 3555
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RESULT 10

US-09-917-800A-1586

; Sequence 1586, Application US/09917800A

; Patent No. US20020119462A1

; GENERAL INFORMATION:

; APPLICANT: Mendrick, Donna

; APPLICANT: Porter, Mark

; APPLICANT: Johnson, Kory

; APPLICANT: Castle, Arthur

; APPLICANT: Elashoff, Michael

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Molecular Toxicology Modeling

; FILE REFERENCE: 44921-5038-US

; CURRENT APPLICATION NUMBER: US/09/917,800A

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/222,040

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880

; PRIOR FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: US 60/290,029

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: US 60/290,645

; PRIOR FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: US 60/292,336

; PRIOR FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: US 60/295,798

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: US 60/297,457

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/298,884

; PRIOR FILING DATE: 2001-06-19

; PRIOR APPLICATION NUMBER: US 60/303,459

; PRIOR FILING DATE: 2001-07-09

; NUMBER OF SEQ ID NOS: 1740

; SOFTWARE: PatentIn Ver. 2.1

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; LENGTH: 6639

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012918

US-09-917-800A-1586

Query Match 35.0%; Score 2582.6; DB 9; Length 6639;

Best Local Similarity 68.3%; Pred. No. 0;

Matches 3955; Conservative 0; Mismatches 1639; Indels 199; Gaps 19;

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DB	1621	TATGGGCTCGGACACAGCGCTTACTTCCACTCTTCTCTTCACTGCTTTGACTGTGGGGTC	1680
QY	1805	ATCGTGGGAGCGTCTTTGAAATGTGCTGTGGCGGCCATCAAGCCGGAAAGTCCCTTTGGG	1864
DB	1681	ATCATCGGAGCATCTTTGAAGTCATCTGGGCCGTCAACAAACGGGTACATCTTTTGA	1740
QY	1865	ATCAGTGTCTGGGGCCCTCGCGCTGTGAGGATCTTTCAAAGTCACGAAGTACTGAGGC	1924
DB	1741	ATCAGCGTGTTCAGGAGCTCTCAGGTTACTGCGTATTTTCAAAGTACAAAGTACTCGGCA	1800
QY	1925	TCCCTCGGAACTGTGTGGTGTCTCGCTGTAACCTCAATGAAGTCCATCAGCGCTGCTC	1984
DB	1801	TCTCTCAGAAACCTGGTTGTCTCCCTCTCACTCCATGAATCCATCATAGTCTGCTG	1860
QY	1985	TTCTTGCTCTTCTGTTCATTTGTGGTCTTTCGCCCTGTGGGGATGCACTGTTTGGGGGA	2044
DB	1861	TTCTCTCTCTTCTCTTCAATGTGTCTTTGCGCTCTTGGGGATGCACTGTTTGTGGTGC	1920
QY	2045	CAGTTTCAACTTCCAGGATGAGACTCCACACCAACTTCCAGACCTTCCCTGCGGCATC	2104
DB	1921	CAGTTTAAATTTGAGGGGAGCTCTCCCAACCACTTCGACATTTTCAGACATTTTCAGACAGCAATA	1980
QY	2105	CTCACTGTCTTCCAGATCTCGACGGGAGAGGACTTGGAAATGCAAGTATGATACAGGGATC	2164
DB	1981	ATGACTGTGTTTCAGATCCTGACTGGCGAGGATTGGAATGAGGTCAATGATGAGATC	2040
QY	2165	GAATCGGAAGCGCGGTGAGAAAGGCATGTTCTCGTCTCTTTACTTCAATGCTCTGACA	2224
DB	2041	AAGTCTCAGGGGGCGTGCAGGGCGGATGGTGTTCTCCATCTACTTCACTGCTCTCACC	2100
QY	2225	CTGTTTCGAAACTACACTCTCTGTAATGTCTTTCTGGCCATCGCTGTGGACAACCTGGCC	2284
DB	2101	CTCTTCGGAACTACACCTGCTCAACGTGTTCTTAGCTATCGGGTGGACCACTGGCC	2160
QY	2285	AACGCCAAGAGCTGAACAAGATGAAGAGAGATGAAGAAGCAGGCCAATACGAAGCTT	2344
DB	2161	AACGCCAGGAACCTCACCAAGGATGAACAAGAAGAGGAGGAGGCCAATCAGAAAATG	2220
QY	2345	GCTCTGAAAGGCAAAAGAAAGTGGCTGAAGTCAAGCCCACTGTCTGCGGCAACATCTCC	2404
DB	2221	GCTCTACAGAAGCCAGGAGGTGGCAGAAGTGAATGCCCTCTCTGTCTGAGCCAAATGTTC	2280
QY	2405	ATCGCCGCCA-----GGCAGCAAACTCGGCCCAAGCGCGCTCGTGTGGGAGCAGCGG	2458
DB	2281	ATAGCTGTGAAGGAACAGCAAGAAACCAAGAAGGAGGAGGAGGCCAATCAGAAAATG	2340
QY	2459	GCCAGCCAGCTACGGCTGCAGAACTTCGGGGCCAGCTGCAGCGGCTGTATCAGCGAGATG	2518
DB	2341	ACCAAGCAGATGCCAAGCAGAACTCTGCTAGCCGCGAGGCGCTGTACGG-----G	2394
QY	2519	GACCCGAGAGCGGCTGCGCTTCGCCACTACGCGCCACTCGCGGCCGACATGAAGACG	2578

[illegible]

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Qy 3543 TAAACCCCAACCACTGCTCGCGCGCTTCTGCCACTACATCGTGACCATGAGGTACTTCG 3602
Db 3533 TCTCCACCAACCAACCCCTTCCGCGGCTGTGCCATTACATCCTGAACTCTGGCTACTTCG 3592
Qy 3603 AGGTGGTCATCTCGTGGTCATCGCTTGAGCAGCATCGCCCTGGCTGCTGAGGACCCAG 3662
Db 3593 AGATGTGCATCCTCATGGTCATTGCCATGAGTAGCATCGCGCTGGCCGCGAGGACCCGG 3652
Qy 3663 TGGCCACAGACTCGCCCAAGAAACAACGCTCTGAAATACCTGGATTAACATTTTCACTGGTG 3722
Db 3653 TGCAGCCCAACGACCCCGCAACACGTCGTGCCATATTTTGACATATGTTTTCACAGAG 3712
Qy 3723 TCTTTA CTTTGAGATGGTGAATAAGATGATCGACTTGGGACTGCTGCTTCAACCTCGAG 3782
Db 3713 TGTTTACCTTTGAGATGGTGATCAAGATGATCGACCTGGGCTCGTCTGCATCAGGGGG 3772
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Db 3773 CCTATTTCCGGTACCTGTGGAACATTTCTGGACTTCATAGTGGTCAGTGGGCGCCCTGGTGG 3832
Qy 3843 CGTTTGTCTTTCGAGCTTTCGTGGAGGATCCAAAGGGAAGACATCAATACCATCAAGT 3902
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Qy 3903 CTCTGAGAGTCTTTCGTGTCTCGTGGGCCCTCAAGACCATCAAAACGCTGCCCAAGCTCA 3962
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Qy 4023 ACATGCTCTTCAATGTTCAATTTTCCGCTCATTTGCGGTGCAGCTCTTCAAGGGGAAGTTT 4082
Db 4004 ACATGCTCTTCAATGTTCAATCTTCCGCTGGTGGCCGTGCAGCTCTTCAAGGGCAAAATCT 4063
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Db 4064 TCCACTGCACGAGAGTCCAAAGAGTTTGAGAGAGACTGTTCGAGGCAAAATACCTCCTTT 4123
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Db 4184 ACAAGTGTCTGGGCCCTGCTCAGCTCTTTACGGTGTCCACGGAGAGGGCTTGGCCAC 4243
Qy 4263 TGGTGTGAAACACTCCGTGGATGCCACCTATGAGGAGCAGGGTCCAAAGCCCTGGGTACC 4322
Db 4244 AGGTCTCAAGCACTCAGTGGATGCCATTTTGAGAACCCAGGGCCCCAGCCCCGGGTACC 4303
Qy 4323 GCATGGAGCTGTCAATCTTCACTGTGTCTACTTTGTGGTCTTTCCCTTCTTCTTCGTCA 4382
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Qy 4983 TGTTCATCTATACGCAATCATCGGATGATGAGTGTGTGGAAATATTCCTCGAT----- 5038
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Db 5018 AAGATGAGGACAGCGATGAGGATGAGTTCCAAAATCAGGAGCACAATACTTCGGACCT 5077
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Qy 5139 TGTGTCTCTGCTGAGCAACAGGCTGTGATGAGCA-----GGCCAAATGCCACCGAGT 5192
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Db 5198 GTGGCAACGAGTTGCGCTATTTTACCTTGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 5257
Qy 5253 TGTGAACTCTTTGTGGCTGTGATGAGCAAAATTTGAGTACCTCACCGGGAGCTCTT 5312
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Qy 5433 CTCTGGGCTGGGAGAAATGCTGCTCGAGTGTCTTACAAGCGCTGGTTCGATGA 5492
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QY 5673 TGCTGGTACACCCCATTAAGCCTGATGAGATGACAGTGGGAAAGGTTTATGACGCTCTGA 5733
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QY 5733 TGATATTTGACTTCTTACAAGCAGAACAAACCA 5765
Db 5735 TGAATCATGGAGTACTTACCGGCAGAGCAAGGCCA 5767

RESULT 11
US-10-375-253-33
; Sequence 33, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10/375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR FILING DATE: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 7808
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (237)...(7769)
; OTHER INFORMATION: standard name = Alpha-1A-1
US-10-375-253-33

Query Match 34.0%; Score 2507.2; DB 16; Length 7808;
Best Local Similarity 63.8%; Pred. No. 0;
Matches 4457; Conservative 0; Mismatches 2093; Indels 434; Gaps 26;

QY 146 ATGGTCGCTTCGGGGACAGAGTCGGGGCGCGCTATGAGAGCCCGCGGCGGAGAGCGG 205
Db 237 ATGGCCGCTTCGAGACGAGATCGCGGCCGCTACGGGGAGGAGGCTCCGGGGCAGCC 296
QY 206 GCCCGGGCGCGGGCGCGCGGGGGCGCGGGTCCCGGGGGGTGACAGCCCGGC 265
Db 297 GCGGGGGTGTCTGTGGGCGAGCGGAGCGGAGCGGGGGAGCGCGGCGAGCGGCGG 356
QY 266 CAGCGGGTCC-----TCTACAGCAATCGATCGCGCAGGCGCGGACCATGGCG 316
Db 357 CAGCCCGGGCGCAAGAGATGTCAAGCAGTCAATGGCGCAGAGCGCGGACCATGGCA 416
QY 317 CTGTACAACCCCATCCCGGTCAAGCAGAACTGTTTCAACCGTCAACCGCTCTTCTGTC 376
Db 417 CTCTACAACCCCATCCCGGTCCGACAGAACTGCCTCACGGTTTAAACGGGTCTCTTCTC 476

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Db 1557 GATCAGCTGGCTGATATAGCTCTGTGGGTCTCCCTTCGCCCGAGCCAGCATTTAAAGT 1616
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Db 1977 GTGTTACAGCCCTCAGGTTATTCGTTATTTTCAAGTTCACAAAGTACTTGGGCATCTC 2036
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Qy 1991 CTCTTCTGTTCATGTGGTCTTCCGCTGCTGGGATGCACTGTTTGGGGACAGTTC 2050
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Qy 2051 AACTTCAGAGTATGACTCCACAAACAACTTCACACACTTCCCTCGCGCCATCCTCACT 2110
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Qy 2171 CAAGCGGCTCAGAAAGGATGTTCTCGTCTTTTACTTCTATGCTGTGACACTGTC 2230
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Db 2517 TCTATAGCTGTGAAGAGCAACAGAAATCAAAAGCCAGCCAAAGTCGTGTGGAGCAG 2576
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Db 2637 ATGGAACCGGACGAGCGCTGGAAAGGCTGCTTACACGGGGCACTCTGCGGCAGACATGAAG 2696
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Db 2697 ACGCACTTGGACCGCGCTGTGTGTGGACCCCGCAGGAGAACCGCAACAACACCAAC 2756
Qy 2618 GCGCGCGGGGCGCGTGGAGGCAAAAGCCGACCTGAGGCTGCGGAGGCCCGGAGGGC 2677
Db 2757 AAGAGCCGGCGCGCCAGGCCACCGTGGACACAGCGCTCGGCCAGCAGCGCGCGAGGAC 2816
Qy 2678 GTGACCTCCGCGCAGGACCAACCGSCACCGGACCAAGCAAGACAGACCCCGCGGCGGGG 2737
Db 2817 TTCTCAGGAAACAGGCCCGCTACAGATCGGGCCCGGACCCACAGCGCTCGGCGGG- 2875
Qy 2738 GACCAGAACCGAGCAGAGGCCCCGAAAGGCGGAGCGGGAGCCCGTGTCCCGGAGGAG 2797
Db 2876 ---CCTGGACGACGAGGCGCTTGGCGGGAAGCCAGGAGCGCGAGCTGAGCGGAGGG 2932
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QY 3400 GGCCCTCTTTGGGGAAGCCACCGTCTCCAGTGGTAAACGTGGAC-----CTGGA 3450
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Db |||||
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4193 CGACTTCAATGAGTGGTCAAGTGGCGGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 4243
QY 3871 ATCCAAAGGGAAGACATCAATACCATCAAGTCTCTGAGAGTCCCTTCTGCTGGCGCC 3930
Db |||||
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Db |||||
4484 TGAGAAAGATTGTGAGGCAAAATACCTCTCTACGAGAAAGTGAAGTGAAGGCGGAGA 4543
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Db |||||
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Db |||||
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QY 4411 CTTCCAGAGCAGGGGCAAGAGTGTCTGAAATGACGCTGGAGAAAGACAGAGGGC 4470
Db |||||
4784 CTTCCAGAGCAAGGGCAAGATGATGGAGGAATACAGCCTGGAGAAATGAGAGGGC 4843

QY 4471 TTGATTGACTTTCGCATCAGCGCAAAACCCCTGACAGGTACATGCCCAAAACCGSCA 4530
Db |||||
4844 CTGATTGATTTCCGATCAGGCGCAAGCGCTGACCGGACACATGCCGAGAAACAAGCA 4903
QY 4531 GTCCTTCCAGTAAAGACGTGGACATTTGTGGTCTCCCGCCCTTTGAATATTTCAAT 4590
Db |||||
4904 GAGCTTCCAGTACCGCATGTGGCAGTTTCTGGTGTCTCCGCTTTCGAGTACAGGATCAT 4963
QY 4591 GGCCATGATAGCCCTCAACACTGTGGTGTGATGATGAAGTTCTATGATCCACCTATGA 4650
Db |||||
4964 GGCCATGATAGCCCTCAACACCATCGTGTCTTATGATGAAGTTCTATGGGCTTCTGTTC 5023
QY 4651 GTACGAGCTGATGTGAAATGCCCTGAAACATCGTGTTCACATCCATGTTCTCCATGGAATG 4710
Db |||||
5024 TTATGAAATGCCCTGCGGGTGTTCACATCGTCTTCACTCCCTCTTCTCTCTGGAATG 5083
QY 4711 CGTCTGAAAGATCATCGCCCTTTGGGGTGTGAACATTTTTCAGAGATGCCCTGGAAATGCTT 4770
Db |||||
5084 TGTCTGAAAGTCAATGGCTTTTGGGATTTCTGAATTTATTTCCGGGATGCCCTGGAACATCTT 5143
QY 4771 TGACTTTGTCACTGTGTGGGAAGTATTAAGTATTTTATTAACAGAGATTTGGGAAAC 4830
Db |||||
5144 CGACTTTGTGACTGTCTGGGCGACATCCGATATCTCTGCTGACTGAGTTTGGGAATCC 5203
QY 4831 GAAACAATTTTCATCAACCTCAGCTTTCCTCCGCTCTTTTCGAGCTGCGCGCTGATCAAGCT 4890
Db |||||
5204 GAATAACTTTTCATCAACCTGAGCTTTCTCCGCTCTTCCGAGCTGCGCGCTCATCAACT 5263
QY 4891 GCTCCGCGAGGGCTACACCATCCGATCTCTGCTGTGGACCTTTTGTCCAGTCTTCAAGGC 4950
Db |||||
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QY 4951 CTTGCCCTCAGTGTCTGCTCTATTCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5010
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QY 5011 GCAGGTGTTTGGGAATTTGCCCCT-----GGATGATGACAC 5046
Db |||||
5384 GCAGGTGTTTGGTAAACATTTGGCATCGACGTGGAGGACGAGACAGTGAAGATGATG 5443
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Db |||||
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QY 5107 GAGCGCCACCGGAGGAGCGCTGCGACAGAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5166
Db |||||
5504 GAGTGCACCGGGAAGCTTGGCAACAATCATGCTTCTCTGCTCAGCGGGAACCGGTG 5563
QY 5167 TGATGAGCAGGC-----CAATGCCACCGAGTGTGGAAGTGAATTTTGGCTTCTTCTTCTTCT 5220
Db |||||
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QY 5221 CGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 5280
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QY 5281 GGACAAATTTTGAATGACTCAACCGGAGCTTCTTCCATCTTAGGTCTTCAACACTTGGATGA 5340
Db |||||
5684 GGACAACTTTGATGACTCAACCGAGACTTCTTCCATCTTGGGCCCCCAACACTGGATGA 5743
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Qy 5761 AACCAACAGACACGATGACGACGAGGCTCTGGAGGCTCTCCAGATGGTCTCTGTGTC 5820
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Qy 5821 CTTGTTCCACCTCTGAAGGCCACCTGGAGCAGACAGCCGGCTGTCTCCGAGGAGC 5880
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Db 6548 AGAGAACAGAGGAGAGGGGCGCGCAGCTGGGAATAACCTCAGTACCATCTCAGACAC 6607
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Db 6788 GACAGACCTGAGCATATGACCCCAATCCGGGGACCTGCGGTGGAAGAGGCGGACAGGA 6847
Qy 6442 TACAGGCTCCGCGGGAACAGAGAGCGCGCAGAGCGGGCGCGGTCCACAGAGCGGAG 6501
Db 6848 GCGGGCGGGCCAAAGATCGGAAGCATCGACAGCAACACACCAACCAACACCA 6907
Qy 6502 GCAGCCCTCATCTCTCTCGAGAAAGACGCGTCTTACTCTCTGCGACCGCTTTGGGGG 6561
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Qy 6562 CCGTGAGCCCCCGGACCAAGCCCTCTCCTCAGAGCCACCCAAAGCTGTCCGCAACAGCTGG 6621

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Qy 6622 CCAGGAGCCGGGACCCCAACACAGGCGAGTGGTTCGTAATGGGAGCCCTTGTGTC 6681
Db 7010 CCAGAGACATGGCGCACCGCAGGCGAGTTCGTAAGTGAAGCCAGGCCCTC 7069
Qy 6682 AACATCTGTGTAGACACCCCGCGCTGGCGGAGGAGCTCCCCACAGAGCCCTC 6741
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Db 7127 CACCCCGGCCACACGTGTCTTA 7150

RESULT 12
US-10-375-253-35
; Sequence 35, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10/375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 7791
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (237)...(7037)
; OTHER INFORMATION: standard name = Alpha-1A-2
US-10-375-253-35

Query Match 33.9%; Score 2502.2; DB 16; Length 7791;
Best Local Similarity 63.8%; Pred. No. 0;
Matches 4443; Conservative 0; Mismatches 2123; Indels 397; Gaps 27;
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Db 237 ATGCGCCGCTTCGGAGACAGATGCCGCGCTACGGGGAGAGAGCTCCGGGCGAGCC 296
Qy 206 GCCCGGGCGCGCGGGCCGCGCGGGGGGGGGCCCGGGTCCCGGGGGGCTGCGAGCCCGGC 265
Db 297 GCCGGGGTGTCTGTGGCAGCGAGGCGGCGGAGGAGCGGGGGCGAGCCGCGAGGGCGG 356
Qy 266 CAGGGGGTCC-----TCTACAGCAATCGATCGCGCAGCGCGCGGACCATGGCG 316

Db 357 CAGCCCGGGCGCAAGAGTGTACAAAGTCAATGGCGCAGAGAGCGCGACCATGGCA 416
QY 317 CTGTACAAACCCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAACCGCTCGCTCTTCGTC 376
Db 417 CTCTACAAACCCCATCCCGGTGCGACAGAACTGCTTCAACCGTCAACCGCTCGCTCTTCGTC 476
QY 377 TTCCAGCGAGGACAAACGTCGTTCGCAAAATACGGGAAGCGCATCACCGAGTGGGCTCCATTC 436
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QY 437 GAGTATATATCTTGGCCACCATCATCGCCAACTGCAATCGTGTGCGCCCTGAGCAGAAC 496
Db 537 GAATATATATATTTAGCCACCATCATAGCGAAATGTCATCGTCTCGCATGAGCAGCAT 596
QY 497 CTCCTCGATGGGACAAAACGCCATGTCGAGCGGCTGGAGACACGAGCGCCATTTTC 556
Db 597 CTGCTGATGATGACAAAGACCCGATGCTGAACGCGCTGGATGACACAGAACCATACTTC 656
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QY 617 AAGGGCTCTTACCTGGGGAACGGCTGGAAAGTCAATGAGTCTCGTGGTGCCTCAACGGG 676
Db 717 AAGGGCTCTTACCTGGGGAATGGCTGGAATGTCATGGAATTTGTGTGTGTCTAAACGGGC 776
QY 677 ATCCTTGGCACCGCTGGAATGACTTTGCACTGCGGAACACTGAGGCGTGTGCTGTGCTG 736
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QY 737 AGGCCCTCTGAAGCTGGTGTCTGGGATTCAGTTTTCAGAGTGGTGTCTCAAGTCCATCATG 796
Db 837 CGGCCGCTCAAGCTGGTGTCTGGAATCCCAAGTTTACAAGTGGTCTCTGAAGTCGATCATG 896
QY 797 AAGGCCATGGTTCACCTCTCGAGATGGGCTGCTTCTCTTCTTGGCATCTCATGTTT 856
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QY 857 GCATCATTTGGCTGGAGTTCTACATGGCAAGTTTCCAAAGGCTGTTTCCCAACAGC 916
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QY 917 ACAGATG---CGAGCCCGTGGTGAATTCCTCTGTGGCAAGGAGGCCCAAGCCCGGCTG 973
Db 1017 ACAGATGACATTCAGGCTGAGTCTCCGGCTCATGTGGGACAGAAAGAGCCCGCGCAC 1076
QY 974 TCGAGGCGGACACTGAGTCCGAGTACTGGCCAGGACCACTTTGGCATCACCAAC 1033
Db 1077 TGCCCAATGGGACCAAAATGTGAGCCCTACTGGGAAGGGGCCCAACACGGGATCACTCAG 1136
QY 1034 TTTGACAAATATCTGTTTGGCATCTTGACGGTGTTCAGTGTGATCACCATGGAGGGCTGG 1093
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QY 1154 ATCCCTCTCATCATCATCGGCTCTTCTTCTCATGCTCAACCTGCTGGGCTGCTCTCG 1213
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QY 1214 GGGGAGTTTGGCAAGGAGGAGAGGTTGGAGAACCGCGGCTTCTTCAAGCTGCGC 1273
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QY 1274 CGGAGCAGCAGATCGAGCAGAGCTCAACGGGTACTTGGAGTGGATCTTCAAGCGGAG 1333
Db 1377 CGGCAACACAGATTTGAACGTGAGTCAATGGGTACATGGAATGGATCTCAAAAGCAGAA 1436
QY 1334 GAAATGATGCTGGCGAGGAGCAGAGGAATGACAGAGGAGAGTCCCTTTTGA---CGTG 1390
Db 1437 GAGGTGATCTTCGCCCGAGGATGAATCTGACGGGAGCAGAGGCAATCCCTTTTGGAGCT 1496

QY 1391 CTGAAGAGAGCGGCGCAACCAAGAGAGCAGAAATGACCTGATCCACGAGGAGGGAGAG 1450
Db 1497 CTGCGAGAACCAACATAAAGAAAGCAAGACAGATTGTCTCAACCCGAGAGGCTGAG 1556
QY 1451 GACCGGTTTGAGATCTCTGTGCTGTTGGATCCCCCTTCGCCCGCGCAGCCTCAAGAGC 1510
Db 1557 GATCAGCTGGCTGATATAGCCTCTGTGGGTTCTCCCTTCGCCCGAGCAGCATTTAAAGT 1616
QY 1511 GGGAGACAGAGAGCTCGTCATCTTCCGGAAGAGAGAGATGTTTCCGGTTTTTTATC 1570
Db 1617 GCCAAGCTGGAGAACTCGACCTTTTTCACAAAAGAGAGAGGAGATGCGTTTCTACATC 1676
QY 1571 CGGCGCATGTTGAAGGCTCAGAGCTTCTAGTGGTGTGTGTCGCTGTTGGCCCTGAAC 1630
Db 1677 CGGCGCATGTTCAAACTCTAGGCTTCTACTGGAATGTTTCTAGTGTGGTAGCTCTCAAC 1736
QY 1631 ACATGCTGTGGCCATGCTGTCATTAACAACGAGCGCGCGGCTTACCAC3ACCCCTGAT 1690
Db 1737 ACGCTGTGTGTGCTATTGTTTCACTACAAACGAGCGAGTGGCTCTCCGACTTCTTTAC 1796
QY 1691 TTTTCAGAGTTTGTCTTCTGGGCTCTTCTCTCACAGAGATGTCCTTGAA3ATGATGGC 1750
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QY 1751 CTGGGCGCCAGAAAGTACTTTCGGTCTCTTCAACTGCTTCGACTTTGG3GTGATCGTG 1810
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QY 1811 GGGAGCCTCTTTGAAGTGTCTGGGGCCCATCAAGCGGGAAGCTCTTTTGGGATCAGT 1870
Db 1917 GGGAGCATCTTCGAGGTCTCTGGGCTGTCTATAAAACCTGGCACATCTTTTGAATCAGC 1976
QY 1871 GTGCTCGGCGCCCTCGGCTGTGAGATCTTCAAAGTCAAGAGTACTG3AGCTCCCTG 1930
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QY 1931 CGGAACCTGTGTGTCTCTGCTGAACTCCATCAAGTCCATCATCAGCCT3CTTCTTCTG 1990
Db 2037 AGAAACCTGTGTCTCTCTCTCACTCCATGAGTCCATCATCAGCCTT3TGTCTCTC 2096
QY 1991 CTCTTCTGTTCATTTGTGCTTTCGCCCTCTCGGGATGAGCTGTTTGG3GACAGTTC 2050
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QY 2051 AACTTCAGATGAGACTCCCAACAACACTTCGACACCTTCCCTGCGGCTATCTCTCACT 2110
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QY 2111 GTCTTCCAGATCCTGAGCGGAGAGGACTGGAATGCAAGTGTATGATCAAGG3ATCGAATCG 2170
Db 2217 GTGTTTCAGATCCTGAGCGGCGAAGACTGGAACGAGGTCTATGTAAGCG3ATCAAGTCT 2276
QY 2171 CAAGCGGCTCAGCAAAAGGATGTTTCTCGTCTCTTTTACTTCAATGTCCT3ACATGTTT 2230
Db 2277 CAGGGGCGGTGCGAGGCGGCTATGTTTCTCCATCTATTTTCAATGTTACT3ACGCTCTTT 2336
QY 2231 GGAACATCACTCTGCTGATGTTTCTTGGCCATCGCTGTGACAACTT3GCAAGGCC 2290
Db 2337 GGAACATCACTCTGCTGATGTTTCTTGGCCATCGCTGTGACAACTT3GCAAGGCC 2396
QY 2291 CAAGAGCTGACCAA-----GGATGAAGAGAGATGGAAGAGCAGCAATCAGAAAG 2341
Db 2397 CAGGAGCTCACCAGGTGGAGGCGGAGCAGCAGAGAGAGAGAGAGAGCAGCAGCAAGAA 2456
QY 2342 CTGTGCTGCAAAAGGCCAAAGAGTGGCTGAAAGTCAAGCCCATGTCCTGCGAATCATC 2401
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QY 2402 TCCATCGCGCCA-----GGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTTGGGAGCAG 2455
Db 2517 TCTATAGCTGTGAAGAGCAACAGAAAGATCAAAAGCCAGCCAGTCCGTTTGGGAGCAG 2576

QY	2456	CGGGCCAGCAGCTACGGCTCGAGAACTCTGGGCGCAGCTCGGAGGCGCTGTATTACGCGAG	2515
Db	2577	CGGACCACTGAGATCGCAAGACGAACTTGTCTGGCCACCGCGGAGGCGCTGTATTAAACGAA	2636
QY	2516	ATGACACCCGAGGAGCGCTCGCTTTCGCCACTACGCGCCACCTGCGGCGCCGACATCAAG	2575
Db	2637	ATGACACCCGAGAGCGCTGTGAAGCTGCTTACACGCGCACCTTCGCGCCAGCATGAAG	2696
QY	2576	ACGCACCTTGGACCGGCGCTGTGTGGAGCTG-----GGCGCGGCAC	2617
Db	2697	ACGCACCTTGGACCGGCGCTGTGTGTGACCCGAGGAGAACCGCAACACCAACACCAAC	2756
QY	2618	GGCGGCGGGGGCGCTGTGGAGGCAAGACCCGACCTGAGGTGTCGGAGGCCCCCGAGGGC	2677
Db	2757	AAGAGCCGGGCGGCGAGCCACCGTGTGACACAGCGCTTCGCGCCAGCAGCGCGCCGAGGAC	2816
QY	2678	GTCGACCTTCGCGCAGGCACACCGGACCCGACCAAGGACAAGACACCCCGCGGCGGGG	2737
Db	2817	TTCTCTCAGAAACAGGCCCGCTACACGATCGGGCCCGGAGCCCGCGGCTCGGCGGG-	2875
QY	2738	GACCAGGACCGAGCAGAGGCGCCGGAAGCGGAGAGCGGGAGCCCGGTGCCCGGAGGAG	2797
Db	2876	---CCTGACGCACGGAGCCCTTGGCGGGAAGCCAGGAGCCGAGCTGAGCCGGAGGG	2932
QY	2798	CGGCGCGGCGCG-----ACCGCAGCCACAGCAAGAGAGCGCGCGGGCC	2841
Db	2933	ACCTTACGGCGCGAGTCGGACCAACACCGCCCGGAGGGCGAGCTTGAGCAACCCCGGTT	2992
QY	2842	CCCGGAGCGCGAGCGAGCGCGGCCGAGGCCCGACG-----	2881
Db	2993	CTGGAGGCGAGGCGGAGCGAGGCAAGCGCGGGACCCCGACCGGAGGCACGTGCAACG	3052
QY	2882	-GAGGGCGCGCGGGCACCAACCGCGCGGCTCCCGGAGGAGCGCGCCGAGCGGGAGCC	2940
Db	3053	GCAGGGGGCAGCAGGAGAGCCGACGCGGTTCCTCCGCGCACGGCGCGGACGCGGAGCA	3112
QY	2941	CCGACGCCACCGCGCGCACCG-----	2961
Db	3113	TCGACGTATCGCGCGCACCCGACGCGCCCGGGGAGAGGGTCCGAGGACAAGCGCGAGCG	3172
QY	2962	-----GCAACGAGATCCGAGCAGGAGTCCGAGGACAAGCGCGAGCG	2988
Db	3173	GAGGGCGCGGCACCGCGAGGCGACGCGGCGCGGCCCGGCGGCGGAGGCGCGGCGGAGGG	3232
QY	2989	CGGCGCCAAGCGCGAGCGCGCGCGCACCGCGGCGGCCCGCGAGCGGGCGCCCGGGA	3048
Db	3233	CCCCGACGGGCGGAGCGCAGAGAGGACCGGCATCGGCTTCCAGCCACTGACGAGGG	3292
QY	3049	GGCGGAGACGGGAGGAGCGCGCGCGCGC-----	3080
Db	3293	GGACGCGGAGGGAGGACAAGGAGCGGAGGCATCGGAGGAGGAAAGAGAACACGAGGCTC	3352
QY	3081	-----ACCGGGC	3087
Db	3353	CGGGTCCCTGTCTGGGCCCCCAACTGTCTCAACCAACCGGCGCAATCCAGCAGGACCTGGG	3412
QY	3088	CCGCGCACAGCGCAGCTGTCTCAGAGGCTGTGGAGAGGAGACCAACGAGGAGGAGGC	3147
Db	3413	CGCCAGAGCCACCCCTTGGCAGAGGATTTGAACAATGAAGAACCAACAGCTGTGGCCAC	3472
QY	3148	CACGGAGAGGAGGCTGAGATAGTGAAGCCGACAAGGAAAGAGGCTCCGGAAACCAACA	3207
Db	3473	CGCGAGTTCGCGCTCTCCACGCGAGCGCTTGGCCACGCGGCGCTGCCACAGAGCCCGAGC	3532
QY	3208	GCCCGGAGGCCACTGTGACTTGGAGACGAGTGGGACTGTGACTGTGGGTGCCATGCA	3267
Db	3533	CAAGATGGGAAACAGCACCGACCCCGGCCCAATGCTGGCCATCCTCTGCCATGGCCACCAA	3592
QY	3268	CACACTGCCAGCACCTGTCTCTCAGAGGTTGGAGGACAG-----	3307
Db	3593	CCCCAGAACCCGCGACGCGCCCGGACGCCCAACCAACCCGGGGAAACCCATCCTCAATCCCGG	3652
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[illegible]

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Db 4784 CTTTCCAGGACCAAGGGACAGATGATGAGGATACAGCCTGGAGAAATGAGAGGC 4843
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Db 4964 GGCCATGATCGCCCTCAACACCATCGTGCTTATGATGAAGTTCTATGGGCTTCTGTTC 5023
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Db 5204 GAATAACTTCATCAACTCAGCTTCTCGCCTCTTCCGAGCTGCCGCTCATCAAACT 5263
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Db 5264 TCTCGTCAGGGTTACACCATCCGATCTTCTGGAACCTTTTGGCAGTCTTCAAGGC 5323
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Db 5384 GCAGGTGTTGGTATACATGGCATCGACGTGGAGGACGAGTGAATGAGATT 5443
Qy 5047 CAGCATCAACCCCAACAACTTCCGGACGTTTTCGAAGCCTGATGCTGCTGTTGAC 5106
Db 5444 CCAATCACTGAGCAATNACTTCGGACCTTCTTCCAGCCCTCATGCTTCTTCCG 5503
Qy 5107 GAGCCGACGGGGAGGCTGACAGATCATGCTGCTTCCCTGAGCAACCGAGCCTG 5166
Db 5504 GAGTGCCACCGGGAGCTTGGCAACATCATGCTTCTTCCCTCAGCGGGAACCGTG 5563
Qy 5167 TGATCAGAGGC-----CAATGCCACCGAGTGTGGAAGTACTTTGCTACTTCTACTT 5220
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Qy 5221 CGTCTCTTCATCTTCTGTGTCTCTTCTGATGTTGAACCTCTTTGTGGCTGTGATCAT 5280
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Qy 5761 AACACACAGACACAGATGACAGAGGCTCTCTGAGGCTCTCCACAGATGCTCTGTGT 5820
Db 6161 GGCCA-----AGAAAGCTGCAGGCCATGCGCGAGGAGCAGGACCGACACC 6205
Qy 5821 CCTGTTCCACCTCTGAAGGCCACCCCTGGAGCAGACACAGCCGCTGTGCTCCGAGGAGC 5880
Db 6206 CCTCATGTTCAAGGCATGAGGCCCTCCCTCCCAAGCAG-----GAAGG 6250
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Db 6786 GGGACAGACTTGAGCATGACCAACCCAAATCCGGGGACCTGCGCTCGAAGGAGGGGACCA 6845
Qy 6476 GAGCGGGGCGGTCCCGAGGCGGAGGAGCCCTCATCTCTCTCTCTCGAGAGAGCAGCGC 6535
Db 6846 GAGCGGGGCGGCCCAAGGATCGGAAGCATTCAGACGACCAACCAACCAACCAACCAAC 6905

QY 1631 A C A C T G T G T G G C C A T G T G C A T T A C A A C C A G C C G C G G C C T T A C C A G A C C C T G T A T 1690
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QY 1691 T T T G C A G A G T T T G T T T T C C T G G T C T C T T C C A C A G A G A T G T C C C T G A A G A T G A T G C 1750
Db 1778 T A T G C A G A A T C A T T T T C T T A G A C T C T T T A T G T C C G A A T G T T T A A A A A T G T A C C G G 1837
QY 1751 C T G G G C C C A G A A G C T A C T C C G G T C C T C T T C A A C T G C T T C G A C T T T G G G G T C A T C G T 1810
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QY 1811 G G A G C G T T T G A A G T G T C T G G G G C C A T C A A G C C G G A A G C T C C T T T G G A T C A G T 1870
Db 1898 G G G A G C A T C T T C G A G T C A T C T G G C T G T C A T A A A A C C T G G C A C A C T C T T T G G A A T C A G C 1957
QY 1871 G T G C T C G G G C C C T C G C C T G T G A G A T C T T C A A G T C A G A A T C A G A A T C T G A G C T C C C T G 1930
Db 1958 G T G T A C G A G C C C T C A G G T A T T G C G T A T T T C A A G T C A A A G T A C A A A G T A C T G G G C A T C T C 2017
QY 1931 C G G A A C C T G T G T G T C C C T G T G A A C C A T G A A G T C C A T C A G C C T G C T C T T C T T G 1990
Db 2018 A G A A C C T G T G T C T C T C T C A C T C A A T C C A T G A A G T C C A T C A G C C T G T T G T T C T C 2077
QY 1991 C T C T C T G T T C A T T G T G T C T T C G C C T G T G G G A T G C A G C T G T T T G G G G A C A G T T C 2050
Db 2078 C T T T T C C T G T C A T T G T C T T C G C C T T T T G G A A T G C A A C T C T T C G G G G C C A G T T 2137
QY 2051 A A C T T C C A G A T G A G A C C C A C A C C A A C T T C G A C A C T T C C C T G C C G C C A C T C T A C T 2110
Db 2138 A A T T T C G A T G A A G G A C T C C T C C C A C C A A C T T T C G A T A C T T T T C A G C A G C A A T A A T A G C 2197
QY 2111 G T C T T C C A G A T C C T G A C G G G A G A G A C T G A A T G C A G T G A T G A T C A C G G G A T C G A A T C G 2170
Db 2198 G T G T T T C A G A T C C T G A C G G G A G A C T G G A C A G G T C A T G A C A C G G A T C A A G T C T 2257
QY 2171 C A A G G G G C T C A G A A A G G A T G T C G T C C T T T T A C T A T T G T C C T G A C A C T G T T C 2230
Db 2258 C A G G G G G C T G C A G G G G C C A T G T G T T C C A T C T A T T T C A T T G T A C T G A C G C T C T T 2317
QY 2231 G G A A A C T A C A C T C T G A A T G T C T T T T T G G C A T C G T G G A C A C C T G G C C A A C C T G C C A A C G C C 2290
Db 2318 G G G A A C T A C A C C C T C T G A A T G T T T T T G G C A T C G T G G A C A A T C T G G C C A A C G C C 2377
QY 2291 C A A G A G C T G A C A A G A T G A A G A G A T G A A G A A G A G C A G C C A A T C A A A G C T G C T C T G 2350
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QY 2351 C A A A G G C A A A A G T G G T G A G T C A G C C C A T G T C T G C G C G A A C A T C T C A T C G C C 2410
Db 2438 C A G A A G C C A A G A G G T G G C A A G T A G T C T C T G T C C G G G C C A A C A T G T C T A T A G C T 2497
QY 2411 G C C A - - - - G G C A C A G A C T C G C C A A G C G C C T G T G T G G A G C A G G G C C A G C 2464
Db 2498 G T G A A G A G C A A C A A A G A A T C A A A G C C A G C C A A G T C C G T G T G G A G C A G C G A C C A G T 2557
QY 2465 C A G C T A C G G C T G C A A A C C T G G G G C C A G C T G C A G G G C T G T A C A G C A G A T G A C C C C 2524
Db 2558 G A G A T G C G A A A G C A A C T T G T G C C A G C C G G A G G C C C T G T A T A C G A A T G A C C G 2617
QY 2525 G A G A G C G C T G C G T T T G C C A C T A G C G C C A C T G C G G C C G A C A T G A A G A C G A C C T G 2584
Db 2618 G A C A G C C T G A A G G C T G C C T A C A C G C G C A C C T G C G G C C A G A C A T A A G A C G A C T T G 2677
QY 2585 G A C G G C C G C T G T G T G T G A G T G - - - - - G C C G C G A C G G C G C G G 2626
Db 2678 G A C C G C C G C T G T G T G T G A C C C G A G A G A C C G C A C A C A C C A C A A G A G C C G G 2737
QY 2627 G G G C C C T G G A G G C A A A G C C G A C C T G A G G T G C G A G G C C C C G A G G G C T G A C C C T 2686
Db 2738 G C G G C G A G C C C A C C G T G G A C C A G C C C T C G C C A G C A G C G C G C G A G A C T T C T C A G G 2797
QY 2687 C C G C A G C A C C C C G C A C C G C A C A A G A C A A G A C C C C G C G G G G G A C C A G A C 2746

Db 2798 A A A C A G C C C G C T A C C A C G A T C G G G C C C G G A C C C C A G C G C T C G G C G G - - - - - C C T G G A 2853
QY 2747 C G A C A G A G G C C C G A A G G C G A G A G C C G G A G C C C G T G C C C G G A G G A G C G C C G C G G 2806
Db 2854 C G A C G A G G C C C T T G G G G G A G C C A G A G C C C A G C T G A G C C G G A G A C C C T A C G G 2913
QY 2807 C C G C - - - - - A C C G A C C A C A G A A G A G C C C G G G C C C C G A G C C 2850
Db 2914 C C G G A G T C G A C C A C A C A G C C C G G A G G C A G C C T G G A G C A A C C C G G T T C T G G A G G G 2973
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QY 2890 C C G C G C A C C A C C C G C G C G C T C C C G A G A G C C G C G A G C C C G A G C C C C A C C A 2949
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QY 2950 C C G C G C A C C G - - - - - C C G C C C A C C G - - - - - 2961
Db 3094 T C G C G C A C C G A G G C C C G G G A G A G G T C C G A G A G A C A A G C G A G C G A G G G C G C G 3153
QY 2962 - - - - - G C A C A G A T C C G A G A A G A G A C C A G G G T C C G G G C C A A 2997
Db 3154 G C A C C G A G G C A G C C G C C C G G G C G C G A G G C C A G G C C C C A G C G 3213
QY 2998 G G G C A G C C G C G C G C A C C G C G C C C C C A G C G G G C C C G G A G C G A G A G 3057
Db 3214 G G G C A G C C A G A A G A G C A C C G C A T G C G C T C C A G C C A C G T A C A G A G G G A G C G C G 3273
QY 3058 C G G A G A G C C G C G C G C G C - - - - - 3080
Db 3274 G A G G A G A C A A G A G C G A G G C A T C G A G A G A A A G A A C C A G G G T C C G G G T C C C 3333
QY 3081 - - - - - A C C G G C C G G C A C A 3096
Db 3334 T G T G T C G G G C C C A A C C T G T C A A C C C C G C C A A T C C A G A G A C C T G G C C G C C A A G A 3393
QY 3097 G G C C A C C T G C T C A C A G G C T G T G A G A A G A G A C C A C G A G A A G A G C C A C G A G A A 3156
Db 3394 C C A C C C T G C A G A G A T A T T A C A C A T G A A G A C A C A A G T G C C A C C G G A G T C 3453
QY 3157 G A G G C T G A G A T G T G A A C C G A C A A G A A A A G A G C T C C G A A C C A C C A G C C C G G A 3216
Db 3454 G C C G C T C C C A C G C A G C C T T G C C A C G C G G C T C C C C A G A G C C C A G C A A G A T G G G 3513
QY 3217 G C C A C T G T G A C C T G A G A C C A G T G G A C T G A C T G T G G T C C C A T G C A C A C A C T G C C 3276
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Db 3634 G A C C C C G A A T A G C C T T A T C G T C A C C A A C C C A G C C C A C C C A G A C C C A A T T C A G C T A A 3693
QY 3351 G T C A G C C C C A G A C C C G A - - A C A C T A T T G A C A T A T C C C A G T A T G T G A G C G G C C C T C T 3408
Db 3694 G A C T G C A G A A A C C C G A C C A C C A C A G T G G A C A T C C C C C A G C C T G C C A C C C C C C T 3753
QY 3409 T G G G A A G C C A C C G T C G T T C C A G T G G T A A C T G G A C - - - - - C T G A A A G C C A A G C 3459
Db 3754 C A A C C A C C G T C G T A C A G T G A C A A A A C C C A C C C A G A C C C A C T G C C A A A A A A G A 3813
QY 3460 A G A G G A A A G A G A G T G G A A C G G A T G A T G A G A G A G C G C C C C G G C C T A T C G T 3519
Db 3814 G G A A G A A A G A G A G A G A G A A C A C A C C C G T G G G A A G A G C C C T A A G C A A T G C C 3873
QY 3520 C C C A T A C A G C T C C A T G T T C T G T T A A G C C C A C C A C C T G C T C C G C G C T T C G C C A C T A 3579

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Qy 4000 TGTCTCAACATCTGATTGTTCTACATGCTCTTCATGTTTCAATTTGCGGCTCATTTGCGGT 4059
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Qy 5410 GATGCTGAAACACATGTCCCGGCTCTGGGGCTGGGGAGAGAAATGCCCTCTCGAGTTGC 5469
Db 5779 TTTATTACGAGTAATATCTCCCTCTCGGCTTTAGCAAGAAATGCTCTCATAGGGTTGC 5838
Qy 5470 TTAAGAGCGCTGTTTCGATGAACATGCCCATCTCCAACGAGGACATGATGTTCACTT 5529
Db 5839 TTCCAGGGCTTCTGGGATGAGCTTGCCTGCTGC-----AGATGACACACCGTCCACTT 5895
Qy 5530 CAGCTCCAGCTGATGGCCCTCATCCGAGCGGCACTGGAGATCAAGTGGCCCCAGCTGG 5889
Db 5896 CAATTCCACCTCATGGCTCTGATCGGCAAGCCCTGGACATCAAGATTGCCAAGGGAGG 5955
Qy 5590 GACAAAGCAGCATCAGTGTGACGGAGTTGAGGAGGAGATTTCCGTTGTGTGGGCCAA 5649
Db 5956 AGCCGCAAAACACAGCATGAGCGCTGAGCTGGCGAAGGAGATGATGGCGATTTGGGCCAA 6015
Qy 5650 TCTGCCCCAGAACACTTTTGGACTTGTGGTGTACCAACCCCAATAAGCCTGATGAGATGACGT 5709
Db 6016 TCTGTCCAGAGACGCTAGACCTGTGTGTCAACCTTCAACAGTCCACGACCTCACCGT 6075

Db 925 GGTCTCAGTGGGCATCTCTGGCCACTGCAGGAAACCACTTCAATACTCACGTGACCTGAG 984
Qy 712 AACACTGAGGGCTGTGCGTGTGCTGAGCGCCCTGGAAGCTGTGTCTGGGATTTCCAAAGTTT 771
Db 985 GACCTCCGGGCTGTGCGTGTGCTGCGGCCCTTTGAAGCTGCTGTCAGGATACCTAGCCT 1044
Qy 772 GCAGTGGTCTCAAGTCCATCATGAAGGCGATGGTTCCACTCTCTGCAGATTTGGGCTGCT 831
Db 1045 GCAGATTTGTGAAGTCCATCATGAAGGCGATGGTTACCTCTTCTGCGAGATTTGGCTTTCT 1104
Qy 832 TCTCTCTTTGGCCATCTCTGATTTGCAATCATTTTGGCTGCGAGTTCTACATGSGCAAGTT 891
Db 1105 GCTCTCTTTGGCCATCTCTGATTTTGTATCATTTGGTTTGAAGTTTCTACAGTGGCAAGTT 1164
Qy 892 CCAGAAGCCTGTTTCCCAACACGACAGATGCGGAGCCGCTGGGTGACTTCCCTCTGTGG 951
Db 1165 ACATCGAGCATGCTTTCATGAACAAATTCAGGTATTTCTAGAAGATTTTGACCCCTCC 1218
Qy 952 CAAGGAGGCCAGCCCGCTGTGCGAGGGGACACTGAGTGC CGGGAGTACTGGCCAGG 1011
Db 1219 ---TCACCCCATGTGTGCGAGGCTGCCAGCTGGTTATGAATGCAAGGACTGGATCGG 1275
Qy 1012 ACCCAACTTTGGCATACCAACTTTGACAATATCTCTGTTTGCCATCTTGACGGTGTTCCTCA 1071
Db 1276 CCCCAATGATGGGATCACCCAGTTTGAATACATCTTTTGTGCTGCTGACTGTCTTCCA 1335
Qy 1072 GTGCATCACCATGAGGGCTGGACTGACATCTCTATAATAACAACGATGCGGCCGCA 1131
Db 1336 GTGCATCACCATGGAAGGTGGACCACTGTCTGTACAAATACCAATGATGCTTAGGAGC 1395
Qy 1132 CACTGGAACTGGCTTACTTATCTTATCTCATCATCATCGCTCTTCTTCAATGCTCAA 1191
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Qy 1192 CCTGGTCTGGGCTGTCTCGGGGAGTTTGCAAGGAGCGAGAGGTGGAGAACCG 1251
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Qy 1252 CCGCGCTTCTGAACTGCGCCGCGACGACGATCGAGCGAGAGCTCAACGGGTACCT 1311
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Qy 1372 GAAGTCCCTTTGCACTGTGAAGAGCGGCGCCACCAAGAGAGCAGAATGACCTGAT 1431
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Qy 1432 CCACGACAGAGGAGGAGGAGGACCGGTTTGCAGATCTCTGTGCTGTGGATCCCGCTTCGC 1491
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Qy 1492 CCGCGCCAGCTTCAAGACGCGGAAGAAGAGAGTCTGTCAATCTTCCGAGGAGAGGAGAA 1551
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Qy 1552 GATGTTCCGGTTTTTATCCGGCCATGTTGMAAGGCTCAGAGCTTCTACTGGGTGTGCT 1611
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Qy 1612 GTGCGTGGTGGCCCTGAACACACTGTGTGTGGCCATGGTGCATTACAAACAGCGCGCGG 1671
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Qy 1672 GCTTACCAACGCTGTATTTTGCAGATTTGTTTTCTCTGGTCTCTTCTTCAAGAGAT 1731
Db 1933 GCTCACCAACCTCTCTACTATGACGAATTTCTGTTTCTGGGACTCTTCTCTTTGGAGAT 1992
Qy 1732 GTCCCTGAAGATGATGGCTGGGGCCAGAGTACTTCCGCTCTCTTCACTGCTT 1791
Db 1993 GTCCCTGAAGATGATGGCATGGGGCCCTCGCCTTTATTTTTCATCTTCAATTCACCTGCTT 2052

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Qy 1852 AAGCTCTTTTGGGATCAGTGTGCTGCGGGCCCTCCGCTGCTGAGGATCTTTCAAAGTCA 1911
Db 2113 TAGCTCTTTTGGAAATCAGTGTCTTGGAGCCCTCCGCTTCTAAGAAATATTTAAATAAC 2172
Qy 1912 GAAGTACTGAGCTCCCTCGGAACTGTGTGTGCTCCCTGCTGAACTCCATGAAGTCCAT 1971
Db 2173 CAAGTATTTGGCTTCTCTACGGAAATTTGGTGTCTCTCTGATGAGCTCAATGAATCTAT 2232
Qy 1972 CATCAGCTGCTCTTCTGCT 2031
Db 2233 CATCAGTTTGTCTTCT 2292
Qy 2032 GCTGTTTGGGGACAGTCAACTTCCAGGATGAGCTCCACACAACCAACTTCCACACCTT 2091
Db 2293 GTTATTTGGAGGAGGTTTAACTTTAATGATGGGACTCTTTCGGCAAAATTTTGATACCTT 2352
Qy 2092 CCCTGCGCCATCTCTCACTGTCTTCCAGATCTCTGACGGGAGGAGACTTGAATGCACTGAT 2151
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Qy 2152 GTATCAAGGATCGAATCGCAAGCGCGCTCAGCAAGGATGTTCTGCTCTTTTACTTT 2211
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Qy 2212 CATGTCTGTGACTGTTTGGAACTTACACTCTGCTGTAATGTCTTTTGGCCATCTCTGT 2271
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Qy 2392 CGGACATCTCATCGCCGCGCAGCAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGGA 2451
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Qy 2692 CAGGCAACCAACCGGCAACCGGCAAGGAAGAACCCCGCGGGGGGGGAACAGACCGAGC 2751
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Qy 2812 CCGCAGCCACAGCAAGAGGCGCGCGGGCCCGGAGGCGCGGAGCGAGCGCGCGCGAGG 2871
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3175 CTCCCGGAGCAGGCTCTGCCAGCGAGAACGCGACTCTGGATGAAGCCATGCCACTGAAG 3234
2992 CGCAAGGGGAGCGCGCGCGGCAACCGCGCGSCCCCGAGCGGGSCCCCGGAGGC 3051
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3052 G-GAGAGCGGGAGGACCGCGCGCGCACCGGGCCCGGACACAGGCGCAGCTGTCTC 3110
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3111 ACGAGCTGTGAGAGGAGACCAACGAGAGGAGGCCACGAGAGAGGAGGCTGAGATAG 3170
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3411 GGAAGCCACGCTGTCTCCAGTGTGAAGCTGTGAAGCTTGGAAAGCAAGAGGAGGAA 3470
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3471 AGAGGTGAAGCGGATGAGCTGATGAGAGGCGGCCCGCGCTATCTGCCATACAGCT 3530
3702 AGAAGAGCAGAGAAAGAGGAGAGCTGTGACAGAGCAAGGCAAGCCATGTGCCACAGCT 3761
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3762 CAATGTTCTATCTTCAGACCAACCAACCGATCCGAGGCGCTGCCACTACATCGTGAACC 3821
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4242 TACTCATTTGTGTACAAGCTCTTCATGTTTCTTGTGTCTTCATCGCAGTTTCAAGCTCTTCA 4301
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4131 AGTATTTGGATTTATGAGAAGGAGGAAGTGAAGAGCTCAAGCCAGGACAGTGAAGAAATACG 4190
4362 ACTATGTAGATCATGAGAAAAACAAGATGAGGTTGAGGGCCGGGAATGGAAGCGCCATG 4421
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4422 AATTTCACTACGACAAATATCTGGGCGCTGTGTGACCTCTTTCACGCTCTCCACAGGGG 4481
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Qy 3177 CCGAACAAGAAAGGAGTCTCGGAACAACAACGACCCCGGGAGCCACACTGTGACCTGGAGA 3236
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QY	5253	TGTTGAACCTCTTTGTGGCTGTGATCATGGACAATTTGAGTACCTCACGCGGACTCTT	5312
Db	5249	TGCTCAACCTGTTTGTGGCGTCATCATGGACAATTTGAGTACCTCGGACTCT	5308
QY	5313	CNATCCTAGTCTCTACCACTTGGATGAGTTTCATCCGGGTCTGGGTGAATACGACCCGG	5372
Db	5309	CCATCCTGGGGCTCACCACTTGGAGAGTTTGTCCGCTCTGGGCGAATATGACCGAG	5368
QY	5373	CTGCGTGTGGGCGCATCAGTTACAATGACATGTTTGAGATGCTGAAACACATGTCCCGC	5432
Db	5369	CAGCATGTGGCGCATCCATTCATCTGAGATGATGAATGCTGACTCTCATGTCACTC	5428
QY	5433	CTCTGGGGCTGGGGAAGAAATGCCCTGCTCGAGTTGCTTACAAGGCGCTGGTTCGCATGA	5492
Db	5429	CGCTAGGCCCTCGGCAAGAGATGTCCCTCCAAAGTGGCATATAAGAGTTGGTCTGATGA	5488
QY	5493	ACATGCCCATCTCCACAGGAGATGACTGTTTCACTTACGTCACGGTGTGATGGCCCTCA	5552
Db	5489	ACATGCCAGTAGC---TGAGGACATGACGCTCCACTTCACTCCACACTTATGGCTCTGA	5545
QY	5553	TCCGACGGCACTGGAGATCAAGCTGGCCCCCAGCTGGGACAAAGCAGCATCAGTGTGACG	5612
Db	5546	TCCGACAGCTCTGGACATTAAATTGCCAAAGGTGGTGACAGAGGAGCTAGACT	5605
QY	5613	CGGAGTTGAGGAGAGATTTCCGTTGTGTGGGCCAAATCTGCCCCAGAGAAGACTTTGGACT	5672
Db	5606	CAGAGCTACAAAGGAGACCTTAGCCATCTGSCCTCACCTATCCCAGAAGATGCTGGATC	5665
QY	5673	TGCTGGTACCCACCCNATAGCCTGATGATGACATGAGTGGGGAAGGTTTATGCAGCTCTGA	5732
Db	5666	TGCTTGTGCCCATGCCCAAGCCTCTGACCTGACTGTGGGCAAAATCTATGCAGCAATGA	5725
QY	5733	TGATATTTGACTTCTACAGCAGAAACAAACCCAGAGACCAGATGCAGCAGG	5786
Db	5726	TGATCATGACTACTATATAGCAGATAGGTGAAGAGGAGGAGCAGCTGG	5779

Search completed: September 27, 2004, 07:05:53
 Job time : 2214 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2004, 15:36:42 ; Search time 11188 Seconds
(without alignments)
19687.473 Million cell updates/sec

Title: US-10-033-026-3
Perfect score: 7376
Sequence: 1 gggcgccgcgtcgcgggt.....tgcttgagtacgtaccgc 7376

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_man:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*
 - 28: gb_gsl:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1987.6	26.9	6813	29	AY406056 Homo sapi
2	1940.8	26.3	6822	29	AY406058 Mus muscu
3	1787	24.2	6675	29	AY406057 Pan trogl
4	1128	15.3	2617	11	AK081230 Mus muscu

5	692	9.4	735	12	BG472603
6	666.4	9.0	802	14	CK000994
7	663	9.0	6035	11	BC051413
8	633.4	8.6	4058	11	AK039991 Mus muscu
9	628.4	8.5	848	14	CF182756
10	625	8.5	807	14	CF743150 UI-M-GVO-
11	624.8	8.5	815	14	CD804209 UI-M-GVO-
12	623	8.4	636	11	BC043482 Mus muscu
13	605	8.2	795	14	CB521867 UI-M-GHO-
14	597.6	8.1	754	14	CF537761 UI-M-GHO-
15	570.6	7.7	756	14	CB518919 UI-M-GHO-
16	569.8	7.7	696	10	BE266069 601190737
17	557.2	7.6	683	12	BM941798 UI-M-CGOp
18	538	7.3	654	14	CA324977 UI-M-FYO-
19	528.6	7.2	942	12	BI905728
20	525.4	7.1	872	13	BU364873
21	514.2	7.0	690	14	CF538264 UI-M-GHO-
22	509.8	6.9	610	14	CF533828 UI-M-GHO-
23	506.2	6.9	957	13	BQ886304 AGENCOURT
24	504.6	6.8	747	14	CF743227 UI-M-GVO-
25	504.2	6.8	600	14	CF534054 UI-M-GHO-
26	500	6.8	645	14	CB518720 UI-M-GHO-
27	500	6.8	657	10	BB621795 BB621795
28	494.6	6.7	958	13	BQ882047 AGENCOURT
29	492.2	6.7	608	14	CB580917 AMGNNUC.N
30	491	6.7	705	13	BU056303 UI-M-FOO-
31	489	6.6	711	13	BY728171
32	473.8	6.4	811	14	CA318259 UI-M-FWO-
33	466.4	6.3	1150	11	AK052625 Mus muscu
34	464.8	6.3	684	14	CB520731 UI-M-GIO-
35	462.2	6.3	646	13	BQ44257 UI-M-EXO-
36	461	6.2	613	14	CF537036 UI-M-FYO-
37	452.6	6.1	2560	11	AK044695 Mus muscu
38	444	6.0	645	14	CB576173 AMGNNUC.C
39	443.4	6.0	658	14	CF739159 UI-M-HDO-
40	443	6.0	524	10	BE234696 141896 MA
41	427.8	5.8	438	9	AA776162 ae80b04.8
42	424.8	5.8	649	14	CD762997 GGE2SM103
43	417.2	5.7	1012	12	BG820937 602780845
44	416.4	5.6	853	9	AU169553
45	415.8	5.6	877	13	BU367254 603584475

ALIGNMENTS

RESULT 1	AY406056	6813 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY406056	Homo sapiens CACNA1E gene, genomic survey sequence.			
DEFINITION	AY406056	GI:39762030			
ACCESSION	AY406056	GI:39762030			
VERSION	AY406056	GI:39762030			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 6813)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 6813)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				

QY 2098 GGCATCTCTCTTCAGATCTTCAGCGGAGAGACTGGAATCGAGTGATGATCA 2157
Db 1935 AGCCATCATGACTGTGTTCAGATCTTCAGCGGTGAGGATGGAATGAGGTATGACAA 1994
QY 2158 CGGGATCGAATCGCAAGCGCGGTGACAAAGGATGTTCTCGTCTTTTACTTTCATTGT 2217
Db 1995 TGGATCCGCTCCAGGGTGGGTCACTCAGGATGTGTCTGCCATCTACTTTCATTGT 2054
QY 2218 CTTGACACTGTTGGAAACTACACTCTGCTGAATGTCTTTCTGGCCATCGCTGTGGACAA 2277
Db 2055 GCTCACCTTGTGGAACATACACGCTACTGAATGTCTTCTGGCTATCGCTGTGGATAA 2114
QY 2278 CTTGGCCAAAGCCCAAGAGCTGACCAAGGATGAAGAGAGATGGAAGAACGCGCAATCA 2337
Db 2115 TCTGCCAAAGCCCAAGAACTGACCAAGGATGAACAGGAGAAAGAGAGCCCTTCAACCA 2174
QY 2338 GAAGCTTGTCTGCAAAAGGCCAAAGAGTGGCTGAAGTCAAGCCCATGCTCTGCGCGAA 2397
Db 2175 GAAACATGCACTGCAGAAAGGCCAAGGAG-----GTGAGCCCGATGCTGACCCAA 2225
QY 2398 CATCTTCATCCGCCAGGAGCAGAACTCGGCCAAGCGCGCTCGGTGTGGAGCAGCG 2457
Db 2226 CATGCTTCGATCGAAAGAGACAGAAAGAGACACCAATGTCGATGTGGAGCCACG 2285
QY 2458 GGCAGCCAGCTAGCGCTGCAGAACTGCGGGCCAGC-----TGCGAGGCGTGTA 2508
Db 2286 CAGCAGCACTGAGGAGCGGAGCGCCGCGCACCAATGCTCGGTGTGGGAGCAGCGTAC 2345
QY 2509 CAGGAGATGGACCCCGAGGAGCGGCTGCGCTTCGCCACTACGCGCCACCTGCGGCCGA 2568
Db 2346 CAGCAGCTGAGGAGCAGATGCAGATGTCAGCAGGAGGCCCTCAACAGAGAGGAGGC 2405
QY 2569 CATGAAGACGCACTGACCGCGCGCTGTGTGGAGCTGGGCGCGCACGCGCGCGGG 2628
Db 2406 GCCACCATGAACCCGCTCAACCCCTCAACCGCTCAGCTCCCTCAACCGCTCAATGC 2465
QY 2629 GCCCGTGGGAGGCAAGCCGACCTGAGGCTGCGGAGGCC-----CCGAGGGGCTGACCC 2685
Db 2466 CCAACCCAGCGCTTATCGGGGACCCAGGGCCATTGAGGGCTGGCCCTGGGCGCTGGCCCT 2525
QY 2686 TCCGCGCAGGCACCCAGCGCACGCAAGGACCAAGACCCCGCGCGGGGAGCACGGA 2745
Db 2526 GGAGAACTTCAGAGAGAGCGCATCAGCGTGGGGGTCTCCTCAGGGGATGAGGGGA 2585
QY 2746 CCGAGCAGAGCCCGGAAGCGGAGAGCGGGAGCCCGGTGCCCGGAGGAGCGCGCG 2805
Db 2586 CCGATCCAGTGCCTTGACAAACAGAGGACCCCTTTGTCTCCCTGGCCAGCGGAGCCACC 2645
QY 2806 GCCGACCCGAGCCACAG-----CAAGAGGCGCGCGGGCC 2841
Db 2646 ATGCTGGCCAGGCGCTGTATGGAACCTGTGACCCGACTCAGCAGGAGCAGGGGAGG 2705
QY 2842 CCGGAGCGCGGAGCAGCGCGCCGAGGCCAGGCCCGGAGGGCGCGCGGACCA 2901
Db 2706 AGAGGCTGTGTGACCTTTGAGGACCCGGGCGAGGCAAGGAGAGCCAAAGCGGAGCCG 2765
QY 2902 CCGCGCGGGTCCCGGAGAGGCGCGGAGCGGGAGCCCGAGCCGACCGCGCGCACCG 2961
Db 2766 GCATCGCGGTGAGGACAGAGCAAGGAGTCTCTTACGCTCCCGGAGCAGTCTGC 2825
QY 2962 GCACAGGATCCGAGCAAGAGTGCGCGCGCCGAGGGGAGCGCGCGCGGACCG 3021
Db 2826 CAGCCAGGAACGCACTGCGATGAAGCCATGCCCTACTGAAGGGGAGAGGACCATGAGCT 2885
QY 3022 CGGCGGCCCGGAGCGGGCCCCCGGAGGCGGAGAGCGGGAGAGCGCGCGCGGGCA 3081
Db 2886 CAGGGGCAACCATGCTGCCAAGGAGCCAAAGATCCAAAGAGAGAGAGCCCGAGATTTAAG 2945
QY 3082 CCGGGCCCGGCACAAGCGCAGCTGCTCAAGGCTGTGGAGAGGAGACCAAGGAGAA 3141
Db 2946 GAGGACCAACAGTCTGATGTGTCCAGAGGCTCCGGGCTGGCAGGAGGCTTGTGAGGC 3005
QY 3142 GGAGGCCACGGAGAGGAGGCTGAGATAGTGGAAAGCCGACCAAGGAAAGGAGCTCCGGA 3201

Db 3006 TGACACCCCTTAGTCTCTGCCCATCTCTGAGCTGGGAAGCACCTGTGTGCTGAC 3065
QY 3202 CCACCAAGCCCGGGAGCCACACTGTGACCTCTGGAGACCAAGTGGAGACTGTGACTGTGGTCC 3261
Db 3066 GGAGCAGGAGCCAGAGGAGCAGTGAAGGCGCTCTGCTGGGGAATGTGCGACTAGACAT 3125
QY 3262 CATGCAACACTGCCCAGACACTGTCTCCAGAAAGGTGGAGGAAACAGCCAGAGATGAGA 3321
Db 3126 GGGCGGGTCTCAGCCAGAGCGAGCTGACCTCTCTGTCATCAGCGCCAAACGAGCAA 3185
QY 3322 CAATCAGCGGAACGTCACTCGCATGGCAGTCAAGCCCGAGCCCAACTATTTGATCA 3381
Db 3186 GGCCACACCGAGAGCAGCGCTCACCGTCGCCATCCCGCAGCTGACCCCTTGGTGG 3245
QY 3382 TATCCCACTGATCTCTGACCGGGCCCTCTTGGGGAAGCCACGCTCTTCCCAGTGTAACT 3441
Db 3246 CTCAACCGTGGTGACATTAGCAACAAGCGATGGGAAGCCAGTCCCTTTGAAGAGGC 3305
QY 3442 GGACCTGGAAAGCAAGCAGAGAGGGGAAGAGGAGGTGGAAAGCGGATGACGTGATGAGGAG 3501
Db 3306 AGAGATCAGAGAGGATGAGGAGGAGGTGGAGAAAGAAAGCAGAAAGAGAGGAGGTGA 3365
QY 3502 CGGCCCCCGGCTTATCGTCCCATACAGCTCCATGTTCTGTTTAAAGCCCAACCACTGCT 3561
Db 3366 GACAGGCAAGCCATGGTCCCAAGCTCAATGTTTCATCTTCAGCACCAACCAACCCGAT 3425
QY 3562 CCGCCCTCTCTGCACTAGATCGTGAACCATGAGGTACTTCGAGGTGTCATTTCTCGTGGT 3621
Db 3426 CCGAGGGCTGCCACTACATCGTGAACCTGCGTACTTGTGATGTGCATCTCTCTGGT 3485
QY 3622 CATCGCTTTGAGCAGCATCGCTCGCTGTAGGACCCAGTCCGACAGACTCGGCCAG 3681
Db 3486 GATTGAGCGAGCAGCATCGCTCGCGGAGAGGACCCCGTCTCTGACCAACTCGGAGCG 3545
QY 3682 GAACAAGCTCTGAATACTGGAATTAATTTTCACTGGTGTCTTTACCTTTTTCAGATGGT 3741
Db 3546 CAACAAGTCTGAGGATTTTGAATGATGTGTTTCAAGGGGCTGTTCACTTTTTCAGATGGT 3605
QY 3742 GATAAAGATGATCGACTTGGGACTGCTGCTTCACTCGGAGCCCTATTTTCGGGACTTGTG 3801
Db 3606 TATAAAGATGATAGACCAAGGCTTGATCTGAGGATGGTCTTACTTTCGAGACTTGTG 3665
QY 3802 GAACATTTCTGGAATCATTTGTGTGAGTGGCGCCCTGTTGGCGCTTGTCTTTTCGAGCTT 3861
Db 3666 GAACATCTGGAATTTGTGTGTGCTGTCGCGCATTTGGTGGCTTGTCTGCGGNNNNN 3725
QY 3862 CGTGGAGGATCCAAAGGGAAGACATCAATCAATCAAGTCTCTGAGAGTCTTCTGCTGT 3921
Db 3726 NNNNNNAACCAACAAAGGAGCGGACATCAAGCAATCAAGTCTCTGCGGTGCTCGAGT 3785
QY 3922 CTTGCGGCGCTCAAGACCATCAACGGCTGCCCAAGCTCAAGGCTTGTGCTTTCAGCTTGTG 3981
Db 3786 TCTAAGGCCACTGAAACCATCAAGCGCTTGCCCAAGCTCAAGNNNNNNNNNNNNNNNN 3845
QY 3982 GGTGAACCTCCCTGAAGAATGTCTCAACATCTTGAATGTGTATCATGCTCTTTCATGTT 4041
Db 3846 NNN 3905
QY 4042 ATTTGCGGTCAATTGCGGTGAGCTCTTCAAGGGAAGTTTCTTACTGCACAGATGAATC 4101
Db 3906 NNN 3965
QY 4102 CAAGGAGCTGGAGAGGAGCTGCAGGGGTGATTTTGGATTATGAGAGGAGGAACTGGA 4161
Db 3966 NNN 4025
QY 4162 AGCTCAGCCCGAGGAGTGAAGAAATACGACTTTTCACTACGACAAATGTGCTCTGGGCTCT 4221
Db 4026 NNN 4085
QY 4222 GCTGACGCTGTTCAAGTGTCCAGGGAGAGGCTCGGCCCATGCTGTAACACTCCGT 4281

ORIGIN

Query Match 26.3%; Score 1940.8; DB 29; Length 6822;
Best Local Similarity 57.1%; Pred. No. 4.7e-291;
Matches 3272: Conservative 0; Mismatches 2316; Indels 145;

Qy	146	ATG	T	G	T	C	G	C	T	T	C	G	G	G	A	C	G	A	C	T	G	G	G	C	G	C	T	A	T	G	A	G	C	C	C	C	G	G	G	A	G	A	C	G	G	205									
Db	1	AT	G	C	T	C	G	T	T	C	G	G	G	A	G	G	G	G	G	T	G	T	C	G	T	G	T	G	T	G	T	G	G	A	G	C	C	A	G	C	A	T	G	A	C	T	G	60							
Qy	206	G	C	C	G	G	G	C	G	C	G	G	C	C	G	G	C	C	G	G	C	C	G	T	C	C	C	G	G	G	G	G	C	T	G	C	A	G	C	C	C	G	C	G	265										
Db	61	G	A	C	C	A	G	A	C	G	A	C	C	C	C	G	T	C	C	G	G	C	T	C	G	G	C	T	C	G	G	G	105																						
Qy	266	C	A	G	C	G	G	T	C	T	A	A	A	G	C	A	A	T	C	G	T	C	G	C	G	C	G	C	G	C	G	A	C	C	A	T	G	G	C	G	T	G	A	C	A	C	325								
Db	106	C	C	G	C	G	C	C	T	A	C	A	A	G	C	G	C	A	A	A	G	C	G	C	A	A	A	G	C	G	C	G	A	C	T	A	T	G	G	C	T	T	T	G	A	C	A	C	165						
Qy	326	C	C	A	T	C	C	G	G	T	C	A	A	G	C	A	G	C	T	C	A	C	G	T	C	A	A	C	C	G	T	C	A	A	C	C	G	T	C	T	T	C	G	A	C	G	385								
Db	166	C	C	C	A	T	C	A	G	T	C	C	G	G	C	A	A	C	T	G	T	T	C	A	C	G	T	C	A	A	C	A	G	A	T	C	C	C	T	G	T	T	C	A	T	C	G	A	A	225					
Qy	386	G	A	C	A	C	G	T	C	G	C	C	A	A	T	C	G	A	A	G	C	G	C	A	C	C	A	C	C	G	A	G	T	G	C	C	T	C	A	T	T	C	G	A	T	A	T	G	445						
Db	226	G	A	T	A	C	A	T	T	G	T	C	A	G	A	A	T	C	G	C	A	G	A	G	C	T	C	A	T	C	G	A	T	T	G	C	C	C	G	C	A	T	T	G	A	T	A	C	285						
Qy	446	A	T	C	T	G	G	C	A	C	A	T	C	G	C	A	A	C	T	G	A	T	C	G	T	G	T	G	G	C	C	T	G	A	G	A	C	A	C	T	C	C	T	G	A	T	505								
Db	286	A	T	C	T	G	G	C	A	C	A	T	T	G	C	A	A	C	T	G	C	A	T	C	T	T	T	G	G	C	C	T	G	A	G	A	C	A	T	T	C	T	C	T	G	A	345								
Qy	506	G	G	G	C	A	A	A	A	C	C	C	A	T	G	T	C	G	A	G	C	G	T	G	A	C	A	C	A	C	A	C	G	A	C	A	C	G	A	C	C	T	A	T	T	C	A	T	C	G	G	A	T	C	565
Db	346	G	A	T	G	A	C	A	A	G	C	C	C	A	A	T	G	T	C	G	A	A	G	C	T	G	G	A	A	G	A	G	A	C	A	A	C	A	A	T	A	T	T	C	A	T	T	C	G	G	A	T	C	405	
Qy	566	T	T	T	T	G	C	T	T	C	A	G	G	C	A	G	G	A	T	C	A	A	A	T	C	A	T	C	G	C	T	T	G	G	C	T	T	G	T	T	C	T	T	C	C	A	A	A	G	G	G	T	C	T	625
Db	406	T	T	C	T	T	T	G	A	G	C	T	G	G	A	T	C	A	A	T	T	G	T	G	C	T	A	G	G	T	T	C	A	T	T	C	C	A	T																

QY 2234 AACTACACTCTGCTGAATGTCTTTCTGGCCATCGCTGTGGACAACCTGGCCAAAGCCCAA 2293
Db |||||
QY 2074 AACTACAGCTCTAAATGTATTCTTTGGCCATCGCTGTGGACAATCTGCCAAATGCCCAG 2133
Db |||||
QY 2294 GAGCTGACCAAGGATGAAGAGAGATGGAAGAGCAGCAATCAGAACTTGCTCTGCAA 2353
Db |||||
QY 2134 GAACTGACCAAGGATGAAGAGAGAGATGGAAGAGCAGCAATCAGAACTTGCTCTGCAA 2193
Db |||||
QY 2354 AAGGCCAAAGAGTGGCTGAAGTCAAGCCCACTGTCTGCCGGGAACATCTCCATGCCGCC 2413
Db |||||
QY 2194 AAGGCCAAGGAG-----GTACAGCCGATGTCTGTCTCCAACTGCTTCCATTGAA 2244
QY 2414 AGGACGAGAACTCGGCCCAAGCGCGCTCGGTGTGGAGCAGCGGCCAGCAGCTACGG 2473
Db |||||
QY 2245 AGAGACAGAGAGAGACACACATGTCTGATGTGGAGCCAGCAGCAGCCACCTGAGG 2304
QY 2474 CTGCGAAGCTCGGG-----CGAGTGGAGCGCTG 2506
Db |||||
QY 2305 GAGCGGAGCGCGGCCACCACTGTCTGTGTGGGAACAACGACAGCCAGCTGAGGAGG 2364
QY 2507 TACAGCGAGATGGACCCCGAGGAGCGCT-----GCGTTTCGCCACTACGCGCCAC 2557
Db |||||
QY 2365 CACATGCAATGTCTAGCAAGAGCCCTCAACAAGAGGAGGCCGCCCAATGAAACCCC 2424
QY 2558 CTGCGGCCGACATGAAGACGACCTGGACCGCGCTGTGTGTGGAGCTGGCGCGCAC 2617
Db |||||
QY 2425 CTCATCTCACTCAACCCACTGAGTCTCTCAACCCCTCAATGTCTACCCAGCCTTTAT 2484
QY 2618 GCGCGCGGGGCCCTGGAGGGAAGACCCGACCTGAGGCTGGAGGCCCGCGAGGCC 2677
Db |||||
QY 2485 CGAGGCCACAGCCCATTTGAGGGCCCTAGCCCTAGGTCTGGGTCTTGAAGTGTGAAGAA 2544
QY 2678 GTGCAACCTCCGCGCAGGACCAACCGCACCGCGACA-----AGCAAGACCCCGC 2729
Db |||||
QY 2545 GAAACGATCAGTCTGGGGGCTCCCTCAAGGGGACATAGGGGCGCTCACTAGCGCCCTG 2604
QY 2730 CGCGGGGGAACAGAACCCGACAGAGGCCCGCGAAGCGCGAGAGCGGGAGCCCGGTGCC 2789
Db |||||
QY 2605 GACAAACAGAGAGGCCCTTGTCTTGGGCAACCGGAGCCACCGTGGCTGCTAGATCC 2664
QY 2790 GGGAGGCGCGCGCGCGCACCGCACAGCAAGAGAGCGCGCGGGCCCGCGAGG 2849
Db |||||
QY 2665 TGTCTATGAAACTGTGACCCCAATC-----CAGCAGGAGCTGGGGAGAGAGACTGTGGT 2720
QY 2850 CGCGAGCGAGCGCGCGCGCGCAGGCCCGCGAGCGCGGCC-----GGCGGACCAACCGCGC 2907
Db |||||
QY 2721 GACTTTTGAGNACCGGCGCAGGCAAGAGTCAAGAGCGAAGCGGCAATCGCGAGT 2780
QY 2908 CGGCTCCCGAGGAGCGCGCGAGCGGAGCCCGACCGCGCACCGCGCACCGGACCA 2967
Db |||||
QY 2781 CAGGACTGAGGCAAGGACTCTGCTCTGCTATCCGAAAGAGGCTGCGCAGCGAGGCG 2840
QY 2968 GGATCCGAGCAGGAGTGGCGCGCGCGCAAGGGCGAGCGCGCGCGCGGCGCGCGGG 3027
Db |||||
QY 2841 GAGTCTGATGAAGGGGTGTCCGTTTGAAGGGGAGAGGAACATGAGCCTCAAGCAGGCA 2900
QY 3028 CCCCAGCGGGGCC-----CCGGGAGCGAGAGCGGGAGAGCGCGCGCGCGCA 3081
Db |||||
QY 2901 CAGGAGCAAGAGCGCACCATCCAGAGAGAGAGAGAACCCAGAGCTTAAGAGAGCAAA 2960
QY 3082 CCGGGCCCGGCAACAGGCGCGCGCTGTCTCAG-AGGCTGTGGAGAGAGAGACCAAGGAGA 3140
Db |||||
QY 2961 CAGTCTGATGTCTCCAGGGGCTTGGACTGTGAGTGTGGGAGCGTACAGCTGTGGGTC 3260
QY 3141 AGGAGGCCACGAGAGAGGCTGAGATGTGGAGCCGACAGGAAGAGAGTCTCGGA 3200
Db |||||
QY 3021 TCTAGTCCAGCCCCAATCTGAGCTGGAAGTGGGAAGGATGCAGCTCTGACAGAGCAGGA 3080
QY 3201 ACCACAGCCCGGAGGCCACACTGTGACCTCTGGAGACCAAGTGGGACTGTGACTGTGGGTC 3260
Db |||||
QY 3081 GGCTGAAGGACGAGTGAACAGCCCTTCTTGGGAGCGTACAGCTGGATGTGGGCCGGG 3140
QY 3261 CCATGCAACACTGCCCCAGCACCTGTCTCCAGAAGGTGGAGGAACAGCCAGAGGATGCGAG 3320

Db |||||
QY 3141 CATTAGCCAGAGTGAACCGGATCTCTC-----CTGCATGACAGCCAAATGGACAAG 3192
QY 3321 ACATACAGCGGAGCTCACTCGCATGGCAGTCAAGCCCGCAGAGCCCGCAACACTATTGTAC 3380
Db |||||
QY 3193 GCTACCAAGGAGAGCAACAGTGTACCGTGGCCAT---CCCTGATGTGGACCCCTTGGTGG 3250
QY 3381 ATATCCCAAGTGTCTGACGGGCCCTCTTGGGGGAAGCAGCGTCTGTTCCCAAGTGGTAACG 3440
Db |||||
QY 3251 ACTCGACAGTGGTGAACATTAGCAACAAGACGGATGGAGAAGCCAGTCCCTTGAAGGAGG 3310
QY 3441 TGGACCTGGAAGCAAGCAGAGGGGAAGAGAGGTGGAGCGGATGACGTGTGATGAGGA 3500
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Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saico,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@ac.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES
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evidence: FASTY, 77.5%ID, 97.1%length, match=531)"

ORIGIN

Query Match 15.3%; Score 1128; DB 11; Length 2617;
Best Local Similarity 81.9%; Pred. No. 7.5e-165;
Matches 1367; Conservative 0; Mismatches 285; Indels 18; Gaps 5;

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source	1. 802 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3070791.7" /lab_host="DH10B Tona" /clone_lib="NIH_MGC 221" /note="Organ: mixed; Vector: pYX-Asc; Site 1: EcoRI; Site 2: NotI; Library is oligo-dT primed and directionally cloned. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. Average insert size 4-5kb. Adaptors 5' (AATTCGCCAGCAGG) 3' and 5' (CTCTGCGCG) 3'. 3' Linker sequence - GCGCGCGCTGAGAGCC T18. Sequencing primers 3' end: T3 promoter primer 5'd (ATTAAACCTCCTAAAGGA) 3'. 5' End: T7 promoter primer 5'd (TAATACGACTCATAGG) 3'. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library"
ORIGIN	
Query Match Best Local Similarity 99.1%; Score 666.4; DB 14; Length 802; Matches 670; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
QY	5694 CTGATGATGACAGTGGGAGGTTTATGCGCTCTGATGATATTTGACTTCTACAGC 5753
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QY	5754 AGAACAAACACACAGAGACAGATGACAGAGGCTCTCGAGGCGCTCTCCAGATGGGTC 5813
Db	121 AGAACAAACACACAGAGACAGATGACAGAGGCTCTCGAGGCGCTCTCCAGATGGGTC 180
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Db	181 CTGTGTCCTGTTCCACCTCTGAAGGCCACCTTGGAGGACACACAGCGCGGTGTGCTCC 240
QY	5874 GAGGAGCCCGGTTTCTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGGGGGCCA 5933
Db	241 GAGGAGCCCGGTTTCTTCGACAGAGAGTTCCACCTCCCTCAGCAATGGGGGGCCA 300
QY	5934 TACAAACCAAGAGAGTGGCATCAAGAGTCTGTCTCTGGGCACTCAAGAGACCCAGG 5993
Db	301 TACAAACCAAGAGAGTGGCATCAAGAGTCTGTCTCTGGGCACTCAAGAGACCCAGG 360
QY	5994 ATGCACCCCATGAGGCCAGGCCACCCCTGAGGCGTGGCCACTCCACAGAGATCCCTGTGG 6053
Db	361 ATGCACCCCATGAGGCCAGGCCACCCCTGAGGCGTGGCCACTCCACAGAGATCCCTGTGG 420
QY	6054 GCGGTCAGAGCACTGGCTGTGACCTTCAGATGACAGCATAACCCGAGGGGCGCTG 6113
Db	421 GCGGTCAGAGCACTGGCTGTGACCTTCAGATGACAGCATAACCCGAGGGGCGCTG 480
QY	6114 ATGGGAGCCCCAGCCTGGGCTGGAGAGCCAGGGTTCGAGCGGCTCCATGCGCCGCTTG 6173
Db	481 ATGGGAGCCCCAGCCTGGGCTGGAGAGCCAGGGTTCGAGCGGCTCCATGCGCCGCTTG 540
QY	6174 CGGCCGAGACTACGCCGTCACAGATGCCAGCCCCCATGAAGCGCTCCATCTCCACGCTGG 6233
Db	541 CGGCCGAGACTACGCCGTCACAGATGCCAGCCCCCATGAAGCGCTCCATCTCCACGCTGG 600
QY	6234 CCAGCGGCCCCGTGGGACTCATTTTGCAGCACCACCCGAGCCGCGCCACCCCTAGCC 6293
Db	601 CCAGCGGCCCCGTGGGACTCATTTTGCAGCACCACCCGAGCCGCGCCACCCCTAGCC 660
QY	6294 AGGCGTGTGACACACACACACCGCTGCCACCGCCGAGGGACAGGAGCAGAGGT 6353
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QY	6354 CCCTGGAGAGGGGCC 6369

Db	721 CCTTGAAGAGGGGCC 736
RESULT 7 BC051413 LOCUS	
DEFINITION	BC051413 6035 bp mRNA linear HTC 19-NOV-2003 Mus musculus calcium channel, voltage-dependent, alpha 1F subunit, mRNA (cDNA clone IMAGE:6493332), containing frame-shift errors.
ACCESSION	BC051413.1 GI:30802106
VERSION	HTC.
KEYWORDS	Mus musculus (house mouse)
SOURCE	Mus musculus
ORGANISM	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 6035)
REFERENCE	Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schneetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
TITLE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL	22388257
MEDLINE	12477932
PUBMED	2 (bases 1 to 6035)
REFERENCE	Strausberg, R.
AUTHORS	Direct Submission
TITLE	Submitted (25-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
JOURNAL	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabs-r@mail.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nih.gov
REMARK	Akhter, N., Ayèle, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 108 Row: O Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972 This clone has the following problem: frame shifted.

FEATURES

Location/Qualifiers
1..6035
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6493332"
/issue_type="Eye, retina, mouse strain C57Bl/6"
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/note="Vector: pCMV-SPORT6"

ORIGIN

Query Watch 9.0%; Score 663; DB 11; Length 6035;
Best Local Similarity 58.2%; Pred. No. 2.1e-92;
Matches 1334; Conservative 0; Mismatches 895; Indels 64; Gaps 7;
QY 3512 CCTATCGTCCCATACAGCTCCATGTTCTGTTTAAGCCCCCAACCTGCTCGCGCTTC 3571
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QY 3572 TGCCTACTACATCGTGACCATGAGTACTTCCGAGGTGGTCAATCTCGTGTATCGCCTTG 3631
DB 2616 TGGCACACACTATACATCACCATATCTTCCAGGCTCTCACTAGTGTTCATCATCTC 2675
QY 3632 AGAGATCGCCCTGCTGCTGAGGACCCAGTGCACAGACTCGCCAGGAACAACGCT 3691
DB 2676 AGTAGTGTGCTGCTGCTGAGGACCCATCCGAGCTCACTCTCCGAACCATATT 2735
QY 3692 CTGAATACCTGGATTACATTTTCACTGGTGTCTTACCTTTGAGATGGTATAAGATG 3751
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QY 3752 ATCGACTTGGGACTGTGCTTCACTCGGAGCTATTTCCGGGACTGTGGAAATTTCTG 3811
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QY 3812 GACTTCAATTTGGTCAAGTGGCCCTCGTGGGGTTTGTCTTCGAGCTTCGAGGAGGA 3871
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QY 3872 TCCAAAGGGAAGACATCAATACCATCAAGTCTCTGAGAGTCTCTGCTCGCGGCC 3931
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QY 3932 CTCAAGACCATCAAAACGGCTGCCAAGCTCAAGGCTGTGTTGACTGTGTGGTGAATCC 3991
DB 2955 CTCGAGGCCATCAACAGAGCCAAAGGACTCAAGCATGTGGTGCAGTGTGTCTGTGGCC 3014
QY 3992 CTGAAGAATGCTCTCAACATCTTGTATGTCTACATGCTCTTCATGTTCAATATTTGCCGTC 4051
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QY 4052 ATTGGGTGACGCTCTTCAAGGGAAGTTTCTACTGCACAGATGAATCCAAAGAGCTG 4111
DB 3075 ATTGGTGTTCAGCTGTTTCAAGGGAATTTCTACAGTGCATGATGAGGCCAAACACACC 3134
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QY 4283 GATGCCACTTATGAGGAGCAGGTTCCAAAGCCCTGGGTACCGCATGGAGCTGTTCATCTTC 4342
DB 3315 GATGCAACCGAGAAGATGAGGGCCCTATCTACAATTAACCATGTTGGAGATATCAGTATTC 3374
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DB 3375 TTCAATGTGTACATCATCATCGCTTCTTTCATGTAACATCTTTGTGGCTTTGTT 3434
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QY 4463 GAGAGGGCTGTGATTTGACTTCCGCTCAGCGCCAAACCCCTGACACAGCTATCATGCCCAA 4522
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QY 4823 GCGGAACGAAACAATTTTCATCAACCTCAGCTTCTCGGCTCTTTTCGAGCTCGCGGCTG 4882
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QY 4943 TTCAAGSCCTGCTGCTGCTGCTCATTTGCGCATGCTGTCTTCACTATAGCCATC 5002
DB 3968 TTCAGGCTTGGCTTATGTTGGCCTCTCTCATAGCAATGATATTTCTTCACTATGAGCT 4027
QY 5003 ATCGCATGAGGTGTTTGGGAATATTTGCGCTGGATGACACAGCATCAACCGCCAC 5062
DB 4028 ATTTGGCATGAGATGTTTGGCAAGTGGCTCTTTCAGGACGCGCAGAGATAATCGAAAC 4087
QY 5063 AACAACTTCCGAGCTTTTGAAGCCCTGATGCTGCTGTTCAGGAGCGCTACGCGGGAG 5122
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Qy 5768 AGACACAGATGC 5780

Db 4796 AAGAAAAGGGGC 4808

RESULT 8

AK039991

LOCUS AK039991 4058 bp mRNA linear HTC 19-SEP-2003

DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430040I15 product:unclassifiable, full insert sequence.

ACCESSION AK039991

VERSION AK039991.1 GI:26087546

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20493974

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 4058)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-23 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/

FEATURES

source Location/Qualifiers

1..4058

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

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/note="unclassifiable"

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Best Local Similarity 69.3%; Pred. No. 7.1e-88;

Matches 938; Conservative 0; Mismatches 376; Indels 39; Gaps 4;

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Qy 199 AGAGCGGCG 258

Db 579 AGACTCGGACACAGAGCAG-----GAACCGAAGGAACCCCCGTCGCGG 623

Qy 259 GCCCGGCGAGCGGCTCTCTTACAAGCAATCGATCGCGCAGCGCGCGGACCATGCGCT 318

Db 624 CTCGGGCGTT 683

Qy 319 GTACAAACCCATCCCGGTCAAGCAGAACTGCTTCAACCGTCAACCGCTCGCTCTTCCTT 378

Db 684 GTACAAACCCCATACCAAGTCCGGCAGAACTGTTTCAACCGTCAACAGATCCCTGTTCACTT 743

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 1635 GCTCCGGCCGACGACAGATTTGACGAGATTTGACCGCTTACCGTGTGCTGATAGACAA 1694
 1327 GCGGAGGAAGTCTGCTGGCGGAGGAGCAGGAATGAGGAGAGTCCCTTTTGA 1386
 1695 AGCAGAGGAAGTCTGCTTGTGTGAAGAAATAAATACTC---GGGAACATCAGCCTTGA 1751
 1387 CTGCTGAAGAGAGCGGCCCCACCAAGACGAGAAATGACCTGTATCCAGCAGAGAGGG 1446
 1752 AGTGCTTGAAGGGCAACCATCAAAAGGAGCGGACGAGGCCATGACCCGAGACTCCAG 1811
 1447 AGAGACCGGTTTGCAGATCTCTGTGCTGTTGG 1479
 1812 CGATGAGCACTCGGTTGATATCTCTTCAGTGG 1844

RESULT 9
 CF182756
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 848)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strauberg, Ph.D.
 Email: cga@xmail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 The following repetitive elements were found in this cDNA
 sequence: 468-529, >CHARLEI#DNA/MERI_type (matched complement)
 Seq primer: pYX-5.
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 /organism="Mus musculus"
 /mol_type="mrna"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:5705193"
 /tissue_type="whole brain"
 /dev_stage="embryo 15.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_EY0"
 /notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with EcoR I adaptor, digested with Not I, and then
 cloned directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA
 tail, is GTGCGTGGAA. This library was created for the
 University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP). 'Gene Discovery in the Developing Mouse Nervous
 System', supported by National Institutes of Mental Health
 (NIMH), Hemin Chin, Ph.D., program coordinator."
 Query Match 8.5%; Score 628.4; DB 14; Length 848;
 Best Local Similarity 88.8%; Pred. No. 2.3e-87;
 Matches 691; Conservative 0; Mismatches 86; Indels 1; Gaps 1;
 QY 4061 CAGCTCTTCAAGGGGAAGTTTCTTACTGCACAGATGAATCCAGGAGCTGGAGCGGAC 4120
 Db 1 CAGCTCTTCAAGGGGAAGTTCTTCTTACTGTATGAATCCAGGAGCTGGAGCGGAC 60
 QY 4121 TGCAGGGGTGAGTATTGGATTATGAGAGGAGGAGTGGAGAGCTCAGCCGAGGCTGG 4180
 Db 61 TGCCGGGGTCAAGTATTGGATTATGAGAGGAGGAGTGGAGAGCTCAGCCGAGGCTGG 120
 QY 4181 AAGAAATAGCACTTTCACCTACGCAATGTCTCTGGGCTCTGCTGACGCTTTCACAGTG 4240

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Db 121 AAGAAATATGACTTCCACTATGACAATGTTCTCTGGGCTTTGTGACGCTGTTCCAGAGT 180
Qy 4241 TCACGGGAGAGGCTGGCCCATGCTGTGAAACACTCCGTGGATGCCACTATGAGGAG 4300
Db 181 TCACGGGAGAGGCTGGCCCATGCTGTGAAACACTCTGTGGATGCCACTATGAGGAA 240
Qy 4301 CAGGCTCAAGCCTGGGTACCGCATGAGAGTGTCCATCTTCTACGTGGTCTACTTTGTG 4360
Db 241 CAGGGGCCAGTCCCGGTTCCGATGGAGCTCTCCATCTTCTACGTGGTCTACTTTGTG 300
Qy 4361 GTCTTTCCCTTCTTCTCGTCAACATCTTGTGCTTGTGATCATCATCACTTCCAGGAG 4420
Db 301 GTCTTCCCTTCTTCTTGTGCAACATCTTGTGCGCTTGATCATATCACTTCCAGGAA 360
Qy 4421 CAGGGGACAGGTGATGTCTGAATCAGCCTGGAGAAGAACGAGAGGCTTGCATTGAC 4480
Db 361 CAGGGAGATAGGTGATGTCTGAATCAGCTTAGAAAAGATGAGAGGCTTGCATTGAT 420
Qy 4481 TTGCCATCAGCGCAACCCCTGACACGCTACATGCTGCCCAAAACCGGCGAGTGTCCAG 4540
Db 421 TTGTCCATCAGTGCACAGCCCTGACACGGTACATGCTCAAAACAAACAGTGTCCAG 480
Qy 4541 TATAAGACGTGACATTTGTGCTCTCCCGCCCTTGAATACTTTCATCATGGCCATGATA 4600
Db 481 TATAAGACATGACATTCGTGCTCTCCACCCCTTGAGTACTTTCATCATGGCTATGATA 540
Qy 4601 GCCCTCAACACTGTGGTCTGATGATGAAGTTCTATGATGACCCCTATGATGACGCTG 4660
Db 541 GCCCTCAACAGTGTGCTGATGATGAAGTTCTATGATGACCTTATGATGACGCTG 600
Qy 4661 ATGCTGAATGCTGAACATGCTGTTTCAATCCATGTTTCCATGGAATGGTGTGAAG 4720
Db 601 ATGCTGAATGCTGAACATGTTCTTCCATCCATGTTTCTCGATGGAGTGCATCTGAAG 660
Qy 4721 ATCATGCTTGGGGTCTGAACATTTTCAGAGATGCTGGATGCTTTGACTTTGTC 4780
Db 661 ATCATGCTTGGGGTATTGAATCTTTCAGAGATGCTGGAGACGCTTTGACTTTGTC 720
Qy 4781 ACTGTGTGGAGTATTACTGATATTTAGTAAACAGAGATTTGGGAAACGAACT 4838
Db 721 ACGGTTTGGAGTA-TACTGATATTAGTACAGAGATGCGGAACACTTCATCAACT 777

RESULT 10
CF743150
LOCUS
DEFINITION
  UI-M-GVO-cln-m-16-0-UI_r1 NIH_BMAP_GV0 Mus musculus cDNA clone
IMAGE:30616527 5', mRNA sequence.
ACCESSION
  CF743150
VERSION
  CF743150.1 GI:37639489
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Dr. James Lin, University of Iowa
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/mousefi.html
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
  The following repetitive elements were found in this cDNA
  sequence: 133-194, >CHARLIE14DNA/MER1_type (matched complement)
  Seq primer: pYX-5.
  Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30616527"
/tissue_type="whole brain"
/dev_stage="1,5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP GV0"
Notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTCAAT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
```

ORIGIN

Query Match 8.5%; Score 625; DB 14; Length 807;
Best Local Similarity 89.4%; Pred. No. 7.5e-87;
Matches 686; Conservative 0; Mismatches 75; Indels 6; Gaps 1;

Qy 4397 TTGATCATCATCACTTCCAGGAGCGGGGCAAGGTGATGTCTGAATGACGCTGGAG 4456
Db 2 TTGATCATTATCACTTCCAGGAACAGGGAGATAAGTGTCTGAATGCAGCTTAGAA 61

Qy 4457 AAGAAAGAGAGGCTTGCATTTGCCATCAGCGCCAAACCCCTGACACGCTACATG 4516
Db 62 AAGAAAGAGAGGCTTGCATTTGCCATCAGTGCACGCTGACGCTGATGATGAA 121

Qy 4517 CCCCAAAACCGGAGCTGTTCCAGTATAAGACGTGGACATTTGTGGTCTCCCCGCCCTTT 4576
Db 122 CCTCAAAACAAACAGTGTTCAGTATAGACATGGACATTCGTGGTCTCTCCACCCCTT 181

Qy 4577 GAATATCTCATCATGCGCCATGATAGCCCTCAACACTGTGGTGTGATGATGAAGTTCTAT 4636
Db 182 GAGTACTTTCATCATGCTGATGATAGCCCTCAACACAGTGGTGTGATGATGAAGTTCTAT 241

Qy 4637 GATGACCCCTATCAGTACGAGCTGATGCTGAATGCTGAACATCGTGTTCACATCCATG 4696
Db 242 GATGCACTTATGAGTACGAGCTGATGCTGAATGCTGAACATTTGCTTTCACATCCATG 301

Qy 4697 TTCTCCATGGAATGCTGTGCTGAAGATCATCGCTTTGGGGTGTCTGAACATTTTCAGAGAT 4756
Db 302 TTCTCCATGGAATGCTGTGCTGAAGATCATCGCTTTGGGGTGTCTGAACATTTTCAGAGAT 361

Qy 4757 GCCTGGAATGCTTCTGACTTTGTCTGCTGTTCGGGAAGTATTACTGATATTTTAGTAACA 4816
Db 362 GCCTGGAACGCTTCTGACTTTGTCTGCTGTTCGGGAAGTATTACTGATATTTTAGTAACA 421

Qy 4817 GAGATTGCGGAACGAAACAATTTTCATCACTCAGCTTCTCCGCCCTCTTTCAGAGTGGC 4876
Db 422 GAGATAG-----CGAACCACTTCATCAACCTTAAGCTTCCTTCGCCCTCTTTCGGGGGGCA 475

Qy 4877 CGGCTGATCAAGTGTCTCGCCAGGGCTACACCATCCGATCTCTGCTGTGGAGCTTTGTC 4936
Db 476 CGGCTGATCAAGTGTCTCGCCAGGGCTACACCATCCGATCTCTGCTGTGGAGCTTCGTC 535

Qy 4937 CAGTCTCTCAAGGCCCTCGCCCTACGCTGTCTGCTCAATGCCATGCTGTGTTCTTCATCTAC 4996
Db 536 CAGTCTCTTAAAGGCGCTGCCCTACGCTGTCTCTCATTTGCCATGCTGTGTTCTTCATCTAC 595

Qy 4997 GCATCATCGGATGAGAGTGTGGGAATATTTGCCCTGGATGATGACACCATCAAC 5056
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Db      596  GCATCATCGGCATGAGGCTTTTGAACAATTGGCCCTTGATGATGACACCAAGTATCAAC 655
QY      5057  CGCCACAACAACCTTCGGAGCGTTTTTGGCAAGCCCTGATGCTGCTTCAGGAGCGCCACG 5116
Db      656  CGACACAACAACCTTCGGACATTTCTGCAAGCCTTAATGCTATTGTTCAAGAGTGCCACT 715
QY      5117  GGGGAGGCTGGCACGAGATCATGCTGCTCCTGCTGAGCAACAGGC 5163
Db      716  GGGGAGGCTGGCATGAGATCATGCTGCTTGTCTGGCAAGCGGCC 762

RESULT 11
CD804209
LOCUS
DEFINITION
  UI-M-GVO-cie-h-24-0-UI.r1 NIH BMAP_GVO Mus musculus cDNA clone
  IMAGE:30545375 5', mRNA sequence.
ACCESSION
  CD804209
VERSION
  CD804209.1 GI:32463035
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 815)
REFERENCE
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Dr. Jim Lin, University of Iowa
  cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
    http://genome.uiowa.edu/distribution/mousefl.html
  This clone was contributed by the Brain Molecular Anatomy Project
  (BMAP)
  The following repetitive elements were found in this cDNA
  sequence: 95-156, >CHARLIE#DNA/MER1_type (matched complement)
  Seq primer: pyX-5.
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    /mol_type="mRNA"
    /strain="C57BL/6"
    /db_xref="taxon:10090"
    /clone="IMAGE:30545375"
    /tissue_type="whole brain"
    /dev_stage="1,5, and 15 days newborn"
    /lab_host="DH10B (T1 phage resistant)"
    /clone_lib="NIH_BMAP_GVO"
    /note="Organ: Brain; Vector: pyX- Asc; Site 1: Ecor I;
    Site 2: Not I; The library was constructed according
    Bonafido, Lennon and Soares, Genome Research, 6:791-806,
    1996. Denatured RNA was size fractionated on a 1% agarose
    gel. First strand cDNA synthesis was primed with oligo-dT
    primer containing a Not I site. Double strand cDNA was
    size selected according to mRNA size fraction, ligated with
    EcoR I adaptor, digested with NotI and then cloned
    directionally into pyX-Asc vector. The library tag
    sequence located between the Not I site and the polyA tail
    is CCAACTGAAT. This library was created for the University
    Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
    Developing Mouse Nervous System', supported by National
    Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
    program coordinator."
ORIGIN
  Query Match      8.5%; Score 624.8; DB 14; Length 815;
  Best Local Similarity 87.9%; Pred. No. 8e-87;
  Matches 716; Conservative 0; Mismatches 90; Indels 9; Gaps 3;
  QY      4434  TGATGCTCTGAATGACGCTCGGAGAGACGAGAGGGCTTGCAATTGATCGCCATCAGCG 4493
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Db      1  TGATGCTCTGAATGACGCTTAGAAAAGAAATGAGAGGGCTTGCAATTGATTTGGCCATCAGTG 60
QY      4494  CCAAAACCCCTGACACGGGTACATGCCCCCAAAACCGGAGTGGTTCACAGTATAGACGTGGA 4553
Db      61  CCAAGCCCCCTGACACGGGTACATGCTCCAAAACCAACAGTGGTTCACAGTATAGACGTGGA 120
QY      4554  CATTTGTGGTCTCCCGCCCTTTGAATACTTTCATCATGGGCATGATAGCCCTCAACACTG 4613
Db      121  CATTCGTGGTCTCTCCACCCCTTTGAGTACTTTCATCATGGCTATGATAGCCCTCAACACAG 180
QY      4614  TGGTGTGATGATGAAGTTCCTATGATGACCCCTATGATGATGATGATGATGATGATGATGATG 4673
Db      181  TGGTGTGATGATGAAGTTCCTATGATGACCCCTATGATGATGATGATGATGATGATGATGATG 240
QY      4674  TGAACATCGTGTTCACATCCATGCTTCCCATGGAATGCGTCTGGAAGATCATCGCCCTTG 4733
Db      241  TGAACATGCTTTCACATCCATGCTTCCGATGAGATGATGATGATGATGATGATGATGATGATG 300
QY      4734  GGGTGTGAACTATTTTCAGAGATGCCCTGGAAATGCTTTTGACTTTTGTCACTGTGTGGGAA 4793
Db      301  GGGTATTGAACTACTTTCAGAGATGCCCTGGAAACGCTTTTGACTTTGTCACTGTGTGGGAA 360
QY      4794  GTATTACTGATATTTTAGTAAACAGAGATTCGGGAAACGAAACAATTTTCATCAACTCAAGCT 4853
Db      361  GTATTACTGATATTTTAGTAAACAGAGAT-----AGCGAAACAACCTTCATCAACTCAAGCT 414
QY      4854  TCCTCCGCCCTCTTTCGAGCTCGCGGCTGATCAAGCTCTCCGCCAGGGGTACACCATCC 4913
Db      415  TCCTTCGCCCTCTTCCCGGCGGCACGGCTGATCAAGCTGCTTCGCCAGGGGTACACCATCC 474
QY      4914  GCATCTCTGCTGTGGACCTTTTGTCCAGTCTCTTCAAGGCCCTTGCCTACGCTGTGCTGCTCA 4973
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QY      4974  TTGCGATGCTGTTCTTCATCTACGCCATCATCGGCATGCGAGGTGTTTGGGAAATATTGCCC 5033
Db      535  TTGCGATGCTGTTCTTCATCTACGCCATCATCGGCATGCGAGGTGTTTGGGAAACATTGCC 594
QY      5034  TGGATGATGACACAGCATCAACCGCCACAAACAACCTTCGGAGCTTTTTCGAAGCCCTGA 5093
Db      595  TTGATGATGACACAGCATCAACCGCCACAAACAACCTTCGGAGCATTTCTCGANGCCCTTAA 654
QY      5094  TGCTGCTGTTTCAGAGCGCCACCGGGAGGCCCTGGCACAGAGATCATGCTGTCTCTGCTCG 5153
Db      655  TGCTATTGTTTCAGAGTNGCACCTGGGAGGCCCTGGCATGAGATCATGCTGTCTGTCTGG 714
QY      5154  GCACACAGGCTGTGATGACAGCGCCAAATGCCACCGAGTGTGGAAGTGAATTTGCCCTACT 5213
Db      715  GC-ACCGGGTCTGTGACCCCATGCCCATCTGCAGTGTGAGTGTGCGGAGCGAGCTTTGCC 771
QY      5214  TCTACTTGGTCTCTCTTCATCTTCTGCTGCTGCTCTTT 5248
Db      772  TTTATTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 806

BC043482      6636 bp      mRNA      linear      HTC 19-NOV-2003
Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,
mRNA (cDNA clone IMAGE:5369391), containing frame-shift errors.
ACCESSION
  BC043482
VERSION
  BC043482.1 GI:28175783
KEYWORDS
  HTC.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 6636)
REFERENCE
  Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
  Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
  Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
  Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.B., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, A., Sanchez, A., Whiting, M., Kettman, M., Madan, A., Rodriguez, A., Bouckard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smal, D.E., Schermer, A., Schein, J.B., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257
12477332
2 (bases 1 to 6636)
Straussberg, R.
Direct Submission
Submitted (09-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Varon Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Kryzanski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smal, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 86 Row: 0 Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972
This clone has the following problem: frame shifted.
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/db_xref="taxon:10090"
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/tissue type="Eye, retina, mouse strain C57Bl/6"
/clone lib="NIH_MGC_94"
/lab host="DH10B"
/note="vector: pCMV-SPORT6"

Query Match 8.4%; Score 623; DB 11; Length 6636;
Best Local Similarity 57.5%; Pred. No. 3.6e-86;
Matches 1308; Conservative 0; Mismatches 875; Indels 90; Gaps 7;
3559 GCTCCGGGCTTTCGCACATACATCGTGACCATGAGGTACTTCGAGGTGTCATTCTCGT 3618
3178 GCTTCGGAAGGCTCGCCACACACATCATACATCATATCTTCCACAGTCTCATCTTAGT 3237
3619 GGTTCATCGCTTGGAGCAGCATCGCCCTGGCTGCTGAGGACCCAGTGGCGACACTCGCC 3678
3238 GTTCATCTCTAGTAGTGTGCTCCCTGGCTGCTGAGGACCCCATCCGAGCTCACTCTCTT 3297

3679 CAGGAACAACGCTCTGAAATACCTGGATTACATTTTCACTGGTGTCTTTTACCTTTGAGAT 3738
3298 CCGAAACCAATATCTGGGATATTTTGAATATGCTTCACTCCATATTCATCTGTGGAGAT 3357
3739 GGTGATAAAGATGATCGACTTTGGGACATGCTGCTTCACTCCCTGGAGCCATTTTCCGGGACTT 3798
3358 TCTACTCAAGATGACAGTGTGTTGGGGCTTCTTCGACCCGAGGGCTCTTTTCTGCGGTAGCTG 3417
3799 GTGGAACATTTCTGGACTTTCAATTTGGTGTGCTGAGGCGCCCTGGTGGCGTTTGTCTTCTCGAG 3858
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3859 CTTCTGTTGGAGGATCCAAAGGGAAGACATCAATACCATCAAGTCTCTGAGAGTCTCTTCG 3918
3478 C-----AGTGCATCTCAGTTGTGAAGATTCTCCGAGTCTCTCCG 3516
3919 TGTCTGCGGCGCTCAAGACCATCAACGGCTGCGCCNAGCTCAAGGCTGTGTTGACTG 3978
3517 AGTCTGCGGCGCTCTCGAGCCATCAACAGGGAATCAAGCATGTGGTGCAGTG 3576
3979 TGTGGTGAACCTCCCTGAAGAAATGCTCAACATCTTGAATGTCTACATGCTCTTTCATGTT 4038
3577 TGTGTTGCTGGCCATCGGACCATCGGAACATCATGATGTCAACACCCTCTTTCGAGTT 3636
4039 CATATTTGCGGTCAATGCGGTGAGCTCTTCAAGGGAAGTCTTCTTCTGACAGATGA 4098
3637 CATGTTGCGCTGATGTTGTTGAGTGTTCAGTGTTCAGGGAATAATCTACAGTTGCTCATGATGA 3696
4099 ATCCAGGAGCTGGAGGAGGACTGCGAGGCTCAGTATTTGGATATGAGAGGAGGAGT 4158
3697 GGGCAACACACACCTGAAGAAATGCAAGGGCTCTCTCTCATCTACCTCATGGAGATG 3756
4159 GGAA-----GCTCAGCCAGGAGTGGAAAGAAATAGACTTTTCACTACGACATGT 4209
3757 GTACAGACTTTGCTCGGAGCGGCTCTGGGTCAACAGTGAATTTTAACTTTGACACGT 3816
4210 GCTCTGGGCTCTGCTGACGCTGTTCACAGTGTCCAGGGAGAGGCTGGCCCATGTTGCT 4269
3817 CTTTTCAGCCATGATGGCCCTGTTCTACTGCTCTCTACCTTTGAAGGCTGGCTGCGCTACT 3876
4270 GAACACTCGTGGATGCCACTATGAGGAGGAGGCTCCAAAGCCCTGGGTACCGCATGGA 4329
3877 ATCAAGGCGCATAGATGCAAAACGAGAGATGAGGCGCTTATCAAAATTTACCATGTGGA 3936
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3937 GATATCAGTATCTTCAATGTCTACATCATCATCTGCGCTTCTTTCATGATGAACATCTT 3996
4390 TGTGGCTTTGATCATCATCACTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4449
3997 TGTGGGCTTTGTTATCATCATCATCTCCGTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4056
4450 CTTGGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4509
4057 ACTGGAACAAGACAGCCGCGAGTGTGTGGAATATGCGCTCAAAAGCTCAGCAGCATCCGCGCG 4116
4510 GTACATGCCCCAAAACCGGAGCTGTTTCCAGTATAAGAGCTGAGACATTTTGTGTCTTCCCC 4569
4117 ATACATCCCTTAAAGTCTCA-----TCAGTACCGGCTGTGGGCCACTGTGAATCTGCG 4170
4570 GCCCTTTGAATACTTTCATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4629
4171 TGCCTTTGAGTACTCATGTTTCTGCTCATCTCTGCTCAACAGGCTGGCCCTGAGCCATGCA 4230
4630 GTTCTATGATGACCCCTATGAGTACAGAGTGTGTAATGCTGAATGCTGAACATCTGTTTCAC 4689
4231 GCATATGAACAGACTGCTCCCTTTAACTATGCGATGGAATCTCTCAACATGCTGTTTCAC 4290
4690 ATCCATGTTCTCCATGGAATGCGTGTGGAAGATCATCGCTTTGGGGGTGCTGAATCTTTT 4749
4291 TGGCTCTTCCACATTTGAGATGTTGCTCAAAATCATCGCTTTTAAACCCAGCATCTT 4350

JOURNAL
MEDLINE
PUBMED
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT

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QY 4750 CAGAGATGCTGGAATGCTCTTTGACATTTGTCTGTTGGGAAGTATTACTGATATTTT 4809
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4351 TGCAGATGCTGGAATGCTCTCTGATGCTCTCTCATTTGAGTGGCAGTGTAGTCGATCGC 4410
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4810 AGTAACA-----GAGATTGGGGAAACGAACAATTTTCAAT 4842
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4411 CGTCACAGAGTCAATPAACGGAGGCCATCTTGCGCAGAGAGTTTCAGAGGACAGCTCCGCAT 4470
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4843 CAACCTCAGCTTCTCCGCTCTTTTCGAGCTGGGGCTGATCAAGCTGCTCCGCCAGGG 4902
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY 4903 CTACACCATCCGATCCTCTGCTGGACCTTTGTCAGTCTCTTCAAGGCCCTGCCCTAGCT 4962
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4531 TGAGGGGATCCGACACTGCTCGGACATTCATCAAGTCTTTCCAGGCCCTTGCCCTATGT 4590
QY 4963 GTGCTGCTCATGTCATGCTCTTCTTCACTACGCCATCATCGGCATCGAGGTGTTTGG 5022
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4591 GGCACCTTCATAGCAATGATATTTCTTCACTATGTCAGTCAATGGCATGCGATGTTTGG 4650
QY 5023 GAATATTGCCCTGGATGATGACACGAGCATCAACCGCCACACAACTTCCGGACGTTTTT 5082
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY 5083 GCAAGCCCTGATGCTGCTTTCAGGAGCCACGCGGGAGGCTGCGCAGAGATCATGCT 5142
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4711 GCAGGCTGTGCTGCTTCTGTTCCAGTGTGCCACTGTTGAGGCTGGCAAGAGATAATGCT 4770
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4771 AGCCAGCCTTCAGGAAATCGATGTGACCTGAGTCTGACTTTGGCCCGAGCGAAT 4830
QY 5188 CGAGTGTGGAAGTGAATTTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5247
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QY 5248 TCTGATGTTGAACCTCTTTGCTGGCTGTGATGATGACAAATTTTGATGATCTCAACGCGGA 5307
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4891 CCGTGAATTAATAATCTCTTTGCTGGCTGTAATCATGATGAATTTGATTAACCTAACGAGA 4950
QY 5308 CTCTTCATCTCTAGTCTCACCACCTGATGAGTTTCATCGGGTCTGGCTGATGATGATG 5367
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QY 4951 TTGGTCTATCTTGGGACCCACCTTGATGATTAAGAGGATCTGGTCTGATGATGATG 5010
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QY 5011 CCCCGGACCAAGGCGCGCATCAAGCACTTGATGTTGGCTGCTGCTGAGACGATCCA 5070
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QY 5071 GCGCCCATTTGGGATTTGAAAGCTATGCCCACACCGAGTGGCTGCAAGAGACTCGTGGC 5130
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Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 5131 ATGATGTTGCCCT---CACTCAGATGGAACAGTGAATTCACGCTACACTCTTTGGC 5187
QY 5548 CTTATCCGACGCGCATCTGGAGATCAAGCTGCGCCACAGCTGGGACAAAGCAGCATGATG 5607
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 5188 CCGTGTGGGACATCCCTGAAAGATCAAG-----ACAGAGGGAACCTGGATCAAGC 5238
QY 5608 TGACCGGAGTTGAGGAGGAGATTTCCGTTGTGTGGGCCAATCTGCCCCGAGAGACTTT 5667
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 5239 CAACGAGGACTTCGGATGGTTCATCAAAAGATCTGGAAGCGGATAAAGCAGAAATTTGT 5298
QY 5668 GGACTTGTGTTACCAACCCCAATAGCCCTGATGATGACAGTGGGAGGTTTATGACG 5727
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QY 5299 GGATGAGTCACTCTCTCCGATGAGAGAGAGTCACTGTGGGAAAATTTCTATGCCAC 5358
QY 5728 TCTGATGATATTGACTTCTCAAGACAGAAACAAACACACAGAGACAGATGC 5780
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 5359 ATTCTGTATCAAGATTTATTTCCGAAAATTCGGAGAGAGGAAAGAAAAGGGGC 5411
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RESULT 13
CB521867
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CB521867 795 bp mRNA linear EST 09-JUL-2003
UI-M-GH0-ceo-i-15-0-UI.r1 NIH_BMAP_GH0 Mus musculus CDNA clone
IMAGE:6842296 5', mRNA sequence.

CB521867
CB521867.1 GI:29355222
EST.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 795)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-x@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.utowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

The following repetitive elements were found in this cDNA

sequence: 124-185, >CHARLIE#DNA/MER1_type (matched complement)

Seq primer: pYX-5.

Location/Qualifiers

1. 795

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6842296"

/tissue_type="Whole brain"

/dev_stage="1, 5, and 15 days newborn"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_GH0"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;

Site 2: Not I; The library was constructed according

Bonaldi, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail

is CGAAGCTGAAT. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,

program coordinator."

ORIGIN

Query Match 8.2%; Score 605; DB 14; Length 795;

Best Local Similarity 89.2%; Pred. No. 9.5e-84;

Matches 677; Conservative 0; Mismatches 75; Indels 7; Gaps 2;

QY 4406 ATCACTTCCAGGACAGGGGGAAGGTGATGCTGTAATGCAAGCTGGAGAAAGACGAG 4465

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

2 ATCACTTCCAGGAAACAGGAGATAAGGTGATGCTGTAATGCAAGCTTAGAAAAGATGAG 61

QY 4466 AGGGCTTGCAATTCCTCGCCATCAGCGCAACCCCTGACACGGTACATGCCCAAAAC 4525

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

62 AGGGCTTGCAATTCCTCGCCATCAGCGCAACCCCTGACACGGTACATGCCCAAAAC 121

QY 4526 CGGCACTGCTTCCAGTATAAGACGTCGATTTGTGGTCTCCCGCCCTTTGATTAATCTTC 4585

Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

122 AAACAGTCGTTCCAGTATAAGACGTCGATTTGTGGTCTCTCCACCCCTTTGATTAATCTTC 181


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Qy 4586 ATCATGCGCATATAGCCCTCAACACATGTTGGTGTGTATGATGAAGTTCTATGATGCAACC 4645
Db 182 ATCATGCTATGATAGCCCTCAACACAGTGTGTGTATGATGAAGTTCTATGATGCAACC 241
Qy 4646 TATGAGTACGAGCTGATGCTGAATGCTGAACATGTTTCAACATCCATGTTCTCCATG 4705
Db 242 TATGAGTACGAGCTGATGCTGAATGCTGAACATGTTTCAACATCCATGTTCTCCATG 301
Qy 4706 GAATGCTGCTGAAGATCATGCGCTTGGGGTGTGAACTATTTTCAAGATGCTCGGAAT 4765
Db 302 GAGTGCATCTGAAGATCATGCGCTTGGGGTATTTGAACATCTTCAAGATGCTCGGAAC 361
Qy 4766 GTCTTTGACCTTTGACATGTTGGGAAGTATTTACTGATATTTTGTAGTAAACAGATTTGG 4825
Db 362 GTCTTTGACCTTTGACATGTTGGGAAGTATTTACTGATATTTTGTAGTAAACAGATAG-- 419
Qy 4826 GAAACGAAACATTTTCAACCTCAGCTTCTCCGCTCTTCCGAGCTGGCGGCTGATC 4885
Db 420 ----CGAACAACTTCAACCTAAGCTTCTTCCGCTCTTCCGCGGCGGACGGCTGATC 475
Qy 4886 AAGCTGCTCCGCCAGGGCTACACCATCGCATCTCTGCT-GTGGACCTTTTGTCCAGTCTTT 4944
Db 476 AAGCTGCTCCGCCAGGGCTACACCATCGCATCTCTATTNGTGGACCTTCTGTCAGTCTTT 535
Qy 4945 CAAGGCGCTGCTGATGCTGTGCTCATATGCGCATGCTGTTTCTATCTACGCGCATCAT 5004
Db 536 TAAGGCGCTGCGCTTACGCTGCTCTCTCATTTGCCATGCTGTTCTTCTATCTACGCGCATCAT 595
Qy 5005 CGGCATCGAGTGTGTTGGGAATATTTGCCGTGATGATGACACAGCATCAACCGCCACAA 5064
Db 596 CGGCATCGAGTGTGTTGGGAACATGTCCTTTGATGATGACACAGTATCAACCGCCACAA 655
Qy 5065 CAATCTCCGACAGTGTGTTGCAAGCCCTGATGCTGCTGTTGAGGAGCCGACGCGGAGGC 5124
Db 656 CAATCTCCGACATTTCTGCAAGCCTTAATGCTATTGTTCAAGAGTGCCTATGCGGGAAG 715
Qy 5125 CTGGCAGAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5163
Db 716 CTGGCATGAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 754

RESULT 14
CF537761 754 bp mRNA linear EST 12-SEP-2003
LOCUS UI-M-G10-chn-k-12-0-UI.r1 NIH_BMAP_G10 Mus musculus cDNA clone
DEFINITION IMAGE:30537755 5', mRNA sequence.
CF537761
VERSION CF537761.1 GI:34589743
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 754)
JOURNAL NIH-MGC http://mgs.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
this clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 161-222, >CHARLIE1#DNA/MER1_type (matched complement)
Seq primer: pYX-5.
FEATURES
source Location/Qualifiers
1..754
/organism="Mus musculus"
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30537755"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_G10"
/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAAGCAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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ORIGIN

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Query Match 8.1%; Score 597.6; DB 14; Length 754;
Best Local Similarity 90.9%; Pred. No. 1.3e-82;
Matches 658; Conservative 0; Mismatches 64; Indels 2; Gaps 2;
Qy 4368 CCTTCTTCTCGTCAACATCTTTGTGGCTTGTATCATCATCCTTCCAGGACAGGGG 4427
Db 1 CTTTTTCTTTGTCAACATCTTTGTGGCTTGTATCATTTACCTTCCAGGAACAGGGAG 60
Qy 4428 ACAAGTGTATGCTGAATGAGGCTCGAGAAAGACGAGAGGGCTTGCAATTGACTTCGCCA 4487
Db 61 ATAAAGTGTATGCTGAATGAGGCTTAGAAAAGAAATGAGAGGGCTTGCAATTGATTTGGCA 120
Qy 4488 TCAGCGCCAAAACCCCTGACACGGTATATGCCCAAAACCGGACAGTGGTCCAGTATTAAGA 4547
Db 121 TCAGTGCCAAAGCCCTGACACGGTATATGCCCTCAAAACAAACAGTGGTCCAGTATTAAGA 180
Qy 4548 CGTGGACATTTGGTGTCTCCCGCCCTTTGAATCTTCATCTCATGCGCATGAGCCCTCA 4607
Db 181 CATGSCATTTCTGGTGTCTTCCACCTTTTGGTGTCTTGGTGTCTTGGTGTCTTGGTGTCT 240
Qy 4608 ACATGTGGTGTGATGATGAAGTCTTATGATGACCCCTATGATGATGATGATGATGATGAT 4667
Db 241 ACACAGTGGTGTGATGATGAAGTCTTATGATGACCCCTATGATGATGATGATGATGATGAT 300
Qy 4668 AATGSCCTGAACATCGTGTTCACATCCATGTTCTCCATGGAATCGTGTGGAAGATCATCG 4727
Db 301 AATGSCCTGAACATCGTGTTCACATCCATGTTCTCGATGGAGTGCATACTGAAGATCATCG 360
Qy 4728 CCTTTGGGTGTGAACTATTTCAAGATGCTCGGAATGCTTTGACTTTGTCTACTGTGT 4787
Db 361 CCTTTGGGTGTGAACTATTTCAAGATGCTCGGAATGCTTTGACTTTGTCTACTGTGT 420
Qy 4788 TGGGAAGTATTACTGATATTTTAACTAACAGAGATTGCGGAAACGAAACAATTTTCATCAACC 4847
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Qy 4848 TCAGTCTTCTCCGCTCTTTTTCAGAGCTCGCGGCTGATCAAGCTGCTCCGCGAGGGGTACA 4907
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Qy 4968 TGTCTCATTCGCATGCTGTTCTTCTCATCTACGCCATCATCGCATGAGGTGTTTGGGAATA 5027
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Qy 5028 TTGCGCTGGATGATGACACAGCATCAACCGCCACAACTTCCGGACGTTTTCGAAG 5087
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Qy 5088 CCCT 5091
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RESULT 15
LOCUS CB518919
DEFINITION CB518919 756 bp mRNA linear EST 09-JUL-2003
IMAGE:6838415 5', mRNA sequence.
ACCESSION CB518919
VERSION CB518919.1 GI:29352274
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 756)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6838415"
/tissue_type="Whole brain"
/dev_stage="1, 5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP GH0"
/note="Organ: Brain; Vector: pYX-Asc; Site: 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN
Query Match 7.7%; Score 570.6; DB 14; Length 756;
Best Local Similarity 86.0%; Pred. No. 2.1e-78;
Matches 644; Conservative 0; Mismatches 104; Indels 1; Gaps 1;

Qy 5520 CTGTTCACTTCAGTCCAGGTGATGGCCCTCATCCGACGGGCACT-GGAGATCAAGCTG 5578
Db 1 CGGTGCACCTTTACGTCCACACTGATGGCCCTCATCCGACAGCACTGGGAGATCAAGCTT 60
Qy 5579 GCGCCAGCTGGGACAAAGCAGCATCAGTGTGACGGGAGTTGAGGAAGGAGATTTCGGT 5638

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Db 61 GCCCAGCGGGGACGAAGCAGCACCAGTGTGATCTGAGCTGAGAAAGAGATCTCTTCT 120
Qy 5639 GTGTGGGCAATCTGCCCCAGAAAGACTTTGGACTTTGGACTTTGGACTTTGGACTTTGG 5698
Db 121 GTGTGGGCTAATCTGCCCCAGAAAGACTCTGGACTTTACTGGTTACCAACCCCA 180
Qy 5699 GAGATGACAGTGGGAAAGGTTTATGACAGCTCTGATGATATTTGATCTTCAACGACGAC 5758
Db 181 GAGATGACAGTGGGAAAGGTTTATGCTGCTCTCATGATATTTGATCTTCAACGACGAC 240
Qy 5759 AAAACCAACGAGACACGATGACAGAGCTCTCTGGAGGSCCTCTCCAGATGGGTCTGTG 5818
Db 241 AAAACCAACGAGATCAGACTCAACAGCTCCCGAGGSCCTGTCTCCAGATGGGTCTCCG 300
Qy 5819 TCCCTGTTCCACCTCTGAAGGCCACCTCGAGGACAGACAGCCGGCTGTGCTCCGAGGA 5878
Db 301 TCCCTGTTCCACCTCTGAAGGCCACCTCTGAAGGCCACAGACAGCCGGCTGTGCTCCGAGGA 360
Qy 5879 GCCCGGTTTTCCTTCGACAGAAAGAGTTCCACCTCCCTCAGCAATGGCGGGCCATACAA 5938
Db 361 GCTCGGGTTTTCCTTCGCGAAAGAGTGCAACTTCCCTCAGCAATGGGGGTGCCATACAA 420
Qy 5939 AACCAAGAGTGGCATCAAGAGATCTGTCTCTCTGGGGCACTCAAAAGGACCCAGGATGCA 5998
Db 421 ACCCAGGAAAGTGGCATCAAGAGATCTGTCTCTCTGGGGCACGACAGAGGCCCAAGATGCA 480
Qy 5999 CCCCATGAGCCAGGCCACCCCTGGAGCGTGGGCCACTCCACAGAGATCCCTGTGGGGCGG 6058
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Qy 6059 TCAGGACACTGGCTGTGGACGTTTCAGATGCAGAGATTAACCCGAGGGGCTCTGTATGGG 6118
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Qy 6119 GAGCCCCAGCTGGGCTGGAGAGCCAGGGTTCGAGCGGCTTCATGCCCGCTTTGGGGCC 6178
Db 601 GAGCCCCAGCTGGGCTGGAAAGCCAAAGCAGAGCTGCCTCTATGCCACGCTTAGCGGCA 660
Qy 6179 GAGACTCAGCCCGTTCACAGATGCCAGCCCATGAAGGCTTCCATCTCCAGCTGGGCCAG 6238
Db 661 GAAACACAGCCGGCCCTTAATGCCAGCCCATGAAGGCTTCCATCTCCAGCTGGGCCAG 720
Qy 6239 CGGCCCGCTGGGACTCATCTTTGACGAC 6267
Db 721 CGGCCACATGGGACTCAGCTTTGACGAC 749

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Job time : 11212 secs